

Process-oriented models of autumn leaf phenology: ways to sound calibration and implications of uncertain projections

Michael Meier, Christof Bigler

<https://doi.org/10.5194/gmd-16-1-2023-supplement>

Correspondence to: Michael Meier (michael.meier@cefe.cnrs.fr)

S1 Non-converting calibration runs and NA values

We calibrated 2 205 000 combinations of phenology models, optimization algorithms, and calibration samples in site-specific mode as well as 139 230 such combinations in species-specific mode. Some of the calibrated models led to NA values in either the calibration or validation and some calibration runs did not convert or ran out of time (Fig. S1). In site-specific calibration, 136 500 runs did not convert or exceeded the time limit and further 373 120 models led to NAs. In species-specific calibration, 7 048 runs did not convert or exceeded the time limit and further 23 312 models led to NAs. The time limit ranged from 4 hours for a single site-specific calibration run to 2 weeks for a single species-specific calibration run with the full sample of 500 sites.

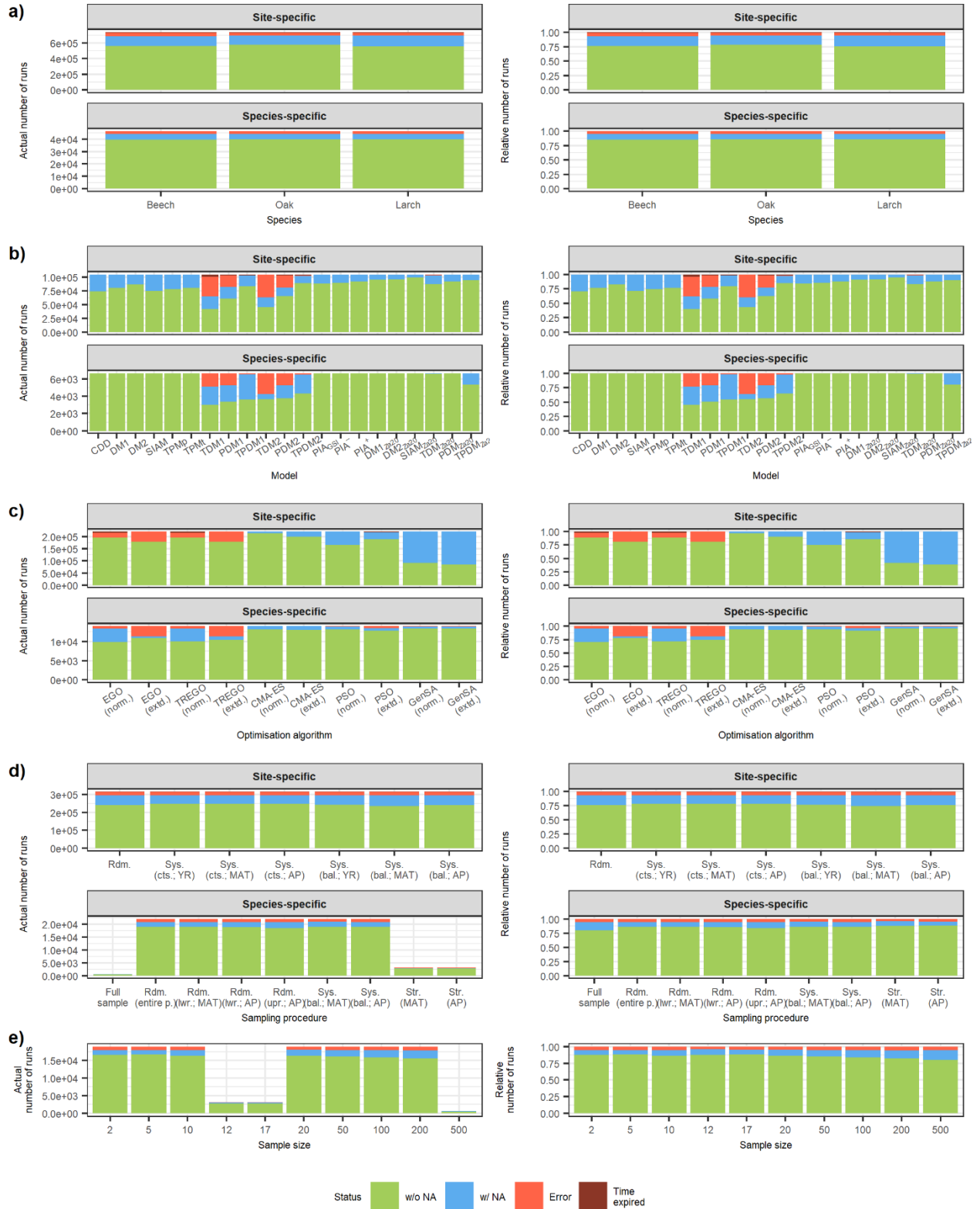


Figure S1. Status of all calibration runs of the site- and species-specific calibration according to species (a), phenology model (b), optimization algorithm (c), sampling procedure (d) and sample size (e; only for species-specific calibration). The figures on the left show the actual number of runs and those on the right show the relative number. The colors indicate the status of the runs, which may have completed without modelled NA values (green; w/o NA), completed with 1 or more modelled NA values (blue; w/ NA), ran into an error (i.e. not completed; red; Error), or ran out of time (brown; Time expired).

S2 Model performance

S2.1 Observed effects

S2.1.1 Observed effects if NA values were substituted

Table S1. Ranked observed statistics mean (μ), median, and standard deviation (σ) of the external (sample) root mean square error per phenology model, optimization algorithm, and sampling procedure (from left to right) as well as per site- and species-specific calibration validated within sample and within population (from top to bottom).

Site-specific calibration mode

| Model | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | Algorithm | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | Sampling procedure | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | | | | | | |
|----------------|--------|---------------|-------------------------|----------|------------------|---------------------|-----------|-------|----------------|-------------------------|----------|------------------|---------------------|--------------------|-------|---------------|-------------------------|------------------|------------------|---------------------|-------|---|-------|---|------|---|
| SIAM $_{Za20}$ | 19.16 | 1 | 10.08 | 3 | 36.61 | 1 | 3.83 | 21 | CMA.ES (norm.) | 19.04 | 1 | 10.83 | 1 | 28.44 | 1 | 4.36 | 10 | Sys. (cts.; MAT) | 51.32 | 1 | 12.30 | 3 | 66.03 | 3 | 1.14 | 7 |
| DM2 $_{Za20}$ | 23.16 | 2 | 9.86 | 1 | 44.30 | 2 | 2.99 | 20 | CMA.ES (extd.) | 29.19 | 2 | 11.28 | 2 | 46.52 | 2 | 2.53 | 9 | Sys. (cts.; YR) | 51.59 | 2 | 12.69 | 6 | 65.86 | 2 | 1.14 | 6 |
| DM1 $_{Za20}$ | 24.94 | 3 | 10.00 | 2 | 46.69 | 3 | 2.77 | 19 | PSO (extd.) | 38.83 | 3 | 11.80 | 5 | 55.94 | 3 | 1.77 | 8 | Sys. (bal.; YR) | 52.94 | 3 | 12.27 | 2 | 67.12 | 4 | 1.08 | 5 |
| PIA $^{+}$ | 29.76 | 4 | 10.57 | 5 | 52.20 | 5 | 2.30 | 18 | EGO (extd.) | 42.95 | 4 | 11.48 | 4 | 62.49 | 6 | 1.50 | 7 | Sys. (cts.; AP) | 54.16 | 4 | 14.09 | 7 | 65.22 | 1 | 1.06 | 4 |
| PDM $_{Za20}$ | 30.96 | 5 | 11.27 | 13 | 52.71 | 6 | 2.25 | 17 | TREGO (norm.) | 45.98 | 5 | 12.94 | 8 | 57.02 | 4 | 1.27 | 5 | Rdm. | 54.22 | 5 | 12.34 | 4 | 67.97 | 5 | 1.03 | 3 |
| PIA $^{-}$ | 33.12 | 6 | 10.69 | 6 | 55.84 | 7 | 2.03 | 16 | EGO (norm.) | 46.05 | 6 | 12.78 | 7 | 57.22 | 5 | 1.27 | 4 | Sys. (bal.; AP) | 54.53 | 6 | 12.15 | 1 | 68.27 | 6 | 1.01 | 2 |
| PIA $_{GSI}$ | 35.82 | 7 | 10.76 | 7 | 58.50 | 9 | 1.85 | 15 | TREGO (extd.) | 46.88 | 7 | 11.38 | 3 | 63.16 | 7 | 1.29 | 6 | Sys. (bal.; MAT) | 56.56 | 7 | 12.58 | 5 | 69.12 | 7 | 0.95 | 1 |
| TDM $_{Za20}$ | 37.62 | 8 | 10.81 | 8 | 59.96 | 10 | 1.74 | 14 | PSO (norm.) | 53.95 | 8 | 12.76 | 6 | 67.83 | 8 | 1.06 | 3 | | | | | | | | | |
| DM2 | 37.90 | 9 | 10.27 | 4 | 60.98 | 11 | 1.70 | 13 | GenSA (norm.) | 104.64 | 9 | 170.00 | 9 | 77.85 | 10 | -0.36 | 2 | | | | | | | | | |
| TPDM $_{Za20}$ | 40.53 | 10 | 12.65 | 15 | 51.39 | 4 | 1.62 | 12 | GenSA (extd.) | 108.66 | 10 | 170.00 | 9 | 77.10 | 9 | -0.47 | 1 | | | | | | | | | |
| TPMt | 47.30 | 11 | 11.19 | 11 | 67.39 | 14 | 1.27 | 11 | | | | | | | | | | | | | | | | | | |
| DM1 | 47.47 | 12 | 10.82 | 9 | 67.85 | 15 | 1.25 | 10 | | | | | | | | | | | | | | | | | | |
| TPMp | 50.53 | 13 | 11.03 | 10 | 69.67 | 18 | 1.13 | 9 | | | | | | | | | | | | | | | | | | |
| SIAM | 56.07 | 14 | 11.24 | 12 | 72.46 | 19 | 0.93 | 8 | | | | | | | | | | | | | | | | | | |
| CDD | 57.23 | 15 | 11.33 | 14 | 73.11 | 20 | 0.89 | 7 | | | | | | | | | | | | | | | | | | |
| TPDM2 | 69.33 | 16 | 39.86 | 16 | 61.35 | 12 | 0.53 | 6 | | | | | | | | | | | | | | | | | | |
| TPDM1 | 80.63 | 17 | 68.71 | 17 | 57.75 | 8 | 0.40 | 5 | | | | | | | | | | | | | | | | | | |
| PDM2 | 87.92 | 18 | 69.88 | 18 | 68.42 | 16 | 0.18 | 4 | | | | | | | | | | | | | | | | | | |
| PDM1 | 95.75 | 19 | 74.97 | 19 | 66.30 | 13 | 0.10 | 3 | | | | | | | | | | | | | | | | | | |
| TDM2 | 105.84 | 20 | 170.00 | 20 | 75.09 | 21 | -0.35 | 2 | | | | | | | | | | | | | | | | | | |
| TDM1 | 114.93 | 21 | 170.00 | 20 | 68.99 | 17 | -0.51 | 1 | | | | | | | | | | | | | | | | | | |

n_{Observations} : 2,205,000

NA values were replaced with 170 days before calculation of statistics.

Species-specific calibration mode (validation within sample)

| Model | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | Algorithm | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | Sampling procedure | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | | | | |
|----------------------|-------|---------------|-------------------------|----------|------------------|---------------------|----------------|-------|---------------|-------------------------|----------|------------------|---------------------|--------------------|-------|------------------|-------------------------|----------|------------------|---------------------|-------|---|------|---|
| TPMp | 11.65 | 1 | 11.68 | 4 | 3.71 | 6 | GenSA (norm.) | 12.90 | 1 | 11.88 | 2 | 5.78 | 2 | 13.11 | 10 | Str. (MAT) | 23.93 | 1 | 12.57 | 7 | 36.63 | 1 | 3.36 | 9 |
| DM1 | 11.66 | 2 | 11.68 | 3 | 3.17 | 3 | CMA.ES (extd.) | 13.26 | 2 | 12.12 | 5 | 5.49 | 1 | 9.12 | 6 | Rdm. (upr.; AP) | 23.94 | 2 | 10.44 | 1 | 40.29 | 9 | 2.97 | 2 |
| SIAM | 11.72 | 3 | 11.66 | 1 | 3.79 | 7 | CMA.ES (norm.) | 13.38 | 3 | 12.13 | 6 | 6.57 | 3 | 11.56 | 8 | Rdm. (lwr.; AP) | 24.94 | 3 | 11.82 | 2 | 39.33 | 5 | 3.05 | 5 |
| DM2 _{Za20} | 11.77 | 4 | 11.71 | 6 | 2.62 | 2 | GenSA (extd.) | 13.47 | 4 | 11.87 | 1 | 11.19 | 5 | 11.98 | 9 | Rdm. (lwr.; MAT) | 25.09 | 4 | 12.08 | 3 | 39.34 | 6 | 3.07 | 7 |
| DM2 | 11.78 | 5 | 11.70 | 5 | 5.03 | 10 | PSO (norm.) | 13.47 | 5 | 11.89 | 3 | 9.87 | 4 | 10.50 | 7 | Sys. (bal.; MAT) | 25.17 | 5 | 12.36 | 6 | 39.13 | 3 | 3.04 | 4 |
| DM1 _{Za20} | 11.89 | 6 | 11.79 | 7 | 3.21 | 4 | PSO (extd.) | 19.10 | 6 | 11.90 | 4 | 30.83 | 6 | 4.51 | 5 | Rdm. (entire p.) | 25.36 | 6 | 12.29 | 5 | 39.66 | 8 | 3.01 | 3 |
| TDM _{Za20} | 11.95 | 7 | 11.67 | 2 | 5.19 | 12 | EGO (norm.) | 38.79 | 7 | 13.96 | 9 | 47.22 | 7 | 1.67 | 4 | Full sample | 25.69 | 7 | 12.29 | 4 | 39.29 | 4 | 3.06 | 6 |
| TPMt | 11.99 | 8 | 11.89 | 12 | 3.26 | 5 | TREGO (norm.) | 40.20 | 8 | 14.19 | 10 | 48.79 | 8 | 1.57 | 3 | Sys. (bal.; AP) | 27.74 | 8 | 13.69 | 8 | 39.46 | 7 | 2.94 | 1 |
| CDD | 12.00 | 9 | 11.95 | 13 | 2.61 | 1 | EGO (extd.) | 43.58 | 9 | 12.45 | 8 | 62.00 | 9 | 1.52 | 2 | Str. (AP) | 28.82 | 9 | 16.75 | 9 | 37.33 | 2 | 3.12 | 8 |
| SIAM _{Za20} | 12.00 | 10 | 11.79 | 8 | 5.47 | 13 | TREGO (extd.) | 46.05 | 10 | 12.35 | 7 | 62.42 | 10 | 1.39 | 1 | | | | | | | | | |
| PIA ⁻ | 12.12 | 11 | 11.87 | 9 | 4.38 | 9 | | | | | | | | | | | | | | | | | | |
| PIA ⁺ | 12.18 | 12 | 11.88 | 10 | 5.16 | 11 | | | | | | | | | | | | | | | | | | |
| PIA _{GSI} | 12.24 | 13 | 11.88 | 11 | 5.50 | 14 | | | | | | | | | | | | | | | | | | |
| PDM _{Za20} | 12.56 | 14 | 12.04 | 14 | 4.27 | 8 | | | | | | | | | | | | | | | | | | |
| TPDM _{Za20} | 23.76 | 15 | 12.21 | 15 | 24.90 | 15 | | | | | | | | | | | | | | | | | | |
| TPDM2 | 42.17 | 16 | 14.12 | 16 | 49.66 | 17 | | | | | | | | | | | | | | | | | | |
| TPDM1 | 44.16 | 17 | 20.37 | 19 | 42.93 | 16 | | | | | | | | | | | | | | | | | | |
| PDM1 | 57.55 | 18 | 21.24 | 20 | 62.08 | 18 | | | | | | | | | | | | | | | | | | |
| PDM2 | 59.29 | 19 | 14.73 | 18 | 67.06 | 20 | | | | | | | | | | | | | | | | | | |
| TDM1 | 66.40 | 20 | 21.65 | 21 | 64.40 | 19 | | | | | | | | | | | | | | | | | | |
| TDM2 | 73.01 | 21 | 14.65 | 17 | 75.53 | 21 | | | | | | | | | | | | | | | | | | |

n_{Observations} : 139,230

NA values were replaced with 170 days before calculation of statistics.

Table S1. Continued.

Species-specific calibration mode (validation within population)

| Model | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | Algorithm | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | Sampling procedure | μ | Rank $_{\mu}$ | Median Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{Skew}$ | | | | | | |
|---------------|-------|---------------|-------------------------|----------|------------------|---------------------|-----------|-------|----------------|-------------------------|----------|------------------|---------------------|--------------------|-------|---------------|-------------------------|------------------|------------------|---------------------|-------|---|-------|---|------|---|
| DM2 $_{Z20}$ | 12.87 | 1 | 12.45 | 1 | 1.19 | 2 | 2.69 | 9 | GenSA (norm.) | 14.83 | 1 | 12.94 | 3 | 6.43 | 1 | 10.48 | 9 | Str. (MAT) | 24.45 | 1 | 12.78 | 4 | 35.95 | 1 | 3.42 | 9 |
| CDD | 12.92 | 2 | 12.66 | 6 | 1.00 | 1 | 2.64 | 8 | CMA.ES (extd.) | 15.26 | 2 | 13.17 | 5 | 6.62 | 2 | 7.01 | 6 | Full sample | 25.69 | 2 | 12.29 | 1 | 39.29 | 5 | 3.06 | 7 |
| DM2 | 12.98 | 3 | 12.49 | 2 | 4.45 | 10 | 33.08 | 15 | CMA.ES (norm.) | 15.38 | 3 | 13.18 | 6 | 7.59 | 3 | 8.72 | 7 | Str. (AP) | 25.88 | 3 | 13.82 | 7 | 37.91 | 2 | 3.13 | 8 |
| DM1 | 13.02 | 4 | 12.49 | 3 | 2.52 | 5 | 38.51 | 19 | GenSA (extd.) | 15.41 | 4 | 12.94 | 2 | 11.45 | 5 | 11.01 | 10 | Sys. (bal.; MAT) | 26.45 | 4 | 12.69 | 2 | 38.81 | 4 | 3.03 | 5 |
| TPMp | 13.06 | 5 | 12.60 | 4 | 2.98 | 6 | 44.43 | 20 | PSO (norm.) | 15.52 | 5 | 12.93 | 1 | 10.36 | 4 | 8.90 | 8 | Rdm. (lwr.; MAT) | 26.81 | 5 | 12.86 | 5 | 39.39 | 6 | 3.00 | 4 |
| TPM1 | 13.14 | 6 | 12.81 | 8 | 2.27 | 3 | 50.01 | 21 | PSO (extd.) | 21.10 | 6 | 12.97 | 4 | 30.61 | 6 | 4.42 | 5 | Rdm. (entire p.) | 26.87 | 6 | 12.72 | 3 | 39.55 | 7 | 2.96 | 3 |
| SIAM | 13.20 | 7 | 12.62 | 5 | 3.22 | 7 | 35.40 | 16 | EGO (norm.) | 40.15 | 7 | 14.69 | 9 | 47.25 | 7 | 1.64 | 4 | Sys. (bal.; AP) | 27.01 | 7 | 12.86 | 6 | 39.67 | 9 | 2.95 | 2 |
| DM1 $_{Z20}$ | 13.27 | 8 | 12.81 | 9 | 2.50 | 4 | 38.16 | 18 | TREGO (norm.) | 41.53 | 8 | 14.90 | 10 | 48.82 | 8 | 1.55 | 3 | Rdm. (lwr.; AP) | 27.22 | 8 | 13.98 | 9 | 38.80 | 3 | 3.04 | 6 |
| SIAM $_{Z20}$ | 13.41 | 9 | 12.82 | 10 | 4.98 | 12 | 28.20 | 13 | EGO (extd.) | 44.61 | 9 | 13.32 | 8 | 61.50 | 9 | 1.52 | 2 | Rdm. (upr.; AP) | 28.81 | 9 | 13.93 | 8 | 39.65 | 8 | 2.84 | 1 |
| PIA $^{-}$ | 13.46 | 10 | 12.95 | 12 | 3.66 | 8 | 35.44 | 17 | TREGO (extd.) | 47.18 | 10 | 13.23 | 7 | 61.97 | 10 | 1.38 | 1 | | | | | | | | | |
| TDM $_{Z20}$ | 13.49 | 11 | 12.69 | 7 | 5.19 | 14 | 22.00 | 10 | | | | | | | | | | | | | | | | | | |
| PIA $^{+}$ | 13.51 | 12 | 12.93 | 11 | 4.58 | 11 | 30.15 | 14 | | | | | | | | | | | | | | | | | | |
| PIA $_{GSI}$ | 13.62 | 13 | 12.98 | 13 | 5.03 | 13 | 27.40 | 12 | | | | | | | | | | | | | | | | | | |
| PDM $_{Z20}$ | 13.99 | 14 | 13.16 | 14 | 3.84 | 9 | 22.64 | 11 | | | | | | | | | | | | | | | | | | |
| TPDM $_{Z20}$ | 25.59 | 15 | 13.45 | 15 | 25.17 | 15 | 1.91 | 7 | | | | | | | | | | | | | | | | | | |
| TPDM2 | 44.79 | 16 | 16.01 | 16 | 49.34 | 17 | 1.33 | 5 | | | | | | | | | | | | | | | | | | |
| TPDM1 | 47.28 | 17 | 22.75 | 19 | 42.75 | 16 | 1.39 | 6 | | | | | | | | | | | | | | | | | | |
| PDM1 | 60.25 | 18 | 25.15 | 20 | 60.87 | 18 | 1.13 | 4 | | | | | | | | | | | | | | | | | | |
| PDM2 | 61.51 | 19 | 17.94 | 18 | 65.81 | 20 | 0.86 | 3 | | | | | | | | | | | | | | | | | | |
| TDM1 | 68.82 | 20 | 26.01 | 21 | 63.07 | 19 | 0.78 | 2 | | | | | | | | | | | | | | | | | | |
| TDM2 | 74.84 | 21 | 17.61 | 17 | 74.21 | 21 | 0.47 | 1 | | | | | | | | | | | | | | | | | | |

n_{observations} : 139,230

NA values were replaced with 170 days before calculation of statistics.

Table S2. Observed statistics mean (μ), median, and standard deviation (σ) of the external (population) root mean square error (RMSE) and corresponding ratios per size bin or sample size in the site- or species-specific calibration (left or right), respectively.

Site-specific calibration mode

RMSE_{external}RMSE_{external}:RMSE_{internal}

| N:q | μ | Median | σ | Skew | N:q | μ | Median | σ | Skew |
|-------------|-------|--------|----------|------|-------------|-------|--------|----------|-------|
| 2.26<xs4.66 | 61.07 | 14.79 | 68.91 | 0.82 | 2.26<xs4.66 | 1.47 | 1.13 | 1.26 | 5.59 |
| 4.66<xs7.03 | 50.40 | 12.05 | 66.43 | 1.17 | 4.66<xs7.03 | 1.26 | 1.09 | 0.80 | 6.70 |
| 7.03<xs9.4 | 43.30 | 11.25 | 63.35 | 1.47 | 7.03<xs9.4 | 1.15 | 1.07 | 0.51 | 10.26 |
| 9.4<xs11.8 | 39.87 | 10.66 | 62.22 | 1.61 | 9.4<xs11.8 | 1.08 | 1.05 | 0.10 | 5.09 |
| 11.8<xs14.1 | 35.76 | 10.67 | 58.50 | 1.85 | 11.8<xs14.1 | 1.07 | 1.04 | 0.09 | 2.35 |
| 14.1<xs16.5 | 40.59 | 10.75 | 62.39 | 1.59 | 14.1<xs16.5 | 1.06 | 1.03 | 0.08 | 1.56 |
| 16.5<xs18.9 | 39.64 | 10.28 | 62.31 | 1.61 | 16.5<xs18.9 | 1.06 | 1.03 | 0.07 | 1.86 |
| 18.9<xs21.3 | 53.64 | 11.36 | 71.07 | 1.02 | 18.9<xs21.3 | 1.05 | 1.02 | 0.07 | 1.93 |
| 21.3<xs23.6 | 53.96 | 10.94 | 71.12 | 1.02 | 21.3<xs23.6 | 1.05 | 1.02 | 0.07 | 1.79 |
| 23.6<xs26 | 54.57 | 10.74 | 71.86 | 0.98 | 23.6<xs26 | 1.04 | 1.02 | 0.07 | 1.96 |

NA values were replaced with 170 days before calculation of statistics.

Species-specific calibration mode

RMSE_{population, external}RMSE_{sample, external}:RMSE_{population, external}

| s.S | Number of sites | μ | Median | σ | Skew | s.S | Number of sites | μ | Median | σ | Skew |
|-------|-----------------|-------|--------|----------|------|-------|-----------------|-------|--------|----------|-------|
| 0.004 | 2 | 30.19 | 14.73 | 40.40 | 2.74 | 0.004 | 2 | 0.83 | 0.78 | 0.36 | 1.39 |
| 0.010 | 5 | 27.62 | 13.63 | 39.10 | 2.96 | 0.010 | 5 | 0.89 | 0.88 | 0.24 | 0.31 |
| 0.020 | 10 | 26.80 | 13.26 | 38.75 | 3.03 | 0.020 | 10 | 0.91 | 0.92 | 0.19 | 0.02 |
| 0.024 | 12 | 24.45 | 12.78 | 35.95 | 3.42 | 0.024 | 12 | 0.95 | 0.98 | 0.13 | -0.06 |
| 0.034 | 17 | 25.88 | 13.82 | 37.91 | 3.13 | 0.034 | 17 | 1.21 | 1.23 | 0.12 | -0.34 |
| 0.040 | 20 | 26.10 | 13.04 | 38.12 | 3.09 | 0.040 | 20 | 0.91 | 0.93 | 0.15 | -0.63 |
| 0.100 | 50 | 26.38 | 13.02 | 39.13 | 3.04 | 0.100 | 50 | 0.93 | 0.96 | 0.12 | -1.44 |
| 0.200 | 100 | 26.28 | 12.95 | 39.14 | 3.04 | 0.200 | 100 | 0.94 | 0.98 | 0.11 | -1.62 |
| 0.400 | 200 | 27.00 | 12.93 | 40.40 | 2.92 | 0.400 | 200 | 0.94 | 0.98 | 0.10 | -1.83 |
| 1.000 | 500 | 25.92 | 12.29 | 39.68 | 3.03 | 1.000 | 500 | 1.00 | 1.00 | 0.00e+00 | NA |

NA values were replaced with 170 days before calculation of statistics.

Note: The RMSE ratios in the site- and species-specific calibrations were derived by dividing the external by the internal RMSE and by dividing the external population RMSE by the external sample RMSE. Size bins are equally distributed over and defined according to the parameter ratio (i.e. number of observations per free parameter of the phenology model). Sample size is further translated into the site ratio, for which the number of sites per sample was divided by 500 (i.e. the number of sites in the entire population).

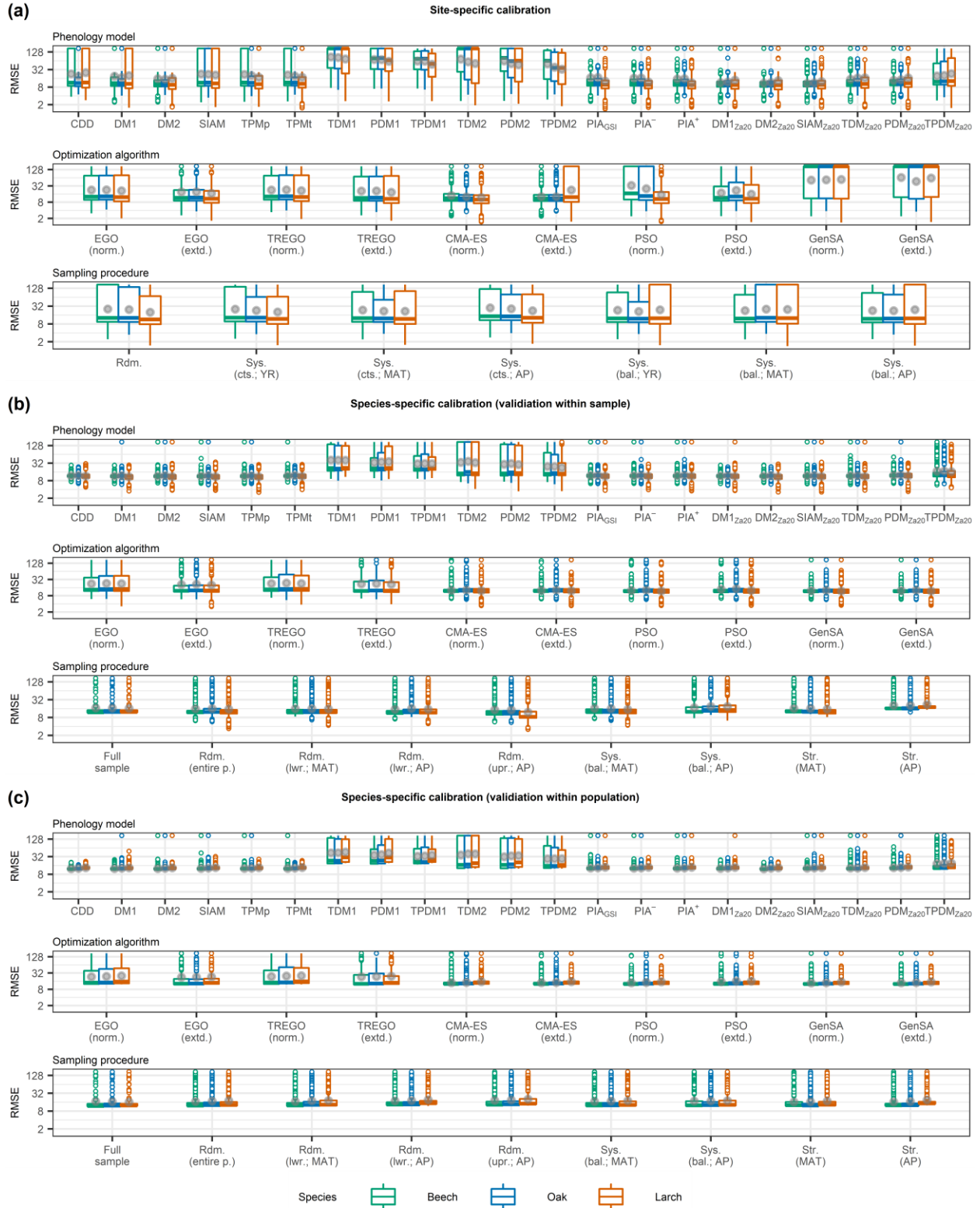


Figure S2. Observed distribution of the external root mean square error (RMSE) according to phenology model, optimization algorithm, or sampling procedure as obtained from the site-specific calibration and species-specific calibration validated within sample or population (a, b, and c, respectively). Thick horizontal lines and grey circles indicate the respective medians and means. Boxes cover the inner quartile range, whiskers extend to the most extreme observations or to 1.5 times the inner quartile range, and outliers are indicated as colored circles. Y-axes are log-transformed and modelled NA values were replaced with an error of 170

days. The abbreviations for the models, algorithms, and sampling procedures are explained in respective Tables Supplement S2: Table S1, Supplement S4: Table S1, and Supplement S4: Table S2/S3.

S2.1.2 Observed effects if calibration runs with NA values were excluded

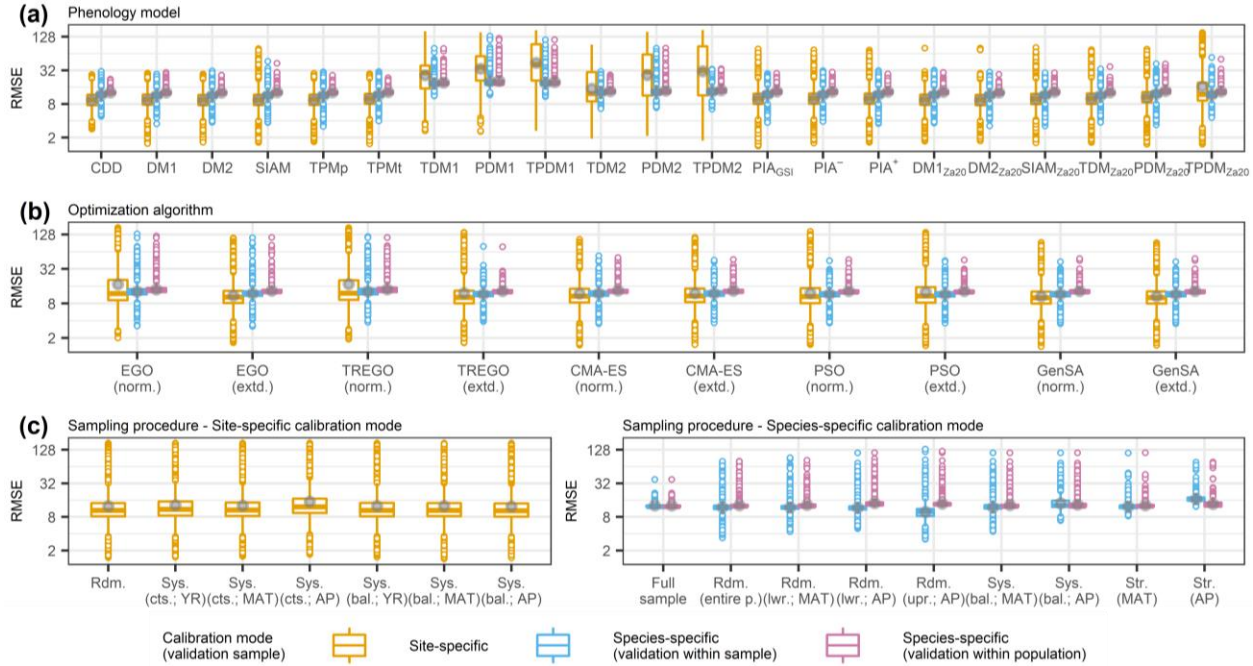


Figure S3. Observed distributions of the external root mean square error (RMSE) according to the three dimensions (a) phenology model, (b) optimization algorithm, and (c) sampling procedure. The thick horizontal lines and grey circles indicate the respective median and mean. Boxes cover the inner quartile range, whiskers extend to the most extreme observations or to 1.5 times the inner quartile range, and outliers are indicated as colored circles. In all figures, the colors represent the calibration and validation modes. The y-axes were log-transformed and modelled NA values were ignored in the calculation of the RMSE. The abbreviations for the models, algorithms, and sampling procedures are explained in respective Tables Supplement S2: Table S1, Supplement S4: Table S1, and Supplement S4: Table S2/S3.

Table S3. Ranked observed statistics mean (μ), median, standard deviation (σ), and skew of the external root mean square error per phenology model, optimization algorithm, and sampling procedure (from left to right) as well as per site-specific calibration and species-specific calibration validated within sample or population (from top to bottom).

| Site-specific calibration mode | | | | | | | | | | | | | | | | | | | |
|--------------------------------|-------|---------------|--------|------------------|----------|------------------|------|----------------|------|----------------|-------|---------------|--------|------------------|----------|------------------|------|----------------|------|
| Model | μ | Rank $_{\mu}$ | Median | Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew | Rank $_{Skew}$ | Skew | Algorithm | μ | Rank $_{\mu}$ | Median | Rank $_{Median}$ | σ | Rank $_{\sigma}$ | Skew | Rank $_{Skew}$ | Skew |
| DM2 | 9.82 | 1 | 9.43 | 1 | 3.24 | 2 | 0.74 | 5 | | GenSA (extd.) | 12.24 | 1 | 10.10 | 2 | 8.83 | 1 | 3.72 | 9 | |
| DM2 _{2a20} | 9.86 | 2 | 9.50 | 2 | 3.32 | 7 | 1.05 | 11 | | GenSA (norm.) | 12.51 | 2 | 10.03 | 1 | 9.68 | 2 | 3.66 | 8 | |
| CDD | 9.91 | 3 | 9.51 | 3 | 3.26 | 3 | 0.78 | 6 | | EGO (extd.) | 12.92 | 3 | 10.30 | 4 | 10.55 | 3 | 3.74 | 10 | |
| DM1 | 9.97 | 4 | 9.58 | 5 | 3.23 | 1 | 0.74 | 4 | | CMA-ES (norm.) | 14.64 | 4 | 10.67 | 6 | 12.21 | 4 | 2.79 | 5 | |
| DM1 _{2a20} | 9.97 | 5 | 9.58 | 6 | 3.27 | 4 | 0.84 | 7 | | CMA-ES (extd.) | 14.80 | 5 | 10.75 | 8 | 12.32 | 5 | 2.81 | 7 | |
| TPMp | 9.97 | 6 | 9.61 | 7 | 3.29 | 6 | 0.89 | 2 | | PSO (norm.) | 15.85 | 6 | 10.57 | 5 | 15.47 | 6 | 2.80 | 6 | |
| SIAM | 10.09 | 7 | 9.51 | 4 | 4.09 | 13 | 3.16 | 21 | | PSO (extd.) | 16.74 | 7 | 10.75 | 7 | 16.42 | 7 | 2.59 | 3 | |
| TPMt | 10.35 | 8 | 9.96 | 9 | 3.29 | 5 | 0.73 | 3 | | TREGO (extd.) | 17.78 | 8 | 10.19 | 3 | 22.43 | 8 | 2.62 | 4 | |
| SIAM _{2a20} | 10.38 | 9 | 9.84 | 8 | 3.93 | 12 | 2.57 | 19 | | TREGO (norm.) | 30.64 | 9 | 12.05 | 10 | 38.92 | 9 | 1.73 | 1 | |
| PIA _{QSI} | 10.40 | 10 | 9.98 | 11 | 3.64 | 10 | 1.94 | 18 | | EGO (norm.) | 30.68 | 10 | 11.87 | 9 | 39.25 | 10 | 1.75 | 2 | |
| PIA* | 10.42 | 11 | 9.99 | 12 | 3.63 | 9 | 1.72 | 17 | | | | | | | | | | | |
| PIA ⁺ | 10.42 | 12 | 10.01 | 13 | 3.55 | 8 | 1.43 | 12 | | | | | | | | | | | |
| TDM _{2a20} | 10.58 | 13 | 9.96 | 10 | 4.34 | 14 | 2.96 | 20 | | | | | | | | | | | |
| PDM _{2a20} | 11.07 | 14 | 10.67 | 14 | 3.82 | 11 | 1.68 | 16 | | | | | | | | | | | |
| TDM2 | 19.62 | 15 | 12.25 | 16 | 15.67 | 15 | 1.66 | 15 | | | | | | | | | | | |
| TPDM _{2a20} | 25.64 | 16 | 11.88 | 15 | 28.21 | 18 | 1.52 | 13 | | | | | | | | | | | |
| TDM1 | 31.58 | 17 | 29.07 | 17 | 20.58 | 16 | 1.58 | 14 | | | | | | | | | | | |
| PDM2 | 38.52 | 18 | 30.17 | 18 | 31.68 | 19 | 0.94 | 10 | | | | | | | | | | | |
| PDM1 | 41.55 | 19 | 36.05 | 20 | 25.35 | 17 | 0.91 | 9 | | | | | | | | | | | |
| TPDM2 | 51.67 | 20 | 31.88 | 19 | 48.32 | 21 | 0.84 | 8 | | | | | | | | | | | |
| TPDM1 | 58.12 | 21 | 40.91 | 21 | 40.70 | 20 | 0.58 | 1 | | | | | | | | | | | |

n_{observations} = 1,695,380
Calibration runs with NA values were excluded from calculation of statistics.

Table S3. Continued.

Species-specific calibration mode (validation within sample)

| Model | μ | Rank $_{\mu}$ | Median Rank $_{\mu}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{\sigma}$ | Algorithm | μ | Rank $_{\mu}$ | Median Rank $_{\mu}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{\sigma}$ | Sampling procedure | μ | Rank $_{\mu}$ | Median Rank $_{\mu}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{\sigma}$ | | | | | | |
|--------------------|-------|---------------|----------------------|----------|------------------|-----------------------|-----------|-------|----------------|----------------------|----------|------------------|-----------------------|--------------------|-------|---------------|----------------------|------------------|------------------|-----------------------|-------|---|------|---|-------|---|
| TDM $_{2a20}$ | 11.59 | 1 | 11.62 | 1 | 2.43 | 1 | 1.38 | 7 | PSO (extd.) | 11.89 | 1 | 11.70 | 1 | 2.90 | 5 | 1.72 | 5 | Rdm. (upr.; AP) | 10.06 | 1 | 10.03 | 1 | 2.95 | 6 | 11.29 | 8 |
| TPMp | 11.61 | 2 | 11.68 | 4 | 2.49 | 4 | 1.34 | 6 | GenSA (extd.) | 11.91 | 2 | 11.72 | 2 | 2.83 | 1 | 1.49 | 3 | Rdm. (lwr.; AP) | 11.99 | 2 | 11.58 | 2 | 2.95 | 5 | 6.07 | 5 |
| DM1 | 11.63 | 3 | 11.68 | 3 | 2.48 | 3 | 1.43 | 9 | GenSA (norm.) | 11.93 | 3 | 11.73 | 4 | 2.83 | 2 | 1.47 | 2 | Rdm. (lwr.; MAT) | 12.08 | 3 | 11.84 | 3 | 2.51 | 2 | 8.62 | 6 |
| SIAM | 11.63 | 4 | 11.65 | 2 | 2.52 | 5 | 1.59 | 12 | PSO (norm.) | 11.94 | 4 | 11.72 | 3 | 2.87 | 4 | 1.47 | 1 | Rdm. (entire p.) | 12.12 | 4 | 12.00 | 4 | 2.80 | 4 | 5.65 | 3 |
| DM2 | 11.66 | 5 | 11.70 | 5 | 2.54 | 7 | 1.48 | 10 | TREGO (extd.) | 11.98 | 5 | 11.82 | 5 | 2.85 | 3 | 2.66 | 7 | Sys. (bal.; MAT) | 12.21 | 5 | 12.06 | 5 | 3.09 | 7 | 5.98 | 4 |
| DM $_{2a20}$ | 11.77 | 6 | 11.71 | 6 | 2.62 | 10 | 1.43 | 8 | EGO (extd.) | 12.29 | 6 | 11.95 | 7 | 3.47 | 8 | 6.62 | 8 | Str. (MAT) | 12.47 | 6 | 12.31 | 7 | 3.14 | 8 | 15.69 | 9 |
| SIAM $_{2a20}$ | 11.81 | 7 | 11.79 | 8 | 2.53 | 6 | 1.22 | 3 | CMA-ES (extd.) | 12.29 | 7 | 11.94 | 6 | 3.05 | 6 | 1.65 | 4 | Full sample | 12.92 | 7 | 12.21 | 6 | 2.03 | 1 | 4.74 | 2 |
| DM1 $_{2a20}$ | 11.86 | 8 | 11.79 | 9 | 2.55 | 8 | 1.15 | 2 | CMA-ES (norm.) | 12.33 | 8 | 11.96 | 8 | 3.15 | 7 | 1.95 | 6 | Sys. (bal.; AP) | 14.43 | 8 | 12.80 | 8 | 4.14 | 9 | 3.40 | 1 |
| TPMt | 11.97 | 9 | 11.89 | 13 | 2.62 | 11 | 1.61 | 13 | EGO (norm.) | 13.33 | 9 | 12.55 | 9 | 4.83 | 10 | 7.07 | 9 | Str. (AP) | 16.91 | 9 | 16.43 | 9 | 2.68 | 3 | 10.21 | 7 |
| CDD | 12.00 | 10 | 11.95 | 14 | 2.61 | 9 | 1.65 | 14 | TREGO (norm.) | 13.44 | 10 | 12.65 | 10 | 4.71 | 9 | 7.22 | 10 | | | | | | | | | |
| TPDM $_{2a20}$ | 12.01 | 11 | 11.77 | 7 | 2.77 | 16 | 2.30 | 17 | | | | | | | | | | | | | | | | | | |
| PIA ⁺ | 12.03 | 12 | 11.87 | 11 | 2.67 | 12 | 1.24 | 4 | | | | | | | | | | | | | | | | | | |
| PIA ⁻ | 12.03 | 13 | 11.87 | 10 | 2.73 | 14 | 1.31 | 5 | | | | | | | | | | | | | | | | | | |
| PIA _{CSI} | 12.09 | 14 | 11.88 | 12 | 2.74 | 15 | 1.13 | 1 | | | | | | | | | | | | | | | | | | |
| PDM $_{2a20}$ | 12.42 | 15 | 12.03 | 15 | 3.01 | 17 | 1.50 | 11 | | | | | | | | | | | | | | | | | | |
| TDM2 | 13.18 | 16 | 12.65 | 17 | 2.46 | 2 | 2.09 | 16 | | | | | | | | | | | | | | | | | | |
| TPDM2 | 13.59 | 17 | 12.91 | 18 | 2.71 | 13 | 1.97 | 15 | | | | | | | | | | | | | | | | | | |
| PDM2 | 13.66 | 18 | 12.63 | 16 | 4.18 | 19 | 5.85 | 19 | | | | | | | | | | | | | | | | | | |
| TDM1 | 19.06 | 19 | 18.21 | 19 | 4.17 | 18 | 6.00 | 20 | | | | | | | | | | | | | | | | | | |
| TPDM1 | 19.58 | 20 | 18.49 | 20 | 6.31 | 20 | 8.27 | 21 | | | | | | | | | | | | | | | | | | |
| PDM1 | 21.83 | 21 | 18.67 | 21 | 10.49 | 21 | 4.54 | 18 | | | | | | | | | | | | | | | | | | |

n_{observations} = 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Species-specific calibration mode (validation within population)

| Model | μ | Rank $_{\mu}$ | Median Rank $_{\mu}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{\sigma}$ | Algorithm | μ | Rank $_{\mu}$ | Median Rank $_{\mu}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{\sigma}$ | Sampling procedure | μ | Rank $_{\mu}$ | Median Rank $_{\mu}$ | σ | Rank $_{\sigma}$ | Skew Rank $_{\sigma}$ |
|--------------------|-------|---------------|----------------------|----------|------------------|-----------------------|----------------|-------|---------------|----------------------|----------|------------------|-----------------------|--------------------|-------|---------------|----------------------|----------|------------------|-----------------------|
| DM2 | 12.86 | 1 | 12.49 | 2 | 1.10 | 2 | TREGO (extd.) | 13.19 | 1 | 12.68 | 3 | 1.68 | 1 | Full sample | 12.92 | 1 | 12.21 | 1 | 2.03 | 1 |
| DM2 $_{Za20}$ | 12.87 | 2 | 12.45 | 1 | 1.19 | 3 | PSO (extd.) | 13.21 | 2 | 12.63 | 1 | 1.83 | 2 | Str. (MAT) | 13.09 | 2 | 12.48 | 4 | 2.77 | 6 |
| TDM $_{Za20}$ | 12.92 | 3 | 12.59 | 4 | 1.26 | 6 | PSO (norm.) | 13.24 | 3 | 12.64 | 2 | 1.90 | 5 | Rdm. (entire p.) | 13.11 | 3 | 12.44 | 3 | 2.33 | 4 |
| CDD | 12.92 | 4 | 12.66 | 7 | 1.00 | 1 | GenSA (extd.) | 13.27 | 4 | 12.69 | 4 | 1.87 | 4 | Sys. (bal.; MAT) | 13.12 | 4 | 12.42 | 2 | 2.40 | 5 |
| DM1 | 12.94 | 5 | 12.49 | 3 | 1.28 | 7 | GenSA (norm.) | 13.28 | 5 | 12.70 | 5 | 1.87 | 3 | Rdm. (lwr.; MAT) | 13.21 | 5 | 12.52 | 6 | 2.24 | 3 |
| TPMp | 13.01 | 6 | 12.60 | 6 | 1.19 | 4 | EGO (extd.) | 13.47 | 6 | 12.79 | 6 | 2.57 | 8 | Sys. (bal.; AP) | 13.53 | 6 | 12.51 | 5 | 2.86 | 8 |
| SIAM | 13.08 | 7 | 12.60 | 5 | 1.55 | 13 | CMA.ES (extd.) | 13.49 | 7 | 12.87 | 8 | 2.03 | 6 | Str. (AP) | 13.81 | 7 | 12.95 | 7 | 2.98 | 9 |
| TPMt | 13.11 | 8 | 12.81 | 9 | 1.20 | 5 | CMA.ES (norm.) | 13.51 | 8 | 12.87 | 7 | 2.13 | 7 | Rdm. (upr.; AP) | 13.86 | 8 | 13.49 | 8 | 2.12 | 2 |
| SIAM $_{Za20}$ | 13.19 | 9 | 12.79 | 8 | 1.35 | 8 | EGO (norm.) | 14.30 | 9 | 13.38 | 9 | 4.18 | 10 | Rdm. (lwr.; AP) | 14.26 | 9 | 13.54 | 9 | 2.82 | 7 |
| DM1 $_{Za20}$ | 13.23 | 10 | 12.81 | 10 | 1.54 | 12 | TREGO (norm.) | 14.40 | 10 | 13.61 | 10 | 4.08 | 9 | | | | | | | |
| PIA ⁺ | 13.37 | 11 | 12.92 | 12 | 1.49 | 10 | | | | | | | | | | | | | | |
| PIA ⁻ | 13.37 | 12 | 12.94 | 13 | 1.50 | 11 | | | | | | | | | | | | | | |
| PIA _{CSI} | 13.44 | 13 | 12.96 | 14 | 1.58 | 14 | | | | | | | | | | | | | | |
| TPDM $_{Za20}$ | 13.49 | 14 | 12.91 | 11 | 1.94 | 15 | | | | | | | | | | | | | | |
| TDM2 | 13.65 | 15 | 13.27 | 17 | 1.47 | 9 | | | | | | | | | | | | | | |
| PDM $_{Za20}$ | 13.82 | 16 | 13.14 | 16 | 2.10 | 17 | | | | | | | | | | | | | | |
| PDM2 | 14.07 | 17 | 13.13 | 15 | 3.64 | 18 | | | | | | | | | | | | | | |
| TPDM2 | 14.17 | 18 | 13.61 | 18 | 1.95 | 16 | | | | | | | | | | | | | | |
| TDM1 | 19.60 | 19 | 18.48 | 19 | 4.11 | 19 | | | | | | | | | | | | | | |
| TPDM1 | 20.21 | 20 | 18.79 | 21 | 6.15 | 20 | | | | | | | | | | | | | | |
| PDM1 | 21.97 | 21 | 18.48 | 20 | 10.27 | 21 | | | | | | | | | | | | | | |

n_{observations} = 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Note: The abbreviations for the models, algorithms, and sampling procedures are explained in respective Tables Supplement S2: Table S1, Supplement S4: Table S1, and Supplement S4: Table S2/S3.

Table S4. Observed statistics mean (μ), median, and standard deviation (σ) of the external (population) root mean square error (RMSE) and corresponding ratios per size bin or sample size in the site- or species-specific calibration (left or right), respectively.

Site-specific calibration mode

RMSE_{external}

RMSE_{external}:RMSE_{internal}

| N:q | μ | Median | σ | Skew | N:q | μ | Median | σ | Skew |
|-------------|-------|--------|-------|------|-------------|------|--------|------|------|
| 2.26<xs4.66 | 23.10 | 11.47 | 28.75 | 2.46 | 2.26<xs4.66 | 1.63 | 1.21 | 1.42 | 4.86 |
| 4.66<xs7.03 | 15.90 | 10.54 | 19.23 | 4.02 | 4.66<xs7.03 | 1.34 | 1.13 | 0.89 | 5.94 |
| 7.03<xs9.4 | 12.44 | 10.18 | 11.33 | 6.26 | 7.03<xs9.4 | 1.19 | 1.09 | 0.56 | 9.31 |
| 9.4<xs11.8 | 10.18 | 9.80 | 3.08 | 1.03 | 9.4<xs11.8 | 1.09 | 1.07 | 0.11 | 5.18 |
| 11.8<xs14.1 | 10.32 | 9.99 | 2.86 | 0.80 | 11.8<xs14.1 | 1.08 | 1.06 | 0.09 | 2.25 |
| 14.1<xs16.5 | 10.58 | 9.93 | 3.21 | 1.18 | 14.1<xs16.5 | 1.07 | 1.05 | 0.08 | 1.33 |
| 16.5<xs18.9 | 9.91 | 9.40 | 2.87 | 1.02 | 16.5<xs18.9 | 1.07 | 1.04 | 0.08 | 1.64 |
| 18.9<xs21.3 | 10.29 | 9.93 | 2.68 | 0.67 | 18.9<xs21.3 | 1.06 | 1.04 | 0.07 | 1.55 |
| 21.3<xs23.6 | 10.45 | 9.84 | 3.00 | 1.61 | 21.3<xs23.6 | 1.07 | 1.03 | 0.08 | 1.40 |
| 23.6<xs26 | 9.89 | 9.83 | 2.00 | 0.68 | 23.6<xs26 | 1.06 | 1.03 | 0.07 | 1.53 |

Species-specific calibration mode

RMSE_{population, external}

RMSE_{sample, external}:RMSE_{population, external}

| s:S | Number of sites | μ | Median | σ | Skew | s:S | Number of sites | μ | Median | σ | Skew |
|-------|-----------------|-------|--------|------|-------|-------|-----------------|------|--------|----------|----------|
| 0.004 | 2 | 14.64 | 13.71 | 3.26 | 7.23 | 0.004 | 2 | 0.83 | 0.77 | 0.33 | 1.00 |
| 0.010 | 5 | 13.74 | 13.11 | 2.70 | 14.11 | 0.010 | 5 | 0.90 | 0.88 | 0.22 | 0.32 |
| 0.020 | 10 | 13.34 | 12.81 | 2.18 | 14.37 | 0.020 | 10 | 0.91 | 0.91 | 0.16 | 7.53e-03 |
| 0.024 | 12 | 13.09 | 12.48 | 2.77 | 21.75 | 0.024 | 12 | 0.95 | 0.98 | 0.11 | -0.92 |
| 0.034 | 17 | 13.81 | 12.95 | 2.98 | 11.22 | 0.034 | 17 | 1.23 | 1.24 | 0.10 | -0.36 |
| 0.040 | 20 | 13.27 | 12.68 | 2.19 | 12.59 | 0.040 | 20 | 0.90 | 0.92 | 0.14 | -0.62 |
| 0.100 | 50 | 13.20 | 12.58 | 2.20 | 9.67 | 0.100 | 50 | 0.92 | 0.95 | 0.12 | -1.32 |
| 0.200 | 100 | 13.22 | 12.59 | 2.35 | 10.15 | 0.200 | 100 | 0.93 | 0.97 | 0.11 | -1.54 |
| 0.400 | 200 | 13.27 | 12.64 | 2.31 | 8.02 | 0.400 | 200 | 0.93 | 0.97 | 0.10 | -1.74 |
| 1.000 | 500 | 12.92 | 12.21 | 2.03 | 4.74 | 1.000 | 500 | 1.00 | 1.00 | 0.00e+00 | NA |

Calibration runs with NA values were excluded from calculation of statistics.

Calibration runs with NA values were excluded from calculation of statistics.

Note: The RMSE ratios in the site- and species-specific calibrations were derived by dividing the external by the internal RMSE and by dividing the external population RMSE by the external sample RMSE. Size bins are equally distributed over and defined according to the parameter ratio (i.e. number of observations per free parameter of the phenology model). Sample size is further translated into the site ratio, for which the number of sites per sample was divided by 500 (i.e. the number of site in the entire population).

S2.2 Estimated effects

S2.2.1 Analysis based on substituted NA values

Table S5. Ranked coefficient estimates per phenology model, optimization algorithm, and calibration sample of the generalized additive models for the site-specific calibration mode.

| Site-specific calibration mode | | | | | | | | | | | | | | | | | | | |
|---|--|-----------------------|---------|------------------------|--|-----------------------------|---------|--------------------|--|-----------------------------------|---------|----|--|--|--|--|--|--|--|
| ln(RMSE) ~ Model + Algorithm + Sampling prc. + ln(N:q) + s(Site) + s(Species) | | | | | | | | | | | | | | | | | | | |
| Phenology model | Transformed estimate (0.5% – 99.5%) | | Rank | Optimisation algorithm | Transformed estimate (0.5% – 99.5%) | | Rank | Sampling procedure | Transformed estimate (0.5% – 99.5%) | | Rank | | | | | | | | |
| SIAM _{2x20} | -50.54% | (-51.64% – -49.41%) | *** ### | 1 | CMA-ES (norm.) | -76.15% (-76.33% – -75.97%) | *** ### | 1 | Sys. (cts.; MAT) | -3.75% (-4.35% – -3.14%) | *** ### | 1 | | | | | | | |
| DM2 _{2x20} | -47.38% | (-48.11% – -46.64%) | *** ### | 2 | CMA-ES (extd.) | -71.38% (-71.60% – -71.16%) | *** ### | 2 | Sys. (cts.; YR) | -1.95% (-2.57% – -1.34%) | *** ### | 2 | | | | | | | |
| DM1 _{2x20} | -45.06% | (-45.82% – -44.29%) | *** ### | 3 | PSO (extd.) | -65.99% (-66.24% – -65.73%) | *** ### | 3 | Sys. (bal.; YR) | -1.73% (-2.35% – -1.11%) | *** ### | 3 | | | | | | | |
| PIA ⁺ | -39.85% | (-41.19% – -38.48%) | *** ### | 4 | EGO (extd.) | -65.73% (-65.98% – -65.47%) | *** ### | 4 | Sys. (bal.; AP) | -0.15% (-0.78% – +0.48%) | *** ### | 4 | | | | | | | |
| PIA ⁻ | -36.07% | (-37.50% – -34.61%) | *** ### | 5 | TREGO (extd.) | -62.84% (-63.12% – -62.56%) | *** ### | 5 | Rdm. | ±0.00% [Ⓢ] | | 5 | | | | | | | |
| PDM _{2x20} | -35.79% | (-37.22% – -34.33%) | *** ### | 6 | EGO (norm.) | -58.85% (-59.15% – -58.53%) | *** ### | 6 | Sys. (bal.; MAT) | +4.53% (+3.87% – +5.19%) | *** ### | 6 | | | | | | | |
| PIA _{CSI} | -33.06% | (-34.55% – -31.53%) | *** ### | 7 | TREGO (norm.) | -58.60% (-58.91% – -58.29%) | *** ### | 7 | Sys. (cts.; AP) | +9.38% (+8.69% – +10.07%) | *** ### | 7 | | | | | | | |
| DM2 | -33.01% | (-34.51% – -31.48%) | *** ### | 8 | PSO (norm.) | -56.83% (-57.15% – -56.50%) | *** ### | 8 | ln(N:q) | -0.46% for +10% (-0.66% – -0.25%) | *** ### | NA | | | | | | | |
| TDM _{2x20} | -30.64% | (-32.18% – -29.05%) | *** ### | 9 | GenSA (norm.) | ±0.00% [Ⓢ] | | 9 | ln(N:q) | -1.93% for +50% (-2.78% – -1.07%) | *** ### | NA | | | | | | | |
| DM1 | -19.44% | (-21.24% – -17.61%) | *** ### | 10 | GenSA (extd.) | +7.28% (+6.48% – +8.10%) | *** ### | 10 | | | | | | | | | | | |
| TPMt | -16.74% | (-18.26% – -15.18%) | *** ### | 11 | | | | | | | | | | | | | | | |
| TPMp | -14.08% | (-15.66% – -12.48%) | *** ### | 12 | | | | | | | | | | | | | | | |
| TPDM _{2x20} | -11.00% | (-13.29% – -8.65%) | *** ### | 13 | | | | | | | | | | | | | | | |
| SIAM | -5.08% | (-6.82% – -3.31%) | *** ### | 14 | | | | | | | | | | | | | | | |
| CDD | ±0.00% [Ⓢ] | | | 15 | | | | | | | | | | | | | | | |
| TPDM2 | +69.37% | (+64.51% – +74.37%) | *** ### | 16 | | | | | | | | | | | | | | | |
| PDM2 | +127.67% | (+121.81% – +133.68%) | *** ### | 17 | | | | | | | | | | | | | | | |
| TPDM1 | +143.57% | (+136.58% – +150.77%) | *** ### | 18 | | | | | | | | | | | | | | | |
| TDM2 | +159.40% | (+152.73% – +166.25%) | *** ### | 19 | | | | | | | | | | | | | | | |
| PDM1 | +189.00% | (+181.57% – +196.63%) | *** ### | 20 | | | | | | | | | | | | | | | |
| TDM1 | +246.51% | (+237.59% – +255.66%) | *** ### | 21 | | | | | | | | | | | | | | | |

@ Reference (intercept) : 57.14 d (52.59 – 62.08 d) *** ###

Adj. R² : 0.41 ; Dev. expl. : 0.41 ; R_{IGAM} : 2.205,000

NA values were replaced with 170 days before calculation of statistics.

Note: Asterisks and dots indicate the significance level: ., *, **, or *** correspond to $p < 0.1$, 0.05, 0.01, or 0.001. Hashtags and crosses indicate the minimum Bayes factor with +, #, ##, ###, or #### corresponding to $\text{BF}_{01} < 1/3$, 1/10, 1/30, 1/100, 1/300, or 1/1000, respectively. Further, @ marks the models, algorithms, and sampling procedures that constituted the reference for the other coefficients. The abbreviations for the models, algorithms, and sampling procedures are explained in respective Tables Supplement S2: Table S1, Supplement S4: Table S1, and Supplement S4: Table S2/S3.

Table S6. Ranked coefficient estimates per phenology model, optimization algorithm, and calibration sample of the generalized additive models for the species-specific calibration mode validated within sample.

Species-specific calibration mode (validation within sample)

$\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Phenology model | Transformed estimate (0.5% – 99.5%) | | Rank | Optimisation algorithm | Transformed estimate (0.5% – 99.5%) | | Rank | Sampling procedure | Transformed estimate (0.5% – 99.5%) | | Rank | | |
|----------------------|--|-----------------------|---------|------------------------|--|-----------------------------|---------|--------------------|--|---------------------|---------------------|---------|----|
| DM1 | -16.20% | (-19.43% – -12.84%) | *** ### | 1 | GenSA (norm.) | ±0.00% [ⓔ] | 1 | Rdm. (upr.; AP) | -13.54% | (-14.66% – -12.41%) | *** ### | 1 | |
| DM2 | -15.92% | (-19.16% – -12.55%) | *** ### | 2 | GenSA (extd.) | +0.87% (-0.76% – +2.53%) | 2 | Rdm. (lwr.; AP) | -1.92% | (-3.18% – -0.64%) | *** ### | 2 | |
| TDM _{Za20} | -14.95% | (-18.23% – -11.54%) | *** ### | 3 | PSO (norm.) | +1.32% (-0.32% – +2.98%) | * | Sys. (bal.; MAT) | -0.13% | (-1.41% – +1.18%) | *** ### | 3 | |
| SIAM _{Za20} | -14.61% | (-17.90% – -11.19%) | *** ### | 4 | CMA-ES (extd.) | +2.76% (+1.10% – +4.45%) | *** ### | 4 | Rdm. (entire p.) | ±0.00% [ⓔ] | *** ### | 4 | |
| PIA [~] | -13.45% | (-16.79% – -9.99%) | *** ### | 5 | CMA-ES (norm.) | +3.06% (+1.40% – +4.76%) | *** ### | 5 | Full sample | +1.44% | (-4.03% – +7.24%) | *** ### | 5 |
| TPMp | -13.38% | (-16.23% – -10.43%) | *** ### | 6 | PSO (extd.) | +10.78% (+8.99% – +12.60%) | *** ### | 6 | Str. (MAT) | +3.01% | (+0.36% – +5.74%) | ** # | 6 |
| PIA [*] | -13.24% | (-16.58% – -9.77%) | *** ### | 7 | EGO (extd.) | +68.54% (+65.81% – +71.31%) | *** ### | 7 | Rdm. (lwr.; MAT) | +11.65% | (+8.71% – +14.68%) | *** ### | 7 |
| PIA _{GSI} | -12.96% | (-16.32% – -9.48%) | *** ### | 8 | TREGO (extd.) | +77.51% (+74.64% – +80.43%) | *** ### | 8 | Sys. (bal.; AP) | +15.50% | (+14.00% – +17.02%) | *** ### | 8 |
| SIAM | -12.93% | (-15.80% – -9.97%) | *** ### | 9 | EGO (norm.) | +83.66% (+80.69% – +86.68%) | *** ### | 9 | Str. (AP) | +35.55% | (+32.04% – +39.16%) | *** ### | 9 |
| TPMt | -10.72% | (-13.66% – -7.68%) | *** ### | 10 | TREGO (norm.) | +87.69% (+84.65% – +90.77%) | *** ### | 10 | ln($\bar{N}:q$) | -1.51% for +10% | (-1.83% – -1.19%) | *** ### | NA |
| PDM _{Za20} | -10.55% | (-14.00% – -6.97%) | *** ### | 11 | | | | | ln($\bar{N}:q$) | -6.27% for +50% | (-7.56% – -4.96%) | *** ### | NA |
| DM2 _{Za20} | -8.22% | (-10.70% – -5.67%) | *** ### | 12 | | | | | ln(s:S) | +0.10% for +10% | (+0.08% – +0.13%) | *** ### | NA |
| DM1 _{Za20} | -7.36% | (-9.87% – -4.79%) | *** ### | 13 | | | | | ln(s:S) | +0.44% for +50% | (+0.34% – +0.54%) | *** ### | NA |
| CDD | ±0.00% [ⓔ] | | *** ### | 14 | | | | | | | | | |
| TPDM _{Za20} | +19.63% | (+14.43% – +25.07%) | *** ### | 15 | | | | | | | | | |
| TPDM2 | +66.71% | (+58.74% – +75.08%) | *** ### | 16 | | | | | | | | | |
| PDM2 | +111.45% | (+102.26% – +121.06%) | *** ### | 17 | | | | | | | | | |
| TPDM1 | +114.50% | (+104.25% – +125.27%) | *** ### | 18 | | | | | | | | | |
| TDM2 | +147.95% | (+137.18% – +159.22%) | *** ### | 19 | | | | | | | | | |
| PDM1 | +150.54% | (+139.65% – +161.92%) | *** ### | 20 | | | | | | | | | |
| TDM1 | +188.38% | (+175.85% – +201.49%) | *** ### | 21 | | | | | | | | | |

[ⓔ]) Reference (intercept) : 13.82 d (12.13 – 15.74 d) *** ###

Adj. R² : 0.52 ; Dev. expl. : 0.52 ; n_{GAM} : 139,230

NA values were replaced with 170 days before calculation of statistics.

Note: See Table S5 for details.

Table S7. Ranked coefficient estimates per phenology model, optimization algorithm, and calibration sample of the generalized additive models for the species-specific calibration mode validated within population.

Species-specific calibration mode (validation within population)

$\ln(\text{RMSE}) = \text{Model} + \text{Algorithm} + \text{Sampling proc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Phenology model | Transformed estimate (0.5% – 99.5%) | | | Rank | Optimisation algorithm | Transformed estimate (0.5% – 99.5%) | | | Rank | Sampling procedure | Transformed estimate (0.5% – 99.5%) | | | Rank |
|----------------------|--|-----------------------|---------|------|------------------------|--|---------|----|--------------------|---------------------|--|---------|----|------|
| DM2 | -6.77% | (-10.04% – -3.38%) | *** ### | 1 | GenSA (norm.) | ±0.00% [Ⓢ] | | 1 | Str. (MAT) | -4.65% | (-6.91% – -2.34%) | *** ### | 1 | |
| DM1 | -6.16% | (-9.45% – -2.75%) | *** ### | 2 | GenSA (extd.) | +0.91% (-0.59% – +2.43%) | | 2 | Sys. (bal.; MAT) | -0.64% | (-1.82% – +0.55%) | *** ### | 2 | |
| TPMp | -4.32% | (-7.20% – -1.36%) | *** ### | 3 | PSO (norm.) | +1.62% (+0.11% – +3.15%) | ** . | 3 | Str. (AP) | -0.20% | (-2.58% – +2.23%) | *** ### | 3 | |
| TDM _{Za20} | -4.09% | (-7.46% – -0.60%) | ** # | 4 | CMA-ES (extd.) | +2.36% (+0.84% – +3.90%) | *** ### | 4 | Rdm. (entire p.) | ±0.00% [Ⓢ] | | *** ### | 4 | |
| SIAM _{Za20} | -4.06% | (-7.43% – -0.57%) | ** # | 5 | CMA-ES (norm.) | +2.62% (+1.09% – +4.17%) | *** ### | 5 | Sys. (bal.; AP) | +0.65% | (-0.55% – +1.86%) | *** ### | 5 | |
| TPMt | -3.58% | (-6.48% – -0.60%) | ** # | 6 | PSO (extd.) | +10.82% (+9.18% – +12.49%) | *** ### | 6 | Full sample | +3.99% | (-1.17% – +9.43%) | * | 6 | |
| SIAM | -3.56% | (-6.46% – -0.57%) | ** # | 7 | EGO (extd.) | +59.12% (+56.75% – +61.52%) | *** ### | 7 | Rdm. (lwr.; AP) | +5.06% | (+3.82% – +6.32%) | *** ### | 7 | |
| DM2 _{Za20} | -3.42% | (-5.81% – -0.97%) | *** ### | 8 | TREGO (extd.) | +67.74% (+65.25% – +70.27%) | *** ### | 8 | Rdm. (lwr.; MAT) | +5.86% | (+3.33% – +8.46%) | *** ### | 8 | |
| PIA ⁻ | -3.31% | (-6.70% – +0.21%) | * . | 9 | EGO (norm.) | +70.97% (+68.43% – +73.55%) | *** ### | 9 | Rdm. (upr.; AP) | +9.74% | (+8.44% – +11.05%) | *** ### | 9 | |
| PIA ⁺ | -3.19% | (-6.59% – +0.33%) | * . | 10 | TREGO (norm.) | +74.49% (+71.90% – +77.12%) | *** ### | 10 | ln(\bar{N} : q) | -0.69% for +10% | (-0.99% – -0.40%) | *** ### | NA | |
| PIA _{GSI} | -2.62% | (-6.03% – +0.93%) | . | 11 | | | | | ln(\bar{N} : q) | -2.92% for +50% | (-4.13% – -1.69%) | *** ### | NA | |
| DM1 _{Za20} | -0.74% | (-3.20% – +1.78%) | | 12 | | | | | ln(s: S) | -0.28% for +10% | (-0.30% – -0.26%) | *** ### | NA | |
| PDM _{Za20} | -0.03% | (-3.54% – +3.60%) | | 13 | | | | | ln(s: S) | -1.18% for +50% | (-1.27% – -1.09%) | *** ### | NA | |
| CDD | ±0.00% [Ⓢ] | | | 14 | | | | | | | | | | |
| TPDM _{Za20} | +34.92% | (+29.59% – +40.48%) | *** ### | 15 | | | | | | | | | | |
| TPDM2 | +92.99% | (+84.60% – +101.76%) | *** ### | 16 | | | | | | | | | | |
| PDM2 | +140.41% | (+130.90% – +150.31%) | *** ### | 17 | | | | | | | | | | |
| TPDM1 | +143.55% | (+132.96% – +154.62%) | *** ### | 18 | | | | | | | | | | |
| TDM2 | +178.46% | (+167.45% – +189.93%) | *** ### | 19 | | | | | | | | | | |
| PDM1 | +179.45% | (+168.40% – +190.95%) | *** ### | 20 | | | | | | | | | | |
| TDM1 | +218.34% | (+205.75% – +231.45%) | *** ### | 21 | | | | | | | | | | |

[Ⓢ] Reference (intercept): 10.94 d (10.06 – 11.90 d) *** ###

Adj. R²: 0.54 ; Dev. expl.: 0.54 ; n_{GAM}: 139,230

NA values were replaced with 170 days before calculation of statistics.

Note: See Table S5 for details.

Table S8. Estimated influence on variance according to type-III ANOVA in site- and species-specific calibration validated within sample or population (top to bottom, respectively).**Site-specific calibration mode** $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Factor | Influence | P value | BF_{01} | Cumulated influence |
|-------------------------|-----------|----------|------------------|---------------------|
| Phenology models | 0.513 | 0.00e+00 | 1/1.0e+09 | 0.5130 |
| Optimisation algorithms | 0.3988 | 0.00e+00 | 1/1.0e+09 | 0.9118 |
| Sites | 0.0849 | 0.00e+00 | 1/1.0e+09 | 0.9967 |
| Sampling procedures | 0.003 | 0.00e+00 | 1/1.0e+09 | 0.9997 |
| Species | 2e-04 | 1.87e-54 | 1/1.1e+51 | 0.9999 |
| $\ln(\bar{N}:q)$ | 0 | 8.57e-06 | 1/2.7e+03 | 0.9999 |

Adj. R^2 : 0.41 ; Dev. expl.: 0.41 ; n_{GAM} : 2,205,000

NA values were replaced with 170 days before calculation of statistics.

Species-specific calibration mode (validation within sample) $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Factor | Influence | P value | BF_{01} | Cumulated influence |
|-------------------------|-----------|----------|------------------|---------------------|
| Phenology models | 0.6219 | 0.00e+00 | 1/1.0e+09 | 0.6219 |
| Optimisation algorithms | 0.3326 | 0.00e+00 | 1/1.0e+09 | 0.9545 |
| Sampling procedures | 0.0395 | 0.00e+00 | 1/1.0e+09 | 0.9940 |
| Species | 0.0035 | 2.59e-85 | 1/4.9e+81 | 0.9975 |
| $\ln(\bar{N}:q)$ | 0.0013 | 1.44e-33 | 1/2.3e+30 | 0.9988 |
| $\ln(s:S)$ | 0.0011 | 1.18e-29 | 1/3.2e+26 | 0.9999 |

Adj. R^2 : 0.52 ; Dev. expl.: 0.52 ; n_{GAM} : 139,230

NA values were replaced with 170 days before calculation of statistics.

Species-specific calibration mode (validation within population) $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Factor | Influence | P value | BF_{01} | Cumulated influence |
|-------------------------|-----------|-----------|------------------|---------------------|
| Phenology models | 0.6864 | 0.00e+00 | 1/1.0e+09 | 0.6864 |
| Optimisation algorithms | 0.2961 | 0.00e+00 | 1/1.0e+09 | 0.9825 |
| $\ln(s:S)$ | 0.0096 | 3.60e-245 | 1/Inf | 0.9921 |
| Sampling procedures | 0.0066 | 2.90e-162 | 1/Inf | 0.9987 |
| Species | 0.001 | 1.54e-25 | 1/2.9e+22 | 0.9997 |
| $\ln(\bar{N}:q)$ | 3e-04 | 6.79e-09 | 1/2.1e+06 | 1.0000 |

Adj. R^2 : 0.54 ; Dev. expl.: 0.54 ; n_{GAM} : 139,230

NA values were replaced with 170 days before calculation of statistics.

Note: For each factor, the explained variance in RMSE (Influence) is listed together with the corresponding p-value and minimum Bayes factor of the null to the alternative hypothesis (BF_{01}). In the last row, the influence of each factor is accumulated. The size proxies are $\bar{N}:q$ and $\bar{N}:q$, i.e. the (average) number of observations per sample relative to the number of free model parameter, and $s:S$, i.e. the number of sites in the sample relative to the number of sites in the population.

Table S9. Coefficient estimates for the phenology models, optimization algorithms, and calibration samples of the generalized additive models for site-specific calibration.

Site-specific calibration mode
 $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(N:q) + s(\text{Site}) + s(\text{Species})$

| Dimension | Coefficient | Estimate | 0.5% | 99.5% | Std. Error | t value | P value | BF ₀₁ |
|------------------------|------------------------------|----------|-------|-------|------------|---------|---------|------------------|
| Base Intercept | CDD GenSA (norm.) Rdm. | 4.05 | 3.96 | 4.13 | 0.03 | 125.63 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM1 | -0.22 | -0.24 | -0.19 | 0.01 | -24.69 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 | -0.40 | -0.42 | -0.38 | 0.01 | -45.75 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM | -0.05 | -0.07 | -0.03 | 0.01 | -7.26 | 0.0000 | 1/2.3e+10 |
| Phenology model | TPMp | -0.15 | -0.17 | -0.13 | 0.01 | -21.14 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMt | -0.18 | -0.20 | -0.16 | 0.01 | -25.51 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM1 | 1.24 | 1.22 | 1.27 | 0.01 | 122.81 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM1 | 1.06 | 1.04 | 1.09 | 0.01 | 104.87 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM1 | 0.89 | 0.86 | 0.92 | 0.01 | 78.76 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM2 | 0.95 | 0.93 | 0.98 | 0.01 | 94.20 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM2 | 0.82 | 0.80 | 0.85 | 0.01 | 81.30 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM2 | 0.53 | 0.50 | 0.56 | 0.01 | 46.61 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA _{GSI} | -0.40 | -0.42 | -0.38 | 0.01 | -45.83 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁻ | -0.45 | -0.47 | -0.42 | 0.01 | -51.09 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁺ | -0.51 | -0.53 | -0.49 | 0.01 | -58.05 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM1 _{Za20} | -0.60 | -0.61 | -0.58 | 0.01 | -110.38 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 _{Za20} | -0.64 | -0.66 | -0.63 | 0.01 | -118.33 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM _{Za20} | -0.70 | -0.73 | -0.68 | 0.01 | -80.39 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM _{Za20} | -0.37 | -0.39 | -0.34 | 0.01 | -41.77 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM _{Za20} | -0.44 | -0.47 | -0.42 | 0.01 | -50.59 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM _{Za20} | -0.12 | -0.14 | -0.09 | 0.01 | -11.52 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | -0.89 | -0.90 | -0.88 | 0.00 | -303.73 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | -1.07 | -1.08 | -1.06 | 0.00 | -366.32 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | -0.88 | -0.89 | -0.87 | 0.00 | -301.69 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | -0.99 | -1.00 | -0.98 | 0.00 | -338.67 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | -1.43 | -1.44 | -1.43 | 0.00 | -490.35 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (extd.) | -1.25 | -1.26 | -1.24 | 0.00 | -428.00 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | PSO (norm.) | -0.84 | -0.85 | -0.83 | 0.00 | -287.34 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | PSO (extd.) | -1.08 | -1.09 | -1.07 | 0.00 | -368.91 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | GenSA (extd.) | 0.07 | 0.06 | 0.08 | 0.00 | 24.06 | 0.0000 | 1/1.0e+09 |
| Calibration sample | $\ln(N:q)$ | -0.05 | -0.07 | -0.03 | 0.01 | -5.74 | 0.0000 | 1/1.5e+06 |
| Calibration sample | Sys. (cts.; YR) | -0.02 | -0.03 | -0.01 | 0.00 | -8.07 | 0.0000 | 1/1.1e+13 |
| Calibration sample | Sys. (cts.; MAT) | -0.04 | -0.04 | -0.03 | 0.00 | -15.63 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (cts.; AP) | 0.09 | 0.08 | 0.10 | 0.00 | 36.65 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (bal.; YR) | -0.02 | -0.02 | -0.01 | 0.00 | -7.15 | 0.0000 | 1/1.1e+10 |
| Calibration sample | Sys. (bal.; MAT) | 0.04 | 0.04 | 0.05 | 0.00 | 18.12 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (bal.; AP) | 0.00 | -0.01 | 0.00 | 0.00 | -0.62 | 0.5323 | 1/1.0 |

Adj. R²: 0.41 ; Dev. expl.: 0.41 ; n_{GAM}: 2,205,000

NA values were replaced with 170 days before calculation of statistics.

Note: For each coefficient, the estimate, 99% confidence interval, standard error, t-value, p-value, and minimum Bayes factor of the null to the alternative hypothesis (BF₀₁) are listed. The size proxies are N:q and \bar{N} :q, i.e. the (average) number of observations per sample relative to the number of free model parameter, and s:S, i.e. the number of sites in the sample relative to the number of sites in the population, while the abbreviations for the models, algorithms, and sampling procedures are explained in respective Tables Supplement S2: Table S1, Supplement S4: Table S1, and Supplement S4: Table S2/S3.

Table S10. Coefficient estimates for the phenology models, optimization algorithms, and calibration samples of the generalized additive models for species-specific calibration, validated within sample.

Species-specific calibration mode (validation within sample)
 $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Dimension | Coefficient | Estimate | 0.5% | 99.5% | Std. Error | t value | P value | BF_{01} |
|------------------------|----------------------|----------|-------|-------|------------|---------|---------|------------------|
| Base Intercept | CDD | | | | | | | |
| | GenSA (norm.) | 2.63 | 2.50 | 2.76 | 0.05 | 51.99 | 0.0000 | 1/1.0e+09 |
| | Rdm. (entire p.) | | | | | | | |
| Phenology model | DM1 | -0.18 | -0.22 | -0.14 | 0.02 | -11.59 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 | -0.17 | -0.21 | -0.13 | 0.02 | -11.37 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM | -0.14 | -0.17 | -0.11 | 0.01 | -10.65 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMp | -0.14 | -0.18 | -0.11 | 0.01 | -11.04 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMt | -0.11 | -0.15 | -0.08 | 0.01 | -8.72 | 0.0000 | 1/2.2e+15 |
| Phenology model | TDM1 | 1.06 | 1.01 | 1.10 | 0.02 | 61.40 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM1 | 0.92 | 0.87 | 0.96 | 0.02 | 53.24 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM1 | 0.76 | 0.71 | 0.81 | 0.02 | 40.13 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM2 | 0.91 | 0.86 | 0.95 | 0.02 | 52.64 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM2 | 0.75 | 0.70 | 0.79 | 0.02 | 43.41 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM2 | 0.51 | 0.46 | 0.56 | 0.02 | 26.87 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA _{GSI} | -0.14 | -0.18 | -0.10 | 0.02 | -9.10 | 0.0000 | 1/6.4e+16 |
| Phenology model | PIA ⁻ | -0.14 | -0.18 | -0.11 | 0.02 | -9.47 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁺ | -0.14 | -0.18 | -0.10 | 0.02 | -9.31 | 0.0000 | 1/5.5e+17 |
| Phenology model | DM1 _{Za20} | -0.08 | -0.10 | -0.05 | 0.01 | -7.19 | 0.0000 | 1/1.4e+10 |
| Phenology model | DM2 _{Za20} | -0.09 | -0.11 | -0.06 | 0.01 | -8.06 | 0.0000 | 1/9.4e+12 |
| Phenology model | SIAM _{Za20} | -0.16 | -0.20 | -0.12 | 0.02 | -10.36 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM _{Za20} | -0.16 | -0.20 | -0.12 | 0.02 | -10.62 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM _{Za20} | -0.11 | -0.15 | -0.07 | 0.02 | -7.31 | 0.0000 | 1/3.4e+10 |
| Phenology model | TPDM _{Za20} | 0.18 | 0.13 | 0.22 | 0.02 | 10.39 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | 0.61 | 0.59 | 0.62 | 0.01 | 96.03 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | 0.52 | 0.51 | 0.54 | 0.01 | 82.46 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | 0.63 | 0.61 | 0.65 | 0.01 | 99.45 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | 0.57 | 0.56 | 0.59 | 0.01 | 90.65 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | 0.03 | 0.01 | 0.05 | 0.01 | 4.77 | 0.0000 | 1/1.1e+04 |
| Optimization algorithm | CMA-ES (extd.) | 0.03 | 0.01 | 0.04 | 0.01 | 4.30 | 0.0000 | 1/1.5e+03 |
| Optimization algorithm | PSO (norm.) | 0.01 | 0.00 | 0.03 | 0.01 | 2.07 | 0.0385 | 1/2.5 |
| Optimization algorithm | PSO (extd.) | 0.10 | 0.09 | 0.12 | 0.01 | 16.17 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | GenSA (extd.) | 0.01 | -0.01 | 0.02 | 0.01 | 1.37 | 0.1703 | 1/1.1 |
| Calibration sample | $\ln(s : S)$ | 0.01 | 0.01 | 0.01 | 0.00 | 11.31 | 0.0000 | 1/1.0e+09 |
| Calibration sample | $\ln(\bar{N} : q)$ | -0.16 | -0.19 | -0.13 | 0.01 | -12.01 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Full sample | 0.01 | -0.04 | 0.07 | 0.02 | 0.67 | 0.5057 | 1/1.0 |
| Calibration sample | Rdm. (lwr.; MAT) | 0.11 | 0.08 | 0.14 | 0.01 | 10.62 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Rdm. (lwr.; AP) | -0.02 | -0.03 | -0.01 | 0.01 | -3.85 | 0.0001 | 1/265 |
| Calibration sample | Rdm. (upr.; AP) | -0.15 | -0.16 | -0.13 | 0.01 | -28.88 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (bal.; MAT) | 0.00 | -0.01 | 0.01 | 0.01 | -0.25 | 0.8029 | 1/1.0 |
| Calibration sample | Sys. (bal.; AP) | 0.14 | 0.13 | 0.16 | 0.01 | 28.48 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Str. (MAT) | 0.03 | 0.00 | 0.06 | 0.01 | 2.93 | 0.0034 | 1/15 |
| Calibration sample | Str. (AP) | 0.30 | 0.28 | 0.33 | 0.01 | 29.83 | 0.0000 | 1/1.0e+09 |

Adj. R² : 0.52 ; Dev. expl. : 0.52 ; n_{GAM} : 139,230

NA values were replaced with 170 days before calculation of statistics.

Note: See Table S9 for details.

Table S11. Coefficient estimates for the phenology models, optimization algorithms, and calibration samples of the generalized additive models for site-specific calibration, validated within population.

Species-specific calibration mode (validation within population)
 $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Dimension | Coefficient | Estimate | 0.5% | 99.5% | Std. Error | t value | P value | BF_{01} |
|------------------------|----------------------|----------|-------|-------|------------|---------|---------|------------------|
| Base Intercept | CDD | | | | | | | |
| | GenSA (norm.) | 2.39 | 2.31 | 2.48 | 0.03 | 73.23 | 0.0000 | 1/1.0e+09 |
| | Rdm. (entire p.) | | | | | | | |
| Phenology model | DM1 | -0.06 | -0.10 | -0.03 | 0.01 | -4.59 | 0.0000 | 1/4.9e+03 |
| Phenology model | DM2 | -0.07 | -0.11 | -0.03 | 0.01 | -5.05 | 0.0000 | 1/4.2e+04 |
| Phenology model | SIAM | -0.04 | -0.07 | -0.01 | 0.01 | -3.06 | 0.0022 | 1/21 |
| Phenology model | TPMp | -0.04 | -0.07 | -0.01 | 0.01 | -3.73 | 0.0002 | 1/170 |
| Phenology model | TPMt | -0.04 | -0.07 | -0.01 | 0.01 | -3.08 | 0.0021 | 1/23 |
| Phenology model | TDM1 | 1.16 | 1.12 | 1.20 | 0.02 | 73.92 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM1 | 1.03 | 0.99 | 1.07 | 0.02 | 65.60 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM1 | 0.89 | 0.85 | 0.93 | 0.02 | 51.58 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM2 | 1.02 | 0.98 | 1.06 | 0.02 | 65.38 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM2 | 0.88 | 0.84 | 0.92 | 0.02 | 56.00 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM2 | 0.66 | 0.61 | 0.70 | 0.02 | 38.10 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA _{GSI} | -0.03 | -0.06 | 0.01 | 0.01 | -1.91 | 0.0559 | 1/2.0 |
| Phenology model | PIA ⁻ | -0.03 | -0.07 | 0.00 | 0.01 | -2.43 | 0.0153 | 1/4.7 |
| Phenology model | PIA ⁺ | -0.03 | -0.07 | 0.00 | 0.01 | -2.34 | 0.0193 | 1/4.0 |
| Phenology model | DM1 _{Za20} | -0.01 | -0.03 | 0.02 | 0.01 | -0.76 | 0.4444 | 1/1.0 |
| Phenology model | DM2 _{Za20} | -0.03 | -0.06 | -0.01 | 0.01 | -3.58 | 0.0003 | 1/102 |
| Phenology model | SIAM _{Za20} | -0.04 | -0.08 | -0.01 | 0.01 | -2.99 | 0.0028 | 1/18 |
| Phenology model | TDM _{Za20} | -0.04 | -0.08 | -0.01 | 0.01 | -3.01 | 0.0026 | 1/19 |
| Phenology model | PDM _{Za20} | 0.00 | -0.04 | 0.04 | 0.01 | -0.02 | 0.9804 | 1/1.0 |
| Phenology model | TPDM _{Za20} | 0.30 | 0.26 | 0.34 | 0.02 | 19.12 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | 0.54 | 0.52 | 0.55 | 0.01 | 92.31 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | 0.46 | 0.45 | 0.48 | 0.01 | 79.95 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | 0.56 | 0.54 | 0.57 | 0.01 | 95.82 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | 0.52 | 0.50 | 0.53 | 0.01 | 89.03 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | 0.03 | 0.01 | 0.04 | 0.01 | 4.45 | 0.0000 | 1/2.7e+03 |
| Optimization algorithm | CMA-ES (extd.) | 0.02 | 0.01 | 0.04 | 0.01 | 4.01 | 0.0001 | 1/470 |
| Optimization algorithm | PSO (norm.) | 0.02 | 0.00 | 0.03 | 0.01 | 2.76 | 0.0058 | 1/9.9 |
| Optimization algorithm | PSO (extd.) | 0.10 | 0.09 | 0.12 | 0.01 | 17.69 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | GenSA (extd.) | 0.01 | -0.01 | 0.02 | 0.01 | 1.55 | 0.1207 | 1/1.3 |
| Calibration sample | $\ln(s : S)$ | -0.03 | -0.03 | -0.03 | 0.00 | -33.51 | 0.0000 | 1/1.0e+09 |
| Calibration sample | $\ln(\bar{N} : q)$ | -0.07 | -0.10 | -0.04 | 0.01 | -6.08 | 0.0000 | 1/1.1e+07 |
| Calibration sample | Full sample | 0.04 | -0.01 | 0.09 | 0.02 | 1.98 | 0.0477 | 1/2.2 |
| Calibration sample | Rdm. (lwr.; MAT) | 0.06 | 0.03 | 0.08 | 0.01 | 6.05 | 0.0000 | 1/9.1e+06 |
| Calibration sample | Rdm. (lwr.; AP) | 0.05 | 0.04 | 0.06 | 0.00 | 10.69 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Rdm. (upr.; AP) | 0.09 | 0.08 | 0.10 | 0.00 | 20.09 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (bal.; MAT) | -0.01 | -0.02 | 0.01 | 0.00 | -1.39 | 0.1640 | 1/1.1 |
| Calibration sample | Sys. (bal.; AP) | 0.01 | -0.01 | 0.02 | 0.00 | 1.40 | 0.1621 | 1/1.2 |
| Calibration sample | Str. (MAT) | -0.05 | -0.07 | -0.02 | 0.01 | -5.12 | 0.0000 | 1/5.8e+04 |
| Calibration sample | Str. (AP) | 0.00 | -0.03 | 0.02 | 0.01 | -0.22 | 0.8281 | 1/1.0 |

Adj. R² : 0.54 ; Dev. expl. : 0.54 ; n_{GAM} : 139,230

NA values were replaced with 170 days before calculation of statistics.

Note: See Table S9 for details.

S2.2.2 Analysis of converging calibration runs that did not led to NA values

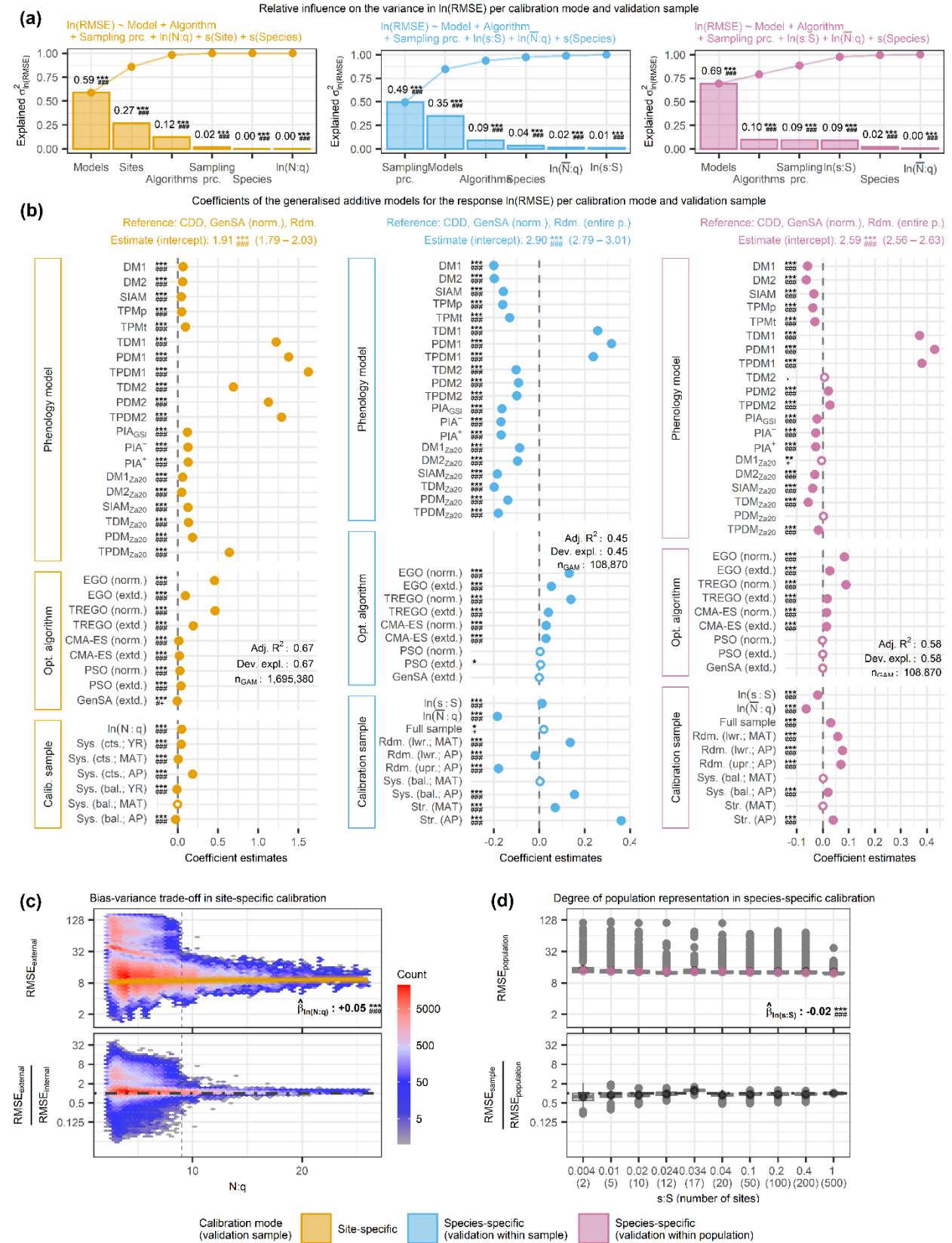


Figure S4. The relative variance in the log-transformed external root mean square error (RMSE) explained by phenology models, optimization algorithms, and calibration samples (i.e. sampling procedures and sample sizes) and the effects of the individual factors together with the observed distribution of the RMSE according to sample size from converged calibration runs that did not lead to any NA value. (See Figure 3 for further description.)

Table S12. Ranked coefficient estimates for site-specific calibration according to converging calibration runs that did not lead to any NA values.

Site-specific calibration mode
 $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(N:q) + s(\text{Site}) + s(\text{Species})$

| Phenology model | Transformed estimate (0.5% – 99.5%) | Rank | Optimisation algorithm | Transformed estimate (0.5% – 99.5%) | Rank | Sampling procedure | Transformed estimate (0.5% – 99.5%) | Rank |
|----------------------|---|------|------------------------|--|------|--------------------|--|------|
| CDD | ±0.00% [Ⓢ] | 1 | GenSA (extd.) | -0.70% (-1.21% – -0.19%) *** ^{##} | 1 | Sys. (bal.; AP) | -2.53% (-2.83% – -2.22%) *** ^{###} | 1 |
| SIAM | +4.35% (+3.35% – +5.36%) *** ^{###} | 2 | GenSA (norm.) | ±0.00% [Ⓢ] | 2 | Sys. (bal.; YR) | -1.02% (-1.33% – -0.72%) *** ^{###} | 2 |
| DM2 _{Za20} | +5.02% (+4.29% – +5.76%) *** ^{###} | 3 | CMA-ES (norm.) | +1.57% (+1.13% – +2.01%) *** ^{###} | 3 | Sys. (bal.; MAT) | -0.09% (-0.40% – +0.23%) | 3 |
| TPMp | +5.16% (+4.15% – +6.17%) *** ^{###} | 4 | CMA-ES (extd.) | +1.97% (+1.52% – +2.41%) *** ^{###} | 4 | Rdm. | ±0.00% [Ⓢ] | 4 |
| DM2 | +6.30% (+5.07% – +7.55%) *** ^{###} | 5 | PSO (norm.) | +2.61% (+2.15% – +3.07%) *** ^{###} | 5 | Sys. (cts.; MAT) | +0.70% (+0.39% – +1.02%) *** ^{###} | 5 |
| DM1 _{Za20} | +6.38% (+5.63% – +7.12%) *** ^{###} | 6 | PSO (extd.) | +4.19% (+3.73% – +4.65%) *** ^{###} | 6 | Sys. (cts.; YR) | +4.32% (+4.00% – +4.65%) *** ^{###} | 6 |
| DM1 | +6.89% (+5.65% – +8.15%) *** ^{###} | 7 | EGO (extd.) | +9.84% (+9.36% – +10.33%) *** ^{###} | 7 | Sys. (cts.; AP) | +20.41% (+20.03% – +20.78%) *** ^{###} | 7 |
| TPMt | +10.09% (+9.04% – +11.15%) *** ^{###} | 8 | TREGO (extd.) | +21.38% (+20.85% – +21.92%) *** ^{###} | 8 | ln(N : q) | +0.48% for +10% (+0.37% – +0.59%) *** ^{###} | NA |
| PIA _{GSI} | +12.89% (+11.58% – +14.21%) *** ^{###} | 9 | EGO (norm.) | +57.92% (+57.24% – +58.61%) *** ^{###} | 9 | ln(N : q) | +2.05% for +50% (+1.59% – +2.52%) *** ^{###} | NA |
| SIAM _{Za20} | +13.51% (+12.20% – +14.83%) *** ^{###} | 10 | TREGO (norm.) | +59.03% (+58.33% – +59.72%) *** ^{###} | 10 | | | |
| PIA ⁻ | +13.56% (+12.25% – +14.90%) *** ^{###} | 11 | | | | | | |
| PIA ⁺ | +13.87% (+12.56% – +15.21%) *** ^{###} | 12 | | | | | | |
| TDM _{Za20} | +14.33% (+13.00% – +15.67%) *** ^{###} | 13 | | | | | | |
| PDM _{Za20} | +20.20% (+18.81% – +21.61%) *** ^{###} | 14 | | | | | | |
| TPDM _{Za20} | +89.65% (+87.11% – +92.23%) *** ^{###} | 15 | | | | | | |
| TDM2 | +99.79% (+97.00% – +102.61%) *** ^{###} | 16 | | | | | | |
| PDM2 | +208.57% (+204.37% – +212.83%) *** ^{###} | 17 | | | | | | |
| TDM1 | +239.84% (+235.08% – +244.66%) *** ^{###} | 18 | | | | | | |
| TPDM2 | +262.77% (+257.32% – +268.30%) *** ^{###} | 19 | | | | | | |
| PDM1 | +296.36% (+290.94% – +301.85%) *** ^{###} | 20 | | | | | | |
| TPDM1 | +406.52% (+398.90% – +414.26%) *** ^{###} | 21 | | | | | | |

[Ⓢ]) Reference (intercept) : 6.75 d (5.97 – 7.64 d) ***^{###}

Adj. R² : 0.67 ; Dev. expl. : 0.67 ; n_{GAM} : 1,695,380

Calibration runs with NA values were excluded from calculation of statistics.

Note: See Table S5 for details.

Table S13. Ranked coefficient estimates for species-specific calibration validated within sample according to converging calibration runs that did not lead to any NA values.**Species-specific calibration mode (validation within sample)** $\ln(\text{RMSE}) = \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Phenology model | Transformed estimate (0.5% – 99.5%) | Rank | Optimisation algorithm | Transformed estimate (0.5% – 99.5%) | Rank | Sampling procedure | Transformed estimate (0.5% – 99.5%) | Rank |
|----------------------|--|------|------------------------|--|------|--------------------|---|------|
| DM1 | -18.17% (-19.34% – -16.98%) *** ### | 1 | GenSA (extd.) | -0.07% (-0.66% – +0.52%) | 1 | Rdm. (upr.; AP) | -16.51% (-16.93% – -16.09%) *** ### | 1 |
| TDM _{Za20} | -18.04% (-19.21% – -16.84%) *** ### | 2 | GenSA (norm.) | ±0.00% [Ⓢ] | 2 | Rdm. (lwr.; AP) | -1.83% (-2.31% – -1.35%) *** ### | 2 |
| DM2 | -18.00% (-19.18% – -16.82%) *** ### | 3 | PSO (norm.) | +0.25% (-0.34% – +0.86%) | 3 | Rdm. (entire p.) | ±0.00% [Ⓢ] | 3 |
| SIAM _{Za20} | -16.92% (-18.11% – -15.72%) *** ### | 4 | PSO (extd.) | +0.48% (-0.12% – +1.09%) * | 4 | Sys. (bal.; MAT) | +0.26% (-0.23% – +0.75%) | 4 |
| TPDM _{Za20} | -16.53% (-17.91% – -15.12%) *** ### | 5 | CMA-ES (extd.) | +2.86% (+2.25% – +3.48%) *** ### | 5 | Full sample | +1.95% (-0.08% – +4.02%) * | 5 |
| PIA ⁺ | -15.57% (-16.78% – -14.35%) *** ### | 6 | CMA-ES (norm.) | +2.97% (+2.35% – +3.58%) *** ### | 6 | Str. (MAT) | +7.16% (+6.10% – +8.24%) *** ### | 6 |
| PIA ⁻ | -15.53% (-16.73% – -14.30%) *** ### | 7 | TREGO (extd.) | +4.04% (+3.40% – +4.69%) *** ### | 7 | Rdm. (lwr.; MAT) | +14.47% (+13.30% – +15.64%) *** ### | 7 |
| PIA _{GSI} | -15.20% (-16.41% – -13.97%) *** ### | 8 | EGO (extd.) | +5.37% (+4.72% – +6.02%) *** ### | 8 | Sys. (bal.; AP) | +16.63% (+16.06% – +17.20%) *** ### | 8 |
| TPMp | -14.94% (-15.95% – -13.90%) *** ### | 9 | EGO (norm.) | +13.98% (+13.27% – +14.70%) *** ### | 9 | Str. (AP) | +43.29% (+41.91% – +44.68%) *** ### | 9 |
| SIAM | -14.70% (-15.72% – -13.66%) *** ### | 10 | TREGO (norm.) | +14.82% (+14.10% – +15.55%) *** ### | 10 | $\ln(\bar{N}:q)$ | -1.75% for +10% (-1.87% – -1.62%) *** ### | NA |
| PDM _{Za20} | -12.99% (-14.23% – -11.73%) *** ### | 11 | | | | $\ln(\bar{N}:q)$ | -7.22% for +50% (-7.71% – -6.72%) *** ### | NA |
| TPMt | -12.29% (-13.34% – -11.22%) *** ### | 12 | | | | $\ln(s:S)$ | +0.11% for +10% (+0.10% – +0.12%) *** ### | NA |
| TDM2 | -9.77% (-11.39% – -8.12%) *** ### | 13 | | | | $\ln(s:S)$ | +0.46% for +50% (+0.42% – +0.50%) *** ### | NA |
| TPDM2 | -9.46% (-11.19% – -7.69%) *** ### | 14 | | | | | | |
| DM2 _{Za20} | -9.14% (-10.01% – -8.27%) *** ### | 15 | | | | | | |
| PDM2 | -8.78% (-10.41% – -7.12%) *** ### | 16 | | | | | | |
| DM1 _{Za20} | -8.35% (-9.22% – -7.47%) *** ### | 17 | | | | | | |
| CDD | ±0.00% [Ⓢ] | 18 | | | | | | |
| TPDM1 | +26.75% (+24.12% – +29.42%) *** ### | 19 | | | | | | |
| TDM1 | +29.21% (+26.64% – +31.83%) *** ### | 20 | | | | | | |
| PDM1 | +37.27% (+34.56% – +40.03%) *** ### | 21 | | | | | | |

[Ⓢ] Reference (intercept) : 18.12 d (16.22 – 20.23 d) *** ###Adj. R² : 0.45 ; Dev. expl. : 0.45 ; n_{GAM} : 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Note: See Table S5 for details.

Table S14. Ranked coefficient estimates for species-specific calibration validated within population according to converging calibration runs that did not lead to any NA values.**Species-specific calibration mode (validation within population)** $\ln(\text{RMSE}) = \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Phenology model | Transformed estimate (0.5% – 99.5%) | Rank | Optimisation algorithm | Transformed estimate (0.5% – 99.5%) | Rank | Sampling procedure | Transformed estimate (0.5% – 99.5%) | Rank |
|----------------------|--|------|------------------------|--|------|--------------------|---|------|
| DM2 | -6.19% (-6.86% – -5.52%) *** ### | 1 | PSO (norm.) | -0.19% (-0.48% – +0.11%) | 1 | Rdm. (entire p.) | ±0.00% [Ⓢ] | 1 |
| DM1 | -5.71% (-6.38% – -5.03%) *** ### | 2 | PSO (extd.) | -0.05% (-0.35% – +0.24%) | 2 | Str. (MAT) | +0.00% (-0.49% – +0.50%) | 2 |
| TDM _{Za20} | -5.46% (-6.13% – -4.78%) *** ### | 3 | GenSA (extd.) | -0.04% (-0.33% – +0.26%) | 3 | Sys. (bal.; MAT) | +0.10% (-0.14% – +0.35%) | 3 |
| SIAM _{Za20} | -3.86% (-4.55% – -3.17%) *** ### | 4 | GenSA (norm.) | ±0.00% [Ⓢ] | 4 | Sys. (bal.; AP) | +2.05% (+1.80% – +2.30%) *** ### | 4 |
| TPMp | -3.80% (-4.37% – -3.22%) *** ### | 5 | CMA-ES (extd.) | +1.38% (+1.08% – +1.68%) *** ### | 5 | Full sample | +3.07% (+2.05% – +4.10%) *** ### | 5 |
| SIAM | -3.41% (-3.98% – -2.83%) *** ### | 6 | CMA-ES (norm.) | +1.46% (+1.16% – +1.76%) *** ### | 6 | Str. (AP) | +4.03% (+3.53% – +4.53%) *** ### | 6 |
| DM2 _{Za20} | -3.07% (-3.52% – -2.61%) *** ### | 7 | TREGO (extd.) | +1.72% (+1.41% – +2.03%) *** ### | 7 | Rdm. (lwr.; MAT) | +5.89% (+5.36% – +6.43%) *** ### | 7 |
| TPMt | -3.02% (-3.59% – -2.44%) *** ### | 8 | EGO (extd.) | +2.71% (+2.40% – +3.02%) *** ### | 8 | Rdm. (upr.; AP) | +7.18% (+6.91% – +7.44%) *** ### | 8 |
| PIA ⁺ | -2.72% (-3.41% – -2.02%) *** ### | 9 | EGO (norm.) | +8.65% (+8.32% – +8.99%) *** ### | 9 | Rdm. (lwr.; AP) | +7.85% (+7.59% – +8.11%) *** ### | 9 |
| PIA ⁻ | -2.70% (-3.39% – -2.00%) *** ### | 10 | TREGO (norm.) | +9.31% (+8.96% – +9.65%) *** ### | 10 | $\ln(\bar{N}:q)$ | -0.61% for +10% (-0.67% – -0.55%) *** ### | NA |
| PIA _{GSI} | -2.23% (-2.93% – -1.53%) *** ### | 11 | | | | $\ln(\bar{N}:q)$ | -2.56% for +50% (-2.82% – -2.31%) *** ### | NA |
| TPDM _{Za20} | -1.70% (-2.51% – -0.88%) *** ### | 12 | | | | $\ln(s:S)$ | -0.19% for +10% (-0.19% – -0.18%) *** ### | NA |
| DM1 _{Za20} | -0.49% (-0.96% – -0.02%) *** ### | 13 | | | | $\ln(s:S)$ | -0.80% for +50% (-0.82% – -0.78%) *** ### | NA |
| CDD | ±0.00% [Ⓢ] | 14 | | | | | | |
| PDM _{Za20} | +0.20% (-0.51% – +0.92%) | 15 | | | | | | |
| TDM2 | +0.64% (-0.25% – +1.55%) | 16 | | | | | | |
| PDM2 | +2.12% (+1.22% – +3.04%) *** ### | 17 | | | | | | |
| TPDM2 | +2.78% (+1.80% – +3.76%) *** ### | 18 | | | | | | |
| TDM1 | +45.10% (+43.67% – +46.56%) *** ### | 19 | | | | | | |
| TPDM1 | +46.37% (+44.86% – +47.89%) *** ### | 20 | | | | | | |
| PDM1 | +53.71% (+52.21% – +55.24%) *** ### | 21 | | | | | | |

[Ⓢ] Reference (intercept) : 13.39 d (12.91 – 13.89 d) *** ###Adj. R² : 0.58 ; Dev. expl. : 0.58 ; n_{GAM} : 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Note: See Table S5 for details.

Table S15. Estimated influence on variance according to type-III ANOVA in site- and species-specific calibration validated within sample or population (top to bottom, respectively) when only converging calibration runs that did not lead to any NA values were considered.**Site-specific calibration mode** $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Factor | Influence | P value | $\underline{\text{BF}}_{01}$ | Cumulated influence |
|-------------------------|-----------|----------|------------------------------|---------------------|
| Phenology models | 0.5883 | 0.00e+00 | 1/1.0e+09 | 0.5883 |
| Sites | 0.2693 | 0.00e+00 | 1/1.0e+09 | 0.8576 |
| Optimisation algorithms | 0.1235 | 0.00e+00 | 1/1.0e+09 | 0.9811 |
| Sampling procedures | 0.0178 | 0.00e+00 | 1/1.0e+09 | 0.9989 |
| Species | 0.001 | 0.00e+00 | 1/1.0e+09 | 0.9999 |
| $\ln(\bar{N}:q)$ | 1e-04 | 3.24e-31 | 1/1.1e+28 | 1.0000 |

Adj. R^2 : 0.67 ; Dev. expl.: 0.67 ; n_{GAM} : 1,695,380

Calibration runs with NA values were excluded from calculation of statistics.

Species-specific calibration mode (validation within sample) $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Factor | Influence | P value | $\underline{\text{BF}}_{01}$ | Cumulated influence |
|-------------------------|-----------|-----------|------------------------------|---------------------|
| Sampling procedures | 0.4946 | 0.00e+00 | 1/1.0e+09 | 0.4946 |
| Phenology models | 0.3512 | 0.00e+00 | 1/1.0e+09 | 0.8458 |
| Optimisation algorithms | 0.0898 | 0.00e+00 | 1/1.0e+09 | 0.9356 |
| Species | 0.037 | 0.00e+00 | 1/1.0e+09 | 0.9726 |
| $\ln(\bar{N}:q)$ | 0.0157 | 7.37e-287 | 1/Inf | 0.9883 |
| $\ln(s:S)$ | 0.0117 | 1.40e-213 | 1/Inf | 1.0000 |

Adj. R^2 : 0.45 ; Dev. expl.: 0.45 ; n_{GAM} : 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Species-specific calibration mode (validation within population) $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Factor | Influence | P value | $\underline{\text{BF}}_{01}$ | Cumulated influence |
|-------------------------|-----------|-----------|------------------------------|---------------------|
| Phenology models | 0.6934 | 0.00e+00 | 1/1.0e+09 | 0.6934 |
| Optimisation algorithms | 0.0971 | 0.00e+00 | 1/1.0e+09 | 0.7905 |
| Sampling procedures | 0.0944 | 0.00e+00 | 1/1.0e+09 | 0.8849 |
| $\ln(s:S)$ | 0.0912 | 0.00e+00 | 1/1.0e+09 | 0.9761 |
| Species | 0.0191 | 0.00e+00 | 1/1.0e+09 | 0.9952 |
| $\ln(\bar{N}:q)$ | 0.0048 | 1.72e-141 | 1/Inf | 1.0000 |

Adj. R^2 : 0.58 ; Dev. expl.: 0.58 ; n_{GAM} : 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Note: See Table S8 for details.

Table S16. Coefficient estimates for phenology models, optimization algorithms, and calibration samples in site-specific calibration based on only converging runs that did not lead to NA values.

Site-specific calibration mode
 $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(N:q) + s(\text{Site}) + s(\text{Species})$

| Dimension | Coefficient | Estimate | 0.5% | 99.5% | Std. Error | t value | P value | BF ₀₁ |
|------------------------|----------------------|----------|-------|-------|------------|---------|---------|------------------|
| Base Intercept | CDD | 1.91 | 1.79 | 2.03 | 0.05 | 40.05 | 0.0000 | 1/1.0e+09 |
| | GenSA (norm.) | | | | | | | |
| | Rdm. | | | | | | | |
| Phenology model | DM1 | 0.07 | 0.05 | 0.08 | 0.00 | 14.65 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 | 0.06 | 0.05 | 0.07 | 0.00 | 13.48 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM | 0.04 | 0.03 | 0.05 | 0.00 | 11.40 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMp | 0.05 | 0.04 | 0.06 | 0.00 | 13.49 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMt | 0.10 | 0.09 | 0.11 | 0.00 | 25.87 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM1 | 1.22 | 1.21 | 1.24 | 0.01 | 223.49 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM1 | 1.38 | 1.36 | 1.39 | 0.01 | 257.79 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM1 | 1.62 | 1.61 | 1.64 | 0.01 | 275.64 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM2 | 0.69 | 0.68 | 0.71 | 0.01 | 127.10 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM2 | 1.13 | 1.11 | 1.14 | 0.01 | 211.80 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM2 | 1.29 | 1.27 | 1.30 | 0.01 | 219.36 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA _{GSI} | 0.12 | 0.11 | 0.13 | 0.00 | 26.77 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁻ | 0.13 | 0.12 | 0.14 | 0.00 | 28.11 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁺ | 0.13 | 0.12 | 0.14 | 0.00 | 28.75 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM1 _{Za20} | 0.06 | 0.05 | 0.07 | 0.00 | 22.70 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 _{Za20} | 0.05 | 0.04 | 0.06 | 0.00 | 18.01 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM _{Za20} | 0.13 | 0.12 | 0.14 | 0.00 | 28.13 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM _{Za20} | 0.13 | 0.12 | 0.15 | 0.00 | 29.55 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM _{Za20} | 0.18 | 0.17 | 0.20 | 0.00 | 40.70 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM _{Za20} | 0.64 | 0.63 | 0.65 | 0.01 | 122.18 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | 0.46 | 0.45 | 0.46 | 0.00 | 269.84 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | 0.09 | 0.09 | 0.10 | 0.00 | 54.52 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | 0.46 | 0.46 | 0.47 | 0.00 | 273.96 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | 0.19 | 0.19 | 0.20 | 0.00 | 112.54 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | 0.02 | 0.01 | 0.02 | 0.00 | 9.32 | 0.0000 | 1/5.5e+17 |
| Optimization algorithm | CMA-ES (extd.) | 0.02 | 0.02 | 0.02 | 0.00 | 11.52 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | PSO (norm.) | 0.03 | 0.02 | 0.03 | 0.00 | 14.76 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | PSO (extd.) | 0.04 | 0.04 | 0.05 | 0.00 | 23.96 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | GenSA (extd.) | -0.01 | -0.01 | 0.00 | 0.00 | -3.53 | 0.0004 | 1/88 |
| Calibration sample | $\ln(N:q)$ | 0.05 | 0.04 | 0.06 | 0.00 | 11.45 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (cts.; YR) | 0.04 | 0.04 | 0.05 | 0.00 | 35.10 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (cts.; MAT) | 0.01 | 0.00 | 0.01 | 0.00 | 5.81 | 0.0000 | 1/2.2e+06 |
| Calibration sample | Sys. (cts.; AP) | 0.19 | 0.18 | 0.19 | 0.00 | 154.11 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (bal.; YR) | -0.01 | -0.01 | -0.01 | 0.00 | -8.50 | 0.0000 | 1/3.6e+14 |
| Calibration sample | Sys. (bal.; MAT) | 0.00 | 0.00 | 0.00 | 0.00 | -0.71 | 0.4749 | 1/1.0 |
| Calibration sample | Sys. (bal.; AP) | -0.03 | -0.03 | -0.02 | 0.00 | -21.05 | 0.0000 | 1/1.0e+09 |

Adj. R²: 0.67 ; Dev. expl.: 0.67 ; n_{GAM}: 1,695,380
 Calibration runs with NA values were excluded from calculation of statistics.

Note: See Table S9 for details.

Table S17. Coefficient estimates for phenology models, optimization algorithms, and calibration samples in species-specific calibration validated within sample based on only converging runs that did not lead to NA values.

Species-specific calibration mode (validation within sample)

 $\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Dimension | Coefficient | Estimate | 0.5% | 99.5% | Std. Error | t value | P value | BF_{01} |
|------------------------|----------------------|----------|-------|-------|------------|---------|---------|-----------|
| Base Intercept | CDD | 2.90 | 2.79 | 3.01 | 0.04 | 67.49 | 0.0000 | 1/1.0e+09 |
| | GenSA (norm.) | | | | | | | |
| | Rdm. (entire p.) | | | | | | | |
| Phenology model | DM1 | -0.20 | -0.21 | -0.19 | 0.01 | -35.89 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 | -0.20 | -0.21 | -0.18 | 0.01 | -35.54 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM | -0.16 | -0.17 | -0.15 | 0.00 | -33.94 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMp | -0.16 | -0.17 | -0.15 | 0.00 | -34.58 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMt | -0.13 | -0.14 | -0.12 | 0.00 | -28.03 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM1 | 0.26 | 0.24 | 0.28 | 0.01 | 32.83 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM1 | 0.32 | 0.30 | 0.34 | 0.01 | 40.98 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM1 | 0.24 | 0.22 | 0.26 | 0.01 | 29.20 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM2 | -0.10 | -0.12 | -0.08 | 0.01 | -14.62 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM2 | -0.09 | -0.11 | -0.07 | 0.01 | -13.13 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM2 | -0.10 | -0.12 | -0.08 | 0.01 | -13.23 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA _{CSI} | -0.16 | -0.18 | -0.15 | 0.01 | -29.50 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁻ | -0.17 | -0.18 | -0.15 | 0.01 | -30.29 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁺ | -0.17 | -0.18 | -0.15 | 0.01 | -30.20 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM1 _{2a20} | -0.09 | -0.10 | -0.08 | 0.00 | -23.56 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 _{2a20} | -0.10 | -0.11 | -0.09 | 0.00 | -25.93 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM _{2a20} | -0.19 | -0.20 | -0.17 | 0.01 | -33.17 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM _{2a20} | -0.20 | -0.21 | -0.18 | 0.01 | -35.44 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM _{2a20} | -0.14 | -0.15 | -0.12 | 0.01 | -24.91 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM _{2a20} | -0.18 | -0.20 | -0.16 | 0.01 | -27.86 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | 0.13 | 0.12 | 0.14 | 0.00 | 53.48 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | 0.05 | 0.05 | 0.06 | 0.00 | 21.97 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | 0.14 | 0.13 | 0.14 | 0.00 | 56.21 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | 0.04 | 0.03 | 0.05 | 0.00 | 16.52 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | 0.03 | 0.02 | 0.04 | 0.00 | 12.63 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (extd.) | 0.03 | 0.02 | 0.03 | 0.00 | 12.19 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | PSO (norm.) | 0.00 | 0.00 | 0.01 | 0.00 | 1.09 | 0.2742 | 1/1.0 |
| Optimization algorithm | PSO (extd.) | 0.00 | 0.00 | 0.01 | 0.00 | 2.06 | 0.0398 | 1/2.4 |
| Optimization algorithm | GenSA (extd.) | 0.00 | -0.01 | 0.01 | 0.00 | -0.30 | 0.7626 | 1/1.0 |
| Calibration sample | $\ln(s:S)$ | 0.01 | 0.01 | 0.01 | 0.00 | 31.26 | 0.0000 | 1/1.0e+09 |
| Calibration sample | $\ln(\bar{N}:q)$ | -0.18 | -0.20 | -0.17 | 0.01 | -36.28 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Full sample | 0.02 | 0.00 | 0.04 | 0.01 | 2.47 | 0.0136 | 1/5.2 |
| Calibration sample | Rdm. (lwr.; MAT) | 0.14 | 0.12 | 0.15 | 0.00 | 34.08 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Rdm. (lwr.; AP) | -0.02 | -0.02 | -0.01 | 0.00 | -9.78 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Rdm. (upr.; AP) | -0.18 | -0.19 | -0.18 | 0.00 | -93.24 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (bal.; MAT) | 0.00 | 0.00 | 0.01 | 0.00 | 1.35 | 0.1777 | 1/1.1 |
| Calibration sample | Sys. (bal.; AP) | 0.15 | 0.15 | 0.16 | 0.00 | 80.86 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Str. (MAT) | 0.07 | 0.06 | 0.08 | 0.00 | 17.84 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Str. (AP) | 0.36 | 0.35 | 0.37 | 0.00 | 95.61 | 0.0000 | 1/1.0e+09 |

Adj. R^2 : 0.45 ; Dev. expl.: 0.45 ; n_{GAM} : 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Note: See Table S9 for details.

Table S18. Coefficient estimates for phenology models, optimization algorithms, and calibration samples in species-specific calibration validated within population based on only converging runs that did not lead to NA values.

Species-specific calibration mode (validation within population)

$\ln(\text{RMSE}) \sim \text{Model} + \text{Algorithm} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Species})$

| Dimension | Coefficient | Estimate | 0.5% | 99.5% | Std. Error | t value | P value | BF ₀₁ |
|------------------------|--|----------|-------|-------|------------|---------|---------|------------------|
| Base Intercept | CDD GenSA (norm.) Rdm. (entire p.) | 2.59 | 2.56 | 2.63 | 0.01 | 182.81 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM1 | -0.06 | -0.07 | -0.05 | 0.00 | -21.24 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM2 | -0.06 | -0.07 | -0.06 | 0.00 | -23.11 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM | -0.03 | -0.04 | -0.03 | 0.00 | -14.95 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMp | -0.04 | -0.04 | -0.03 | 0.00 | -16.71 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPMt | -0.03 | -0.04 | -0.02 | 0.00 | -13.23 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM1 | 0.37 | 0.36 | 0.38 | 0.00 | 96.32 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM1 | 0.43 | 0.42 | 0.44 | 0.00 | 112.31 | 0.0000 | 1/1.0e+09 |
| Phenology model | TPDM1 | 0.38 | 0.37 | 0.39 | 0.00 | 94.79 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM2 | 0.01 | 0.00 | 0.02 | 0.00 | 1.84 | 0.0651 | 1/1.8 |
| Phenology model | PDM2 | 0.02 | 0.01 | 0.03 | 0.00 | 6.07 | 0.0000 | 1/9.9e+06 |
| Phenology model | TPDM2 | 0.03 | 0.02 | 0.04 | 0.00 | 7.36 | 0.0000 | 1/4.7e+10 |
| Phenology model | PIA _{GSI} | -0.02 | -0.03 | -0.02 | 0.00 | -8.16 | 0.0000 | 1/2.2e+13 |
| Phenology model | PIA ⁻ | -0.03 | -0.03 | -0.02 | 0.00 | -9.88 | 0.0000 | 1/1.0e+09 |
| Phenology model | PIA ⁺ | -0.03 | -0.03 | -0.02 | 0.00 | -9.96 | 0.0000 | 1/1.0e+09 |
| Phenology model | DM1 _{Za20} | 0.00 | -0.01 | 0.00 | 0.00 | -2.70 | 0.0069 | 1/8.6 |
| Phenology model | DM2 _{Za20} | -0.03 | -0.04 | -0.03 | 0.00 | -17.00 | 0.0000 | 1/1.0e+09 |
| Phenology model | SIAM _{Za20} | -0.04 | -0.05 | -0.03 | 0.00 | -14.23 | 0.0000 | 1/1.0e+09 |
| Phenology model | TDM _{Za20} | -0.06 | -0.06 | -0.05 | 0.00 | -20.19 | 0.0000 | 1/1.0e+09 |
| Phenology model | PDM _{Za20} | 0.00 | -0.01 | 0.01 | 0.00 | 0.73 | 0.4626 | 1/1.0 |
| Phenology model | TPDM _{Za20} | -0.02 | -0.03 | -0.01 | 0.00 | -5.34 | 0.0000 | 1/1.8e+05 |
| Optimization algorithm | EGO (norm.) | 0.08 | 0.08 | 0.09 | 0.00 | 68.49 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | 0.03 | 0.02 | 0.03 | 0.00 | 22.69 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | 0.09 | 0.09 | 0.09 | 0.00 | 73.07 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | 0.02 | 0.01 | 0.02 | 0.00 | 14.37 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | 0.01 | 0.01 | 0.02 | 0.00 | 12.63 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | CMA-ES (extd.) | 0.01 | 0.01 | 0.02 | 0.00 | 11.93 | 0.0000 | 1/1.0e+09 |
| Optimization algorithm | PSO (norm.) | 0.00 | 0.00 | 0.00 | 0.00 | -1.62 | 0.1044 | 1/1.4 |
| Optimization algorithm | PSO (extd.) | 0.00 | 0.00 | 0.00 | 0.00 | -0.47 | 0.6375 | 1/1.0 |
| Optimization algorithm | GenSA (extd.) | 0.00 | 0.00 | 0.00 | 0.00 | -0.34 | 0.7342 | 1/1.0 |
| Calibration sample | $\ln(s:S)$ | -0.02 | -0.02 | -0.02 | 0.00 | -111.02 | 0.0000 | 1/1.0e+09 |
| Calibration sample | $\ln(\bar{N}:q)$ | -0.06 | -0.07 | -0.06 | 0.00 | -25.42 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Full sample | 0.03 | 0.02 | 0.04 | 0.00 | 7.82 | 0.0000 | 1/1.4e+12 |
| Calibration sample | Rdm. (lwr.; MAT) | 0.06 | 0.05 | 0.06 | 0.00 | 29.15 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Rdm. (lwr.; AP) | 0.08 | 0.07 | 0.08 | 0.00 | 80.75 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Rdm. (upr.; AP) | 0.07 | 0.07 | 0.07 | 0.00 | 72.32 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Sys. (bal.; MAT) | 0.00 | 0.00 | 0.00 | 0.00 | 1.10 | 0.2718 | 1/1.0 |
| Calibration sample | Sys. (bal.; AP) | 0.02 | 0.02 | 0.02 | 0.00 | 21.51 | 0.0000 | 1/1.0e+09 |
| Calibration sample | Str. (MAT) | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.9960 | 1/1.0 |
| Calibration sample | Str. (AP) | 0.04 | 0.03 | 0.04 | 0.00 | 21.21 | 0.0000 | 1/1.0e+09 |

Adj. R²: 0.58 ; Dev. expl.: 0.58 ; n_{GAM}: 108,870

Calibration runs with NA values were excluded from calculation of statistics.

Note: See Table S9 for details.

S3 Estimated effects on model projections

Table S19. Range of coefficient estimates according to five samples and ranked according to their mean, for climate projection scenarios, phenology models, optimization algorithms, and calibration samples according to generalized additive models for 100-shifts in autumn phenology projected with site-specific models.

Projections according to site-specific phenology models

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(N:q) + s(\text{Site}) + s(\text{Species})$

| Climate projection scenario | Estimate range | Rank | Phenology model | Estimate range | Rank | Optimisation algorithm | Estimate range | Rank | Sampling procedure | Estimate range | Rank |
|-----------------------------|-----------------------------|------|----------------------|-----------------------------|------|------------------------|---------------------------|------|--------------------|--|------|
| RCP 4.5 & CMC 6 | -11.06 – -10.97 [d] *** ### | 1 | PDM1 | -11.85 – -11.50 [d] *** ### | 1 | GenSA (extd.) | -0.14 – -0.07 [d] . | 1 | Sys. (bal.; MAT) | -0.04 – +0.01 [d] | 1 |
| RCP 4.5 & CMC 8 | -10.84 – -10.81 [d] *** ### | 2 | TPDM1 | -11.10 – -10.86 [d] *** ### | 2 | GenSA(norm.) | ±0.00 [d] @ | 2 | Sys. (bal.; AP) | -0.05 – +0.04 [d] | 2 |
| RCP 4.5 & CMC 7 | -10.73 – -10.66 [d] *** ### | 3 | TDM1 | -10.01 – -9.81 [d] *** ### | 3 | PSO (norm.) | +0.15 – +0.22 [d] *** ### | 3 | Rdm. | ±0.00 [d] | 3 |
| RCP 4.5 & CMC 16 | -8.29 – -8.19 [d] *** ### | 4 | TPDM2 | -9.15 – -9.02 [d] *** ### | 4 | PSO (extd.) | +0.16 – +0.23 [d] *** ### | 4 | Sys. (bal.; YR) | -0.01 – +0.03 [d] | 4 |
| RCP 4.5 & CMC 4 | -7.33 – -7.22 [d] *** ### | 5 | TDM2 | -9.12 – -8.93 [d] *** ### | 5 | EGO (extd.) | +0.32 – +0.39 [d] *** ### | 5 | Sys. (cts.; MAT) | +0.02 – +0.05 [d] | 5 |
| RCP 4.5 & CMC 3 | -6.60 – -6.48 [d] *** ### | 6 | PDM2 | -8.73 – -8.60 [d] *** ### | 6 | TREGO (extd.) | +0.36 – +0.40 [d] *** ### | 6 | Sys. (cts.; YR) | +0.01 – +0.08 [d] | 6 |
| RCP 4.5 & CMC 13 | -6.42 – -6.34 [d] *** ### | 7 | TDM _{Za20} | -6.10 – -5.91 [d] *** ### | 7 | EGO (norm.) | +0.77 – +0.80 [d] *** ### | 7 | Sys. (cts.; AP) | +0.01 – +0.08 [d] | 7 |
| RCP 4.5 & CMC 9 | -5.76 – -5.68 [d] *** ### | 8 | SIAM | -6.01 – -5.83 [d] *** ### | 8 | TREGO (norm.) | +0.90 – +0.96 [d] *** ### | 8 | (N : q) | +0.03 – +0.05 [d (N : q) ⁻¹] *** ### | NA |
| RCP 4.5 & CMC 5 | -4.34 – -4.27 [d] *** ### | 9 | DM1 | -5.70 – -5.56 [d] *** ### | 9 | CMA-ES (extd.) | +1.94 – +2.02 [d] *** ### | 9 | | | |
| RCP 4.5 & CMC 10 | -3.96 – -3.87 [d] *** ### | 10 | DM2 _{Za20} | -4.64 – -4.53 [d] *** ### | 10 | CMA-ES (norm.) | +2.00 – +2.06 [d] *** ### | 10 | | | |
| RCP 4.5 & CMC 11 | -3.68 – -3.62 [d] *** ### | 11 | DM2 | -4.59 – -4.41 [d] *** ### | 11 | | | | | | |
| RCP 4.5 & CMC 15 | -3.18 – -3.05 [d] *** ### | 12 | SIAM _{Za20} | -4.00 – -3.81 [d] *** ### | 12 | | | | | | |
| RCP 4.5 & CMC 12 | -2.83 – -2.77 [d] *** ### | 13 | PDM _{Za20} | -2.82 – -2.63 [d] *** ### | 13 | | | | | | |
| RCP 8.5 & CMC 3 | -2.20 – -2.14 [d] *** ### | 14 | TPMp | -2.02 – -1.90 [d] *** ### | 14 | | | | | | |
| RCP 4.5 & CMC 14 | -1.45 – -1.39 [d] *** ### | 15 | DM1 _{Za20} | -1.18 – -1.09 [d] *** ### | 15 | | | | | | |
| RCP 8.5 & CMC 9 | -0.27 – -0.18 [d] *** ### | 16 | CDD | ±0.00 [d] @ | 16 | | | | | | |
| RCP 4.5 & CMC 1 | ±0.00 [d] @ | 17 | PIA _{GSI} | +0.45 – +0.66 [d] *** ### | 17 | | | | | | |
| RCP 8.5 & CMC 2 | +0.28 – +0.36 [d] *** ### | 18 | TPMt | +0.89 – +1.04 [d] *** ### | 18 | | | | | | |
| RCP 8.5 & CMC 5 | +0.41 – +0.51 [d] *** ### | 19 | TPDM _{Za20} | +0.91 – +1.11 [d] *** ### | 19 | | | | | | |
| RCP 8.5 & CMC 4 | +3.13 – +3.20 [d] *** ### | 20 | PIA ⁺ | +1.46 – +1.60 [d] *** ### | 20 | | | | | | |
| RCP 8.5 & CMC 8 | +3.92 – +4.04 [d] *** ### | 21 | PIA ⁺ | +1.73 – +1.84 [d] *** ### | 21 | | | | | | |
| RCP 8.5 & CMC 7 | +3.95 – +4.07 [d] *** ### | 22 | | | | | | | | | |
| RCP 8.5 & CMC 10 | +6.42 – +6.59 [d] *** ### | 23 | | | | | | | | | |
| RCP 8.5 & CMC 1 | +6.53 – +6.58 [d] *** ### | 24 | | | | | | | | | |
| RCP 8.5 & CMC 6 | +7.33 – +7.39 [d] *** ### | 25 | | | | | | | | | |
| RCP 4.5 & CMC 2 | +34.66 – +34.95 [d] *** ### | 26 | | | | | | | | | |

@ Reference (intercept): +10.02 – +10.29 [d] *** ###

Adj. R²: 0.5361–0.5397 ; Dev. expl.: 0.5363–0.5399 ; n_{GAM}: 5 × 2,600,000

Note: The abbreviations for the climate projection scenarios are explained in Supplement S1: Sect. 2. See Table S5 for further details.

Table S20. Range of coefficient estimates according to five samples and ranked according to their mean, for climate projection scenarios, phenology models, optimization algorithms, and calibration samples according to generalized additive models for 100-shifts in autumn phenology projected with species-specific models and within the sites of the sample.

Projections according to species-specific phenology models and within sample

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Climate projection scenario | Estimate range | Rank | Phenology model | Estimate range | Rank | Optimisation algorithm | Estimate range | Rank | Sampling procedure | Estimate range | Rank |
|-----------------------------|-----------------------------|------|----------------------|-----------------------------|------|------------------------|---------------------------|------|--------------------|--|------|
| RCP 4.5 & CMC 6 | -8.81 – -8.74 [d] *** ### | 1 | PDM1 | -11.98 – -11.85 [d] *** ### | 1 | GenSA(norm.) | ±0.00 [d] @ | 1 | Rdm. (lwr.; AP) | -5.63 – -5.59 [d] *** ### | 1 |
| RCP 4.5 & CMC 8 | -8.83 – -8.68 [d] *** ### | 2 | TPDM1 | -11.71 – -11.55 [d] *** ### | 2 | GenSA (extd.) | +0.06 – +0.10 [d] ** * | 2 | Str. (AP) | -1.95 – -1.71 [d] *** ### | 2 |
| RCP 4.5 & CMC 7 | -8.23 – -8.17 [d] *** ### | 3 | PDM2 | -11.24 – -11.15 [d] *** ### | 3 | PSO (extd.) | +0.33 – +0.37 [d] *** ### | 3 | Sys. (bal.; AP) | -0.27 – -0.21 [d] *** ### | 3 |
| RCP 4.5 & CMC 16 | -6.82 – -6.74 [d] *** ### | 4 | TPDM2 | -11.17 – -11.07 [d] *** ### | 4 | PSO (norm.) | +0.38 – +0.43 [d] *** ### | 4 | Rdm. (entire p.) | ±0.00 [d] @ | 4 |
| RCP 4.5 & CMC 4 | -6.05 – -5.90 [d] *** ### | 5 | TDM1 | -10.91 – -10.77 [d] *** ### | 5 | EGO (extd.) | +1.56 – +1.61 [d] *** ### | 5 | Sys. (bal.; MAT) | +0.04 – +0.07 [d] | 5 |
| RCP 4.5 & CMC 3 | -5.34 – -5.27 [d] *** ### | 6 | TDM _{2a20} | -10.77 – -10.66 [d] *** ### | 6 | TREGO (extd.) | +1.70 – +1.73 [d] *** ### | 6 | Full sample | +0.26 – +0.40 [d] *** ### | 6 |
| RCP 4.5 & CMC 13 | -5.04 – -4.97 [d] *** ### | 7 | TDM2 | -10.18 – -10.06 [d] *** ### | 7 | EGO (norm.) | +2.19 – +2.27 [d] *** ### | 7 | Str. (MAT) | +1.85 – +2.06 [d] *** ### | 7 |
| RCP 4.5 & CMC 9 | -4.30 – -4.24 [d] *** ### | 8 | DM1 | -8.83 – -8.70 [d] *** ### | 8 | CMA-ES (extd.) | +2.95 – +2.98 [d] *** ### | 8 | Rdm. (lwr.; MAT) | +2.65 – +2.71 [d] *** ### | 8 |
| RCP 4.5 & CMC 5 | -3.42 – -3.38 [d] *** ### | 9 | SIAM | -8.81 – -8.70 [d] *** ### | 9 | TREGO (norm.) | +3.02 – +3.09 [d] *** ### | 9 | Rdm. (upr.; AP) | +4.47 – +4.54 [d] *** ### | 9 |
| RCP 4.5 & CMC 11 | -2.93 – -2.89 [d] *** ### | 10 | DM2 | -7.48 – -7.36 [d] *** ### | 10 | CMA-ES (norm.) | +3.26 – +3.32 [d] *** ### | 10 | (s:S) | 0.00 – 0.00 [d s ⁻¹] *** ### | NA |
| RCP 4.5 & CMC 10 | -2.82 – -2.74 [d] *** ### | 11 | DM2 _{2a20} | -6.44 – -6.38 [d] *** ### | 11 | | | | ($\bar{N}:q$) | -0.22 – -0.21 [d (N:q) ⁻¹] *** ### | NA |
| RCP 4.5 & CMC 15 | -2.33 – -2.27 [d] *** ### | 12 | SIAM _{2a20} | -6.29 – -6.19 [d] *** ### | 12 | | | | | | |
| RCP 4.5 & CMC 12 | -1.99 – -1.87 [d] *** ### | 13 | TPMp | -6.01 – -5.90 [d] *** ### | 13 | | | | | | |
| RCP 8.5 & CMC 3 | -1.77 – -1.69 [d] *** ### | 14 | PDM _{2a20} | -5.01 – -4.92 [d] *** ### | 14 | | | | | | |
| RCP 4.5 & CMC 14 | -0.73 – -0.65 [d] *** ### | 15 | TPDM _{2a20} | -4.67 – -4.50 [d] *** ### | 15 | | | | | | |
| RCP 8.5 & CMC 9 | -0.29 – -0.22 [d] *** ### | 16 | DM1 _{2a20} | -4.43 – -4.31 [d] *** ### | 16 | | | | | | |
| RCP 4.5 & CMC 1 | ±0.00 [d] @ | 17 | PIA ⁻ | -3.75 – -3.68 [d] *** ### | 17 | | | | | | |
| RCP 8.5 & CMC 2 | +0.18 – +0.22 [d] *** ### | 18 | PIA ⁺ | -3.59 – -3.49 [d] *** ### | 18 | | | | | | |
| RCP 8.5 & CMC 5 | +0.55 – +0.59 [d] *** ### | 19 | PIA _{GSI} | -3.52 – -3.44 [d] *** ### | 19 | | | | | | |
| RCP 8.5 & CMC 4 | +2.72 – +2.77 [d] *** ### | 20 | TPMt | -2.73 – -2.65 [d] *** ### | 20 | | | | | | |
| RCP 8.5 & CMC 8 | +3.48 – +3.54 [d] *** ### | 21 | CDD | ±0.00 [d] @ | 21 | | | | | | |
| RCP 8.5 & CMC 7 | +3.55 – +3.62 [d] *** ### | 22 | | | | | | | | | |
| RCP 8.5 & CMC 10 | +5.00 – +5.17 [d] *** ### | 23 | | | | | | | | | |
| RCP 8.5 & CMC 1 | +5.28 – +5.41 [d] *** ### | 24 | | | | | | | | | |
| RCP 8.5 & CMC 6 | +5.81 – +5.95 [d] *** ### | 25 | | | | | | | | | |
| RCP 4.5 & CMC 2 | +40.99 – +41.24 [d] *** ### | 26 | | | | | | | | | |

@ Reference (intercept): +11.43 – +11.55 [d] *** ###

Adj. R²: 0.6705–0.6731 ; Dev. expl.: 0.6706–0.6733 ; n_{GAM}: 5× 2,600,000

Note: See Table S19 for details.

Table S21. Range of coefficient estimates according to five samples and ranked according to their mean, for climate projection scenarios, phenology models, optimization algorithms, and calibration samples according to generalized additive models for 100-shifts in autumn phenology projected with species-specific models and within the population.

Projections according to species-specific phenology models and within population

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Climate projection scenario | Estimate range | | Rank | Phenology model | Estimate range | | Rank | Optimisation algorithm | Estimate range | | Rank | Sampling procedure | Estimate range | | Rank |
|-----------------------------|---------------------|-----|------|----------------------|---------------------|-----|------|------------------------|-------------------|-----|------|--------------------|--|-----|------|
| RCP 4.5 & CMC 8 | -9.42 – -9.23 [d] | *** | 1 | PDM1 | -10.40 – -10.27 [d] | *** | 1 | GenSA(norm.) | ±0.00 [d] | @ | 1 | Rdm. (lwr.; AP) | -5.89 – -5.82 [d] | *** | 1 |
| RCP 4.5 & CMC 6 | -9.41 – -9.30 [d] | *** | 2 | TPDM1 | -10.35 – -10.22 [d] | *** | 2 | GenSA (extd.) | -0.03 – +0.06 [d] | | 2 | Str. (AP) | -2.58 – -2.42 [d] | *** | 2 |
| RCP 4.5 & CMC 7 | -8.82 – -8.76 [d] | *** | 3 | TDM1 | -9.89 – -9.69 [d] | *** | 3 | PSO (extd.) | +0.26 – +0.36 [d] | *** | 3 | Sys. (bal.; AP) | -0.38 – -0.34 [d] | *** | 3 |
| RCP 4.5 & CMC 16 | -7.31 – -7.20 [d] | *** | 4 | PDM2 | -8.64 – -8.51 [d] | *** | 4 | PSO (norm.) | +0.28 – +0.36 [d] | *** | 4 | Rdm. (entire p.) | ±0.00 [d] | @ | 4 |
| RCP 4.5 & CMC 4 | -6.40 – -6.33 [d] | *** | 5 | TPDM2 | -8.46 – -8.32 [d] | *** | 5 | EGO (extd.) | +1.22 – +1.35 [d] | *** | 5 | Sys. (bal.; MAT) | +0.83 – +0.87 [d] | *** | 5 |
| RCP 4.5 & CMC 3 | -5.67 – -5.55 [d] | *** | 6 | TDM2 | -8.07 – -7.95 [d] | *** | 6 | TREGO (extd.) | +1.33 – +1.40 [d] | *** | 6 | Rdm. (lwr.; MAT) | +0.98 – +1.04 [d] | *** | 6 |
| RCP 4.5 & CMC 13 | -5.52 – -5.37 [d] | *** | 7 | TDM _{2a20} | -7.54 – -7.46 [d] | *** | 7 | EGO (norm.) | +1.66 – +1.74 [d] | *** | 7 | Full sample | +1.19 – +1.50 [d] | *** | 7 |
| RCP 4.5 & CMC 9 | -4.73 – -4.58 [d] | *** | 8 | SIAM | -6.51 – -6.41 [d] | *** | 8 | TREGO (norm.) | +2.11 – +2.21 [d] | *** | 8 | Str. (MAT) | +1.95 – +2.05 [d] | *** | 8 |
| RCP 4.5 & CMC 5 | -3.74 – -3.58 [d] | *** | 9 | DM1 | -6.07 – -5.94 [d] | *** | 9 | CMA-ES (extd.) | +2.97 – +3.07 [d] | *** | 9 | Rdm. (upr.; AP) | +5.44 – +5.51 [d] | *** | 9 |
| RCP 4.5 & CMC 11 | -3.25 – -3.07 [d] | *** | 10 | DM2 _{2a20} | -4.94 – -4.80 [d] | *** | 10 | CMA-ES (norm.) | +3.04 – +3.09 [d] | *** | 10 | (s:S) | 0.00 – 0.00 [d s ⁻¹] | *** | NA |
| RCP 4.5 & CMC 10 | -3.20 – -3.08 [d] | *** | 11 | DM2 | -4.89 – -4.78 [d] | *** | 11 | | | | | ($\bar{N}:q$) | +0.07 – +0.08 [d (N:q) ⁻¹] | *** | NA |
| RCP 4.5 & CMC 15 | -2.58 – -2.46 [d] | *** | 12 | SIAM _{2a20} | -3.81 – -3.69 [d] | *** | 12 | | | | | | | | |
| RCP 4.5 & CMC 12 | -2.32 – -2.19 [d] | *** | 13 | TPMp | -3.57 – -3.42 [d] | *** | 13 | | | | | | | | |
| RCP 8.5 & CMC 3 | -1.96 – -1.81 [d] | *** | 14 | PDM _{2a20} | -2.71 – -2.57 [d] | *** | 14 | | | | | | | | |
| RCP 4.5 & CMC 14 | -0.94 – -0.81 [d] | *** | 15 | DM1 _{2a20} | -2.59 – -2.52 [d] | *** | 15 | | | | | | | | |
| RCP 8.5 & CMC 9 | -0.40 – -0.18 [d] | *** | 16 | TPDM _{2a20} | -1.41 – -1.29 [d] | *** | 16 | | | | | | | | |
| RCP 4.5 & CMC 1 | ±0.00 [d] | @ | 17 | PIA ⁻ | -0.84 – -0.70 [d] | *** | 17 | | | | | | | | |
| RCP 8.5 & CMC 2 | +0.09 – +0.21 [d] | * | 18 | PIA _{SSl} | -0.68 – -0.60 [d] | *** | 18 | | | | | | | | |
| RCP 8.5 & CMC 5 | +0.41 – +0.56 [d] | *** | 19 | PIA ⁺ | -0.44 – -0.35 [d] | *** | 19 | | | | | | | | |
| RCP 8.5 & CMC 4 | +2.68 – +2.85 [d] | *** | 20 | TPMt | -0.18 – -0.07 [d] | *** | 20 | | | | | | | | |
| RCP 8.5 & CMC 8 | +3.44 – +3.62 [d] | *** | 21 | CDD | ±0.00 [d] | @ | 21 | | | | | | | | |
| RCP 8.5 & CMC 7 | +3.56 – +3.68 [d] | *** | 22 | | | | | | | | | | | | |
| RCP 8.5 & CMC 10 | +5.36 – +5.51 [d] | *** | 23 | | | | | | | | | | | | |
| RCP 8.5 & CMC 1 | +5.61 – +5.73 [d] | *** | 24 | | | | | | | | | | | | |
| RCP 8.5 & CMC 6 | +6.08 – +6.23 [d] | *** | 25 | | | | | | | | | | | | |
| RCP 4.5 & CMC 2 | +37.18 – +37.59 [d] | *** | 26 | | | | | | | | | | | | |

@) Reference (intercept): +8.18 – +8.40 [d] ***

Adj. R²: 0.6438–0.6469 ; Dev. expl.: 0.6440–0.6471 ; n_{GAM}: 5× 2,600,000

Note: See Table S19 for details.

Table S22. Relative variance in the 100-shifts of autumn phenology (influence) explained by the evaluated factors when projected with site-specific models (top) or species-specific models within sample (middle) and within population (bottom).

Projections according to site-specific phenology models

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-------------------------|--------------------------|---------------------|-----------------------|--------------------------|
| CMC | 0.6426 (0.6417 – 0.6434) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6426 |
| Sites | 0.2375 (0.2367 – 0.2387) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8801 |
| Phenology models | 0.1142 (0.1139 – 0.1148) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9943 |
| Optimisation algorithms | 0.0047 (0.0046 – 0.0048) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9990 |
| Species | 0.0010 (0.0010 – 0.0011) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| Sampling procedures | 0.0000 (0.0000 – 0.0000) | 4.25e-04 – 0.1320 | 1/86 – 1/1.3 | 1.0000 |
| $\ln(\bar{N}:q)$ | 0.0000 (0.0000 – 0.0000) | 7.25e-11 – 1.53e-04 | 1/1.5e+08 – 1/207 | 1.0000 |

Adj. R^2 : 0.5361–0.5397 ; Dev. expl.: 0.5363–0.5399 ; n_{GAM} : $5 \times 2,600,000$

Projections according to species-specific phenology models and within sample

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-------------------------|--------------------------|---------------------|-----------------------|--------------------------|
| CMC | 0.5021 (0.5015 – 0.5028) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5021 |
| Sites | 0.4097 (0.4085 – 0.4103) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9118 |
| Phenology models | 0.0429 (0.0425 – 0.0431) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9547 |
| Sampling procedures | 0.0336 (0.0334 – 0.0339) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9883 |
| Optimisation algorithms | 0.0093 (0.0092 – 0.0093) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9976 |
| Species | 0.0021 (0.0020 – 0.0022) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9997 |
| $\ln(\bar{N}:q)$ | 0.0003 (0.0003 – 0.0003) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| $\ln(s:S)$ | 0.0000 (0.0000 – 0.0000) | 4.95e-41 – 1.20e-23 | 1/5.4e+37 – 1/4.0e+20 | 1.0000 |

Adj. R^2 : 0.6705–0.6731 ; Dev. expl.: 0.6706–0.6733 ; n_{GAM} : $5 \times 2,600,000$

Projections according to species-specific phenology models and within population

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-------------------------|--------------------------|-----------------------|-------------------------|--------------------------|
| Sites | 0.4596 (0.4590 – 0.4609) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4596 |
| CMC | 0.4233 (0.4219 – 0.4241) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8830 |
| Sampling procedures | 0.0586 (0.0583 – 0.0587) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9415 |
| Phenology models | 0.0486 (0.0484 – 0.0486) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9901 |
| Optimisation algorithms | 0.0073 (0.0072 – 0.0074) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9974 |
| Species | 0.0023 (0.0023 – 0.0024) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9997 |
| $\ln(s:S)$ | 0.0002 (0.0002 – 0.0002) | 7.11e-251 – 4.11e-221 | 1/5.2e+246 – 1/1.1e+217 | 0.9999 |
| $\ln(\bar{N}:q)$ | 0.0000 (0.0000 – 0.0000) | 1.04e-45 – 1.63e-33 | 1/2.3e+42 – 1/2.0e+30 | 0.9999 |

Adj. R^2 : 0.6438–0.6469 ; Dev. expl.: 0.6440–0.6471 ; n_{GAM} : $5 \times 2,600,000$

Note: The mean influence together with the influence range according to the five ANOVA based on five samples are given and cumulated according to decreasing influence, together with respective ranges of the p-value and minimum Bayes factors (BF01). See Table S8 for further details.

Table S23. Coefficient estimates for the effects of climate projection scenarios, phenology models, optimization algorithms, and calibration samples on the 100-shifts of autumn phenology when projected with site-specific models.

Note: The abbreviations for the climate projection scenarios are explained in Supplement S1: Sect. 2. See Table S9 for further details.

Projections according to site-specific phenology models

$$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(N:q) + s(\text{Site}) + s(\text{Species})$$

| Dimension | Coefficient | Estimate | CI _{95%} range | P value | BF ₀₁ |
|-----------------------------|---|-----------------|-------------------------|-----------------|-----------------------|
| Base Intercept | RCP 4.5 & CMC 1 CDD GenSA (norm.) Rdm. | +10.02 – +10.29 | +8.32 – +12.05 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 2 | +34.66 – +34.95 | +34.54 – +35.07 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 3 | -6.60 – -6.48 | -6.71 – -6.36 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 4 | -7.33 – -7.22 | -7.45 – -7.10 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 5 | -4.34 – -4.27 | -4.46 – -4.15 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 6 | -11.06 – -10.97 | -11.18 – -10.85 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 7 | -10.73 – -10.66 | -10.85 – -10.55 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 8 | -10.84 – -10.81 | -10.96 – -10.69 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 9 | -5.76 – -5.68 | -5.88 – -5.56 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 10 | -3.96 – -3.87 | -4.08 – -3.75 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 11 | -3.68 – -3.62 | -3.79 – -3.50 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 12 | -2.83 – -2.77 | -2.95 – -2.65 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 13 | -6.42 – -6.34 | -6.54 – -6.22 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 14 | -1.45 – -1.39 | -1.57 – -1.27 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 15 | -3.18 – -3.05 | -3.30 – -2.93 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 16 | -8.29 – -8.19 | -8.41 – -8.08 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 1 | +6.53 – +6.58 | +6.41 – +6.70 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 2 | +0.28 – +0.36 | +0.16 – +0.48 | 0.0000 – 0.0000 | 1/1.3e+12 – 1/1.5e+07 |
| Climate projection scenario | RCP 8.5 & CMC 3 | -2.20 – -2.14 | -2.32 – -2.03 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 4 | +3.13 – +3.20 | +3.01 – +3.32 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 5 | +0.41 – +0.51 | +0.29 – +0.62 | 0.0000 – 0.0000 | 1/5.9e+15 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 6 | +7.33 – +7.39 | +7.21 – +7.51 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 7 | +3.95 – +4.07 | +3.83 – +4.18 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 8 | +3.92 – +4.04 | +3.80 – +4.16 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 9 | -0.27 – -0.18 | -0.38 – -0.07 | 0.0000 – 0.0001 | 1/1.5e+06 – 1/459 |
| Climate projection scenario | RCP 8.5 & CMC 10 | +6.42 – +6.59 | +6.30 – +6.71 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM1 | -5.70 – -5.56 | -5.88 – -5.38 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM2 | -4.59 – -4.41 | -4.77 – -4.23 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | SIAM | -6.01 – -5.83 | -6.17 – -5.66 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPMp | -2.02 – -1.90 | -2.19 – -1.74 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPMt | +0.89 – +1.04 | +0.73 – +1.20 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM1 | -10.01 – -9.81 | -10.23 – -9.60 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM1 | -11.85 – -11.50 | -12.05 – -11.30 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM1 | -11.10 – -10.86 | -11.31 – -10.65 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM2 | -9.12 – -8.93 | -9.33 – -8.72 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM2 | -8.73 – -8.60 | -8.92 – -8.40 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM2 | -9.15 – -9.02 | -9.36 – -8.81 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA _{GS} | +0.45 – +0.66 | +0.27 – +0.84 | 0.0000 – 0.0000 | 1/1.2e+16 – 1/1.4e+08 |
| Phenology model | PIA ⁻ | +1.46 – +1.60 | +1.28 – +1.78 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA ⁺ | +1.73 – +1.84 | +1.55 – +2.02 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM1 _{Za20} | -1.18 – -1.09 | -1.32 – -0.96 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM2 _{Za20} | -4.64 – -4.53 | -4.77 – -4.40 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | SIAM _{Za20} | -4.00 – -3.81 | -4.18 – -3.63 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM _{Za20} | -6.10 – -5.91 | -6.28 – -5.73 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM _{Za20} | -2.82 – -2.63 | -3.00 – -2.45 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM _{Za20} | +0.91 – +1.11 | +0.72 – +1.31 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | +0.77 – +0.80 | +0.69 – +0.89 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | +0.32 – +0.39 | +0.24 – +0.48 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | +0.90 – +0.96 | +0.82 – +1.05 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | +0.36 – +0.40 | +0.27 – +0.49 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | +2.00 – +2.06 | +1.92 – +2.14 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | CMA-ES (extd.) | +1.94 – +2.02 | +1.85 – +2.10 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | PSO (norm.) | +0.15 – +0.22 | +0.06 – +0.31 | 0.0000 – 0.0000 | 1/2.9e+08 – 1/2.1e+03 |
| Optimization algorithm | PSO (extd.) | +0.16 – +0.23 | +0.08 – +0.32 | 0.0000 – 0.0000 | 1/3.9e+09 – 1/1.8e+04 |
| Optimization algorithm | GenSA (extd.) | -0.14 – -0.07 | -0.24 – +0.03 | 0.0002 – 0.0629 | 1/173 – 1/1.8 |
| Calibration sample | (N : q) | +0.03 – +0.05 | +0.01 – +0.07 | 0.0000 – 0.0001 | 1/3.8e+08 – 1/361 |
| Calibration sample | Sys. (cts.; YR) | +0.01 – +0.08 | -0.05 – +0.14 | 0.0006 – 0.6592 | 1/66 – 1/1.0 |
| Calibration sample | Sys. (cts.; MAT) | +0.02 – +0.05 | -0.04 – +0.11 | 0.0347 – 0.4739 | 1/2.7 – 1/1.0 |
| Calibration sample | Sys. (cts.; AP) | +0.01 – +0.08 | -0.05 – +0.14 | 0.0006 – 0.7694 | 1/65 – 1/1.0 |
| Calibration sample | Sys. (bal.; YR) | -0.01 – +0.03 | -0.07 – +0.09 | 0.2381 – 0.8585 | 1/1.0 – 1/1.0 |
| Calibration sample | Sys. (bal.; MAT) | -0.04 – +0.01 | -0.10 – +0.07 | 0.1069 – 0.8848 | 1/1.4 – 1/1.0 |
| Calibration sample | Sys. (bal.; AP) | -0.05 – +0.04 | -0.11 – +0.10 | 0.0516 – 0.9958 | 1/2.1 – 1/1.0 |

Adj. R² : 0.5361–0.5397 ; Dev. expl. : 0.5363–0.5399 ; n_{GAM} : 5×2,600,000

Table S24. Coefficient estimates for the effects of climate projection scenarios, phenology models, optimization algorithms, and calibration samples on the 100-shifts of autumn phenology when projected with species-specific models and within sample.

Note: See Table S23 for details.

Projections according to species-specific phenology models and within sample

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling pr.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Dimension | Coefficient | Estimate | CI _{99%} range | P value | BF ₀₁ |
|-----------------------------|---|-----------------|-------------------------|-----------------|-----------------------|
| Base Intercept | RCP 4.5 & CMC 1 CDD GenSA (norm.) Rdm. (entire p.) | +11.43 – +11.55 | +9.08 – +13.88 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 2 | +40.99 – +41.24 | +40.88 – +41.34 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 3 | -5.34 – -5.27 | -5.45 – -5.16 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 4 | -6.05 – -5.90 | -6.15 – -5.80 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 5 | -3.42 – -3.38 | -3.52 – -3.28 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 6 | -8.81 – -8.74 | -8.92 – -8.64 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 7 | -8.23 – -8.17 | -8.33 – -8.07 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 8 | -8.83 – -8.68 | -8.93 – -8.58 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 9 | -4.30 – -4.24 | -4.40 – -4.13 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 10 | -2.82 – -2.74 | -2.92 – -2.63 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 11 | -2.93 – -2.89 | -3.04 – -2.78 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 12 | -1.99 – -1.87 | -2.10 – -1.76 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 13 | -5.04 – -4.97 | -5.15 – -4.86 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 14 | -0.73 – -0.65 | -0.83 – -0.55 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 15 | -2.33 – -2.27 | -2.44 – -2.16 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 16 | -6.82 – -6.74 | -6.93 – -6.63 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 1 | +5.28 – +5.41 | +5.18 – +5.51 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 2 | +0.18 – +0.22 | +0.07 – +0.32 | 0.0000 – 0.0000 | 1/2.5e+05 – 1/2.4e+03 |
| Climate projection scenario | RCP 8.5 & CMC 3 | -1.77 – -1.69 | -1.88 – -1.58 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 4 | +2.72 – +2.77 | +2.61 – +2.88 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 5 | +0.55 – +0.59 | +0.45 – +0.69 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 6 | +5.81 – +5.95 | +5.70 – +6.05 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 7 | +3.55 – +3.62 | +3.45 – +3.72 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 8 | +3.48 – +3.54 | +3.38 – +3.64 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 9 | -0.29 – -0.22 | -0.39 – -0.12 | 0.0000 – 0.0000 | 1/1.2e+10 – 1/5.1e+05 |
| Climate projection scenario | RCP 8.5 & CMC 10 | +5.00 – +5.17 | +4.90 – +5.27 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM1 | -8.83 – -8.70 | -8.97 – -8.56 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM2 | -7.48 – -7.36 | -7.63 – -7.21 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | SIAM | -8.81 – -8.70 | -8.94 – -8.57 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPMp | -6.01 – -5.90 | -6.14 – -5.77 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPMt | -2.73 – -2.65 | -2.86 – -2.52 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM1 | -10.91 – -10.77 | -11.08 – -10.59 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM1 | -11.98 – -11.85 | -12.16 – -11.68 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM1 | -11.71 – -11.55 | -11.89 – -11.37 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM2 | -10.18 – -10.06 | -10.35 – -9.90 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM2 | -11.24 – -11.15 | -11.41 – -10.98 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM2 | -11.17 – -11.07 | -11.34 – -10.89 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA _{SSI} | -3.52 – -3.44 | -3.67 – -3.29 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA* | -3.75 – -3.68 | -3.90 – -3.54 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA† | -3.59 – -3.49 | -3.74 – -3.34 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM1 _{Za20} | -4.43 – -4.31 | -4.54 – -4.20 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM2 _{Za20} | -6.44 – -6.38 | -6.55 – -6.27 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | SIAM _{Za20} | -6.29 – -6.19 | -6.43 – -6.04 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM _{Za20} | -10.77 – -10.66 | -10.92 – -10.51 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM _{Za20} | -5.01 – -4.92 | -5.16 – -4.77 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM _{Za20} | -4.67 – -4.50 | -4.83 – -4.34 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | +2.19 – +2.27 | +2.12 – +2.33 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | +1.56 – +1.61 | +1.50 – +1.68 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | +3.02 – +3.09 | +2.95 – +3.16 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | +1.70 – +1.73 | +1.63 – +1.79 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | +3.26 – +3.32 | +3.19 – +3.39 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | CMA-ES (extd.) | +2.95 – +2.98 | +2.89 – +3.04 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | PSO (norm.) | +0.38 – +0.43 | +0.31 – +0.49 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | PSO (extd.) | +0.33 – +0.37 | +0.27 – +0.43 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | GenSA (extd.) | +0.06 – +0.10 | +0.00 – +0.16 | 0.0000 – 0.0078 | 1/1.6e+03 – 1/7.8 |
| Calibration sample | (s:S) | -0.56 – -0.42 | -0.66 – -0.31 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | (N̄:q) | -0.22 – -0.21 | -0.23 – -0.19 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Full sample | +0.26 – +0.40 | +0.14 – +0.51 | 0.0000 – 0.0000 | 1/3.1e+15 – 1/1.6e+06 |
| Calibration sample | Rdm. (lwr.; MAT) | +2.65 – +2.71 | +2.56 – +2.80 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Rdm. (lwr.; AP) | -5.63 – -5.59 | -5.68 – -5.53 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Rdm. (upr.; AP) | +4.47 – +4.54 | +4.42 – +4.59 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Sys. (bal.; MAT) | +0.04 – +0.07 | -0.02 – +0.12 | 0.0023 – 0.1019 | 1/21 – 1/1.4 |
| Calibration sample | Sys. (bal.; AP) | -0.27 – -0.21 | -0.32 – -0.15 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Str. (MAT) | +1.85 – +2.06 | +1.63 – +2.28 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Str. (AP) | -1.95 – -1.71 | -2.13 – -1.52 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |

Adj. R²: 0.6705–0.6731 ; Dev. expl.: 0.6706–0.6733 ; n_{SAM}: 5× 2,600,000

Table S25. Coefficient estimates for the effects of climate projection scenarios, phenology models, optimization algorithms, and calibration samples on the 100-shifts of autumn phenology when projected with species-specific models and within population.

Note: See Table S23 for details.

Projections according to species-specific phenology models and within population

$\Delta_{100} \sim \text{RCP\&CMC} + \text{Model} + \text{Alg.} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$

| Dimension | Coefficient | Estimate | CI _{95%} range | P value | BF ₀₁ |
|-----------------------------|---|-----------------|-------------------------|-----------------|-----------------------|
| Base Intercept | RCP 4.5 & CMC 1 CDD GenSA (norm.) Rdm. (entire p.) | +8.18 – +8.40 | +5.74 – +10.83 | 0.0000 – 0.0000 | 1/1.3e+16 – 1/1.3e+15 |
| Climate projection scenario | RCP 4.5 & CMC 2 | +37.18 – +37.59 | +37.06 – +37.70 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 3 | -5.67 – -5.55 | -5.78 – -5.43 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 4 | -6.40 – -6.33 | -6.52 – -6.22 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 5 | -3.74 – -3.58 | -3.85 – -3.47 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 6 | -9.41 – -9.30 | -9.52 – -9.18 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 7 | -8.82 – -8.76 | -8.94 – -8.64 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 8 | -9.42 – -9.23 | -9.54 – -9.11 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 9 | -4.73 – -4.58 | -4.84 – -4.47 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 10 | -3.20 – -3.08 | -3.32 – -2.97 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 11 | -3.25 – -3.07 | -3.36 – -2.95 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 12 | -2.32 – -2.19 | -2.44 – -2.07 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 13 | -5.52 – -5.37 | -5.63 – -5.26 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 14 | -0.94 – -0.81 | -1.06 – -0.69 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 15 | -2.58 – -2.46 | -2.69 – -2.34 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 4.5 & CMC 16 | -7.31 – -7.20 | -7.43 – -7.08 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 1 | +5.61 – +5.73 | +5.49 – +5.85 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 2 | +0.09 – +0.21 | -0.03 – +0.32 | 0.0000 – 0.0455 | 1/6.1e+03 – 1/2.2 |
| Climate projection scenario | RCP 8.5 & CMC 3 | -1.96 – -1.81 | -2.08 – -1.70 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 4 | +2.68 – +2.85 | +2.56 – +2.96 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 5 | +0.41 – +0.56 | +0.30 – +0.68 | 0.0000 – 0.0000 | 1/1.4e+17 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 6 | +6.08 – +6.23 | +5.96 – +6.35 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 7 | +3.56 – +3.68 | +3.45 – +3.80 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 8 | +3.44 – +3.62 | +3.33 – +3.74 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Climate projection scenario | RCP 8.5 & CMC 9 | -0.40 – -0.18 | -0.51 – -0.06 | 0.0000 – 0.0001 | 1/5.8e+15 – 1/432 |
| Climate projection scenario | RCP 8.5 & CMC 10 | +5.36 – +5.51 | +5.25 – +5.63 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM1 | -6.07 – -5.94 | -6.22 – -5.79 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM2 | -4.89 – -4.78 | -5.03 – -4.63 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | SIAM | -6.51 – -6.41 | -6.64 – -6.28 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPMp | -3.57 – -3.42 | -3.70 – -3.29 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPMt | -0.18 – -0.07 | -0.31 – +0.06 | 0.0007 – 0.1531 | 1/59 – 1/1.2 |
| Phenology model | TDM1 | -9.89 – -9.69 | -10.07 – -9.52 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM1 | -10.40 – -10.27 | -10.57 – -10.10 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM1 | -10.35 – -10.22 | -10.52 – -10.04 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM2 | -8.07 – -7.95 | -8.24 – -7.78 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM2 | -8.64 – -8.51 | -8.80 – -8.35 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM2 | -8.46 – -8.32 | -8.63 – -8.14 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA _{0SI} | -0.68 – -0.60 | -0.83 – -0.45 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA* | -0.84 – -0.70 | -0.98 – -0.55 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PIA† | -0.44 – -0.35 | -0.59 – -0.20 | 0.0000 – 0.0000 | 1/3.6e+11 – 1/1.2e+07 |
| Phenology model | DM1 _{Za20} | -2.59 – -2.52 | -2.70 – -2.40 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | DM2 _{Za20} | -4.94 – -4.80 | -5.05 – -4.69 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | SIAM _{Za20} | -3.81 – -3.69 | -3.96 – -3.55 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TDM _{Za20} | -7.54 – -7.46 | -7.69 – -7.31 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | PDM _{Za20} | -2.71 – -2.57 | -2.86 – -2.42 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Phenology model | TPDM _{Za20} | -1.41 – -1.29 | -1.58 – -1.13 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | EGO (norm.) | +1.66 – +1.74 | +1.59 – +1.82 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | EGO (extd.) | +1.22 – +1.35 | +1.14 – +1.42 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | TREGO (norm.) | +2.11 – +2.21 | +2.03 – +2.28 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | TREGO (extd.) | +1.33 – +1.40 | +1.26 – +1.47 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | CMA-ES (norm.) | +3.04 – +3.09 | +2.97 – +3.15 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | CMA-ES (extd.) | +2.97 – +3.07 | +2.90 – +3.14 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | PSO (norm.) | +0.28 – +0.36 | +0.21 – +0.43 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | PSO (extd.) | +0.26 – +0.36 | +0.20 – +0.42 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Optimization algorithm | GenSA (extd.) | -0.03 – +0.06 | -0.10 – +0.13 | 0.0139 – 0.7760 | 1/5.1 – 1/1.0 |
| Calibration sample | (s:S) | -1.61 – -1.52 | -1.73 – -1.39 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | (N̄:q) | +0.07 – +0.08 | +0.05 – +0.09 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Full sample | +1.19 – +1.50 | +0.92 – +1.76 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Rdm. (lwr.; MAT) | +0.98 – +1.04 | +0.89 – +1.13 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Rdm. (lwr.; AP) | -5.89 – -5.82 | -5.95 – -5.76 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Rdm. (upr.; AP) | +5.44 – +5.51 | +5.38 – +5.56 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Sys. (bal.; MAT) | +0.83 – +0.87 | +0.77 – +0.93 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Sys. (bal.; AP) | -0.38 – -0.34 | -0.44 – -0.28 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Str. (MAT) | +1.95 – +2.05 | +1.84 – +2.17 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |
| Calibration sample | Str. (AP) | -2.58 – -2.42 | -2.69 – -2.30 | 0.0000 – 0.0000 | 1/1.0e+09 – 1/1.0e+09 |

Adj. R²: 0.6438–0.6469 ; Dev. expl.: 0.6440–0.6471 ; n_{GAM}: 5* 2,600,000

S3.1 Estimated influence on variance in Δ_{100} per model

Table S26. Kendall rank correlation between ranked coefficients of explanatory variables for log-transformed root mean square error (RMSE) and 100-year shift of autumn phenology (top row) and between ranked coefficients of phenology models for $\ln(\text{RMSE})$ and the relative influence on Δ_{100} of the other factors (bottom row).

| Site-specific | | | | | Species-specific (calib. & proj. within sample) | | | | | Species-specific (calib. & proj. within population) | | | | |
|------------------------|--------|------------|-----------|----|--|--------|------------|-----------|----|--|--------|------------|-----------|----|
| Dimension | τ | p -value | BF_{01} | N | Dimension | τ | p -value | BF_{01} | N | Dimension | τ | p -value | BF_{01} | N |
| Phenology model | -0.32 | 0.0516 | 1/2.2 | 21 | Phenology model | -0.24 | 0.1356 | 1/1.3 | 21 | Phenology model | -0.35 | 0.0322 | 1/3.1 | 21 |
| Optimization algorithm | +0.28 | 0.2971 | 1/1 | 10 | Optimization algorithm | +0.50 | 0.0606 | 1/2.2 | 10 | Optimization algorithm | +0.33 | 0.2109 | 1/1.1 | 10 |
| Sampling prc. | +0.71 | 0.0243 | 1/5.1 | 7 | Sampling prc. | -0.06 | 0.8348 | 1/1 | 9 | Sampling prc. | -0.11 | 0.6767 | 1/1 | 9 |

| Site-specific | | | | | Species-specific (calib. & proj. within sample) | | | | | Species-specific (calib. & proj. within population) | | | | |
|-----------------|--------|------------|-----------|----|--|--------|------------|-----------|----|--|--------|------------|-----------|----|
| Dimension | τ | p -value | BF_{01} | N | Dimension | τ | p -value | BF_{01} | N | Dimension | τ | p -value | BF_{01} | N |
| RCP & CMC | -0.64 | 5.2e-05 | 1/788 | 21 | RCP & CMC | -0.20 | 0.2047 | 1/1.1 | 21 | RCP & CMC | -0.32 | 0.04 | 1/2.6 | 21 |
| Opt. algorithms | +0.32 | 0.043 | 1/2.5 | 21 | Opt. algorithms | +0.10 | 0.5065 | 1/1 | 21 | Opt. algorithms | +0.34 | 0.0297 | 1/3.3 | 21 |
| Sampling prc. | NA | NA | NA | 21 | Sampling prc. | -0.22 | 0.1648 | 1/1.2 | 21 | Sampling prc. | -0.30 | 0.0533 | 1/2.2 | 21 |
| N : q | -0.29 | 0.1031 | 1/1.5 | 21 | N : q | -0.01 | 0.9518 | 1/1 | 21 | N : q | -0.33 | 0.0429 | 1/2.5 | 21 |
| Sites | +0.59 | 0.000181 | 1/249 | 21 | s : S | +0.06 | 0.7117 | 1/1 | 21 | s : S | -0.09 | 0.5639 | 1/1 | 21 |
| Species | -0.14 | 0.3635 | 1/1 | 21 | Sites | +0.20 | 0.2047 | 1/1.1 | 21 | Sites | +0.12 | 0.4324 | 1/1 | 21 |
| | | | | | Species | -0.22 | 0.1556 | 1/1.2 | 21 | Species | +0.08 | 0.629 | 1/1 | 21 |

Note: The 100-year shifts were projected with site-specific models (left) and with species-specific models within sample (middle) or within population (right). Correlations in the bottom row were visualized in Figure S5 and derived from five ANOVAs per model, each based on a corresponding generalized additive model fitted to random samples of 105 projected 100-shifts of autumn phenology per model and projection mode. These ANOVAs were plotted in Figures S6–S8 and results are listed in Tables S27–S29.

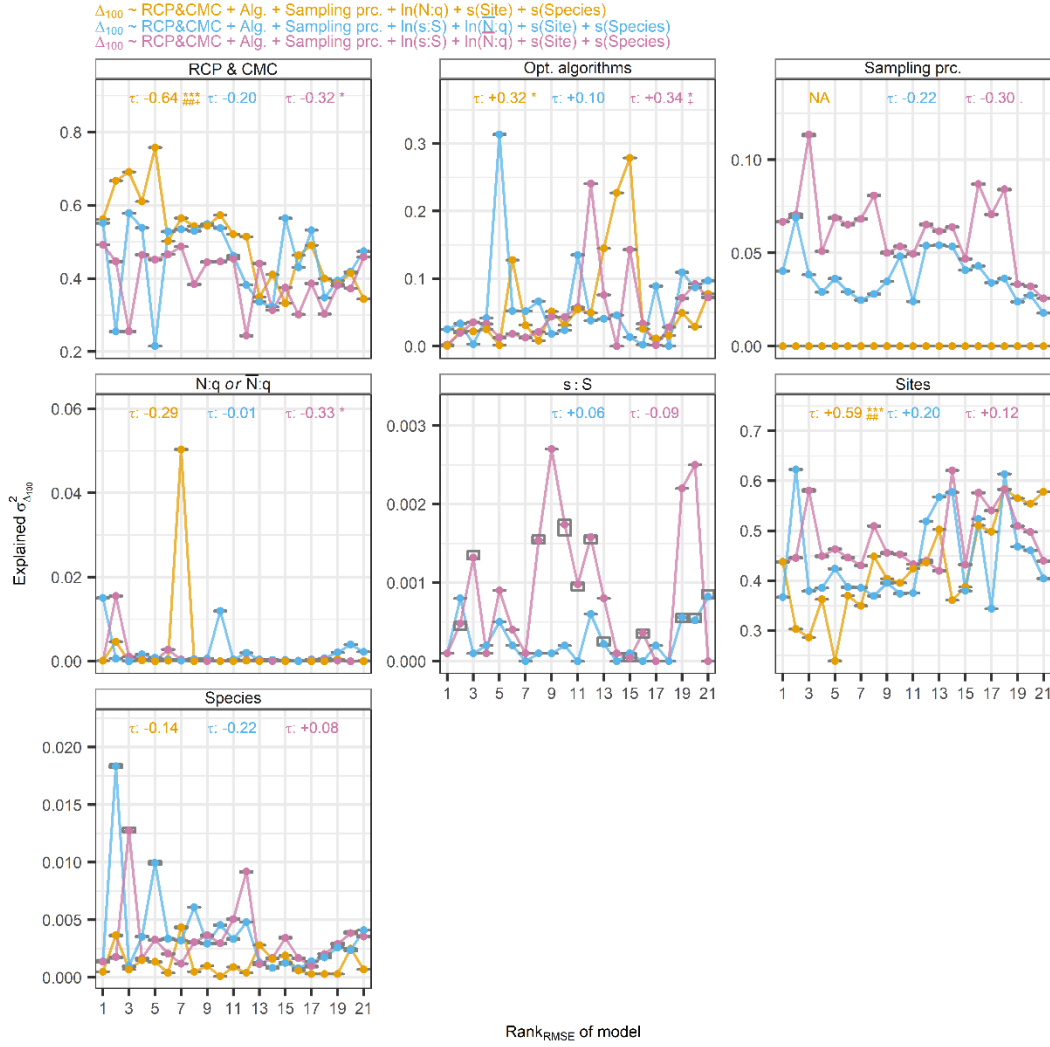


Figure S5. Relative influence of aggregated climate projection scenarios (RCP & CMC), optimization algorithms, sampling procedures, sample size proxies (N:q, \bar{N} :q, and s:S), sites and species per each of the 21 phenology models. The x-axis refers to the rank of the phenology models according to their estimated effect on model performance when only converging runs without NA values were considered. The y-axis refers to the relative influence, that was estimated with five ANOVAs based on a corresponding generalized additive model fitted to random samples of 105 projected 100-shifts of autumn phenology per model and projection mode. The entire range of estimated influence is plotted with error bars. The Kendall rank correlation (τ) between the influence and model rank is given together with the p-value and minim Bayes factor (see Figure 3 for the meaning of corresponding symbols).

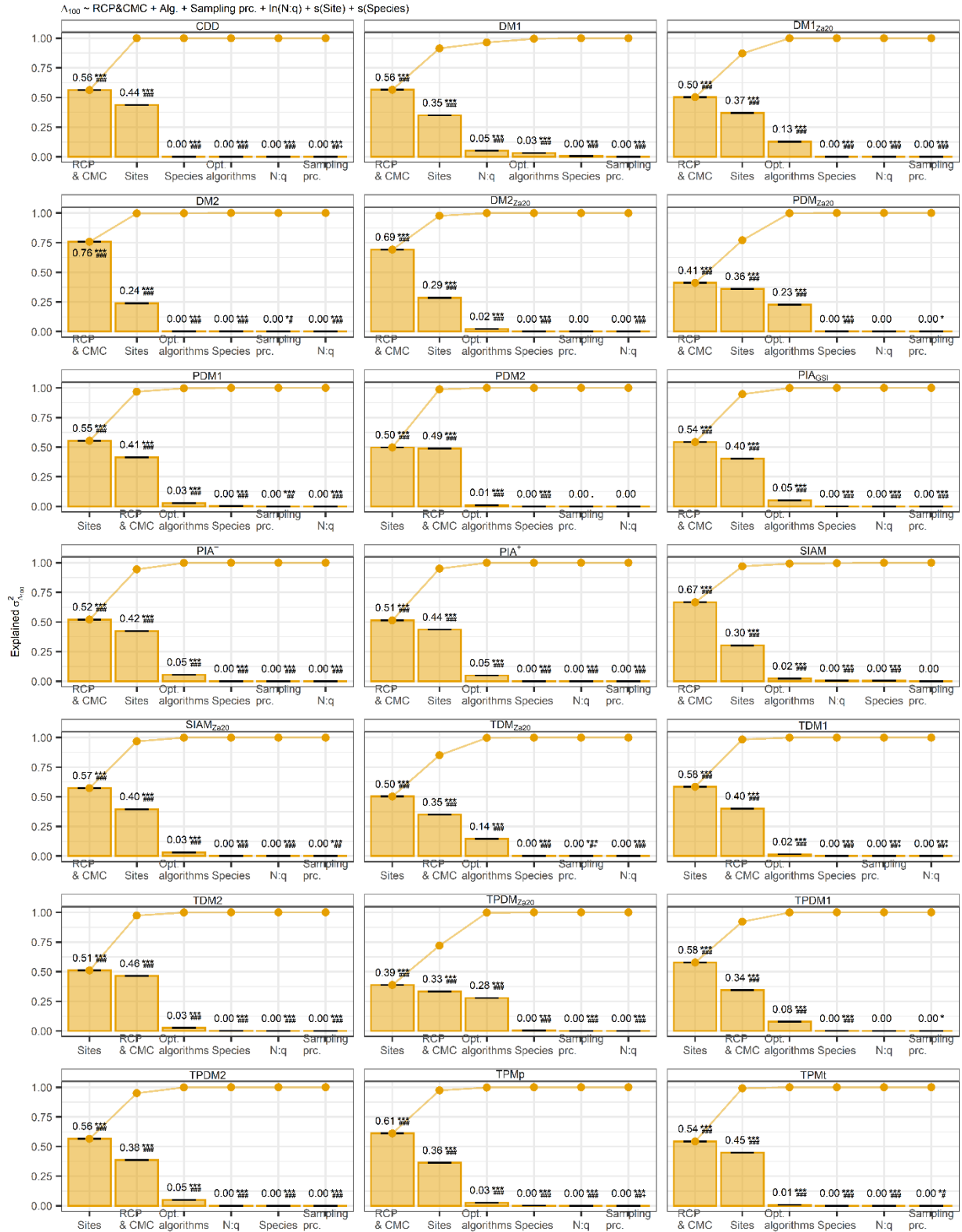


Figure S6. Estimated influence of the climate projection scenarios (i.e. representative concentration pathways, RCP, and climate model chains, CMC), optimization algorithms, and calibration samples on the 100-year shifts of autumn phenology at site level derived from site-specific models. Influence was estimated from the analyses of variance per phenology model based on five generalized additive models (GAM) from random samples from site-specific projections. The bars indicate the estimated mean influence on the variance in Δ_{100} , the connected dots show the cumulated mean influence, and the black error-bars indicate the range of estimated influence according to the five GAMs. The symbols for p-values and minimum Bayes factors are explained in the description of Figure 3 and abbreviations for the phenology models are explained in Supplement S2: Table S1.

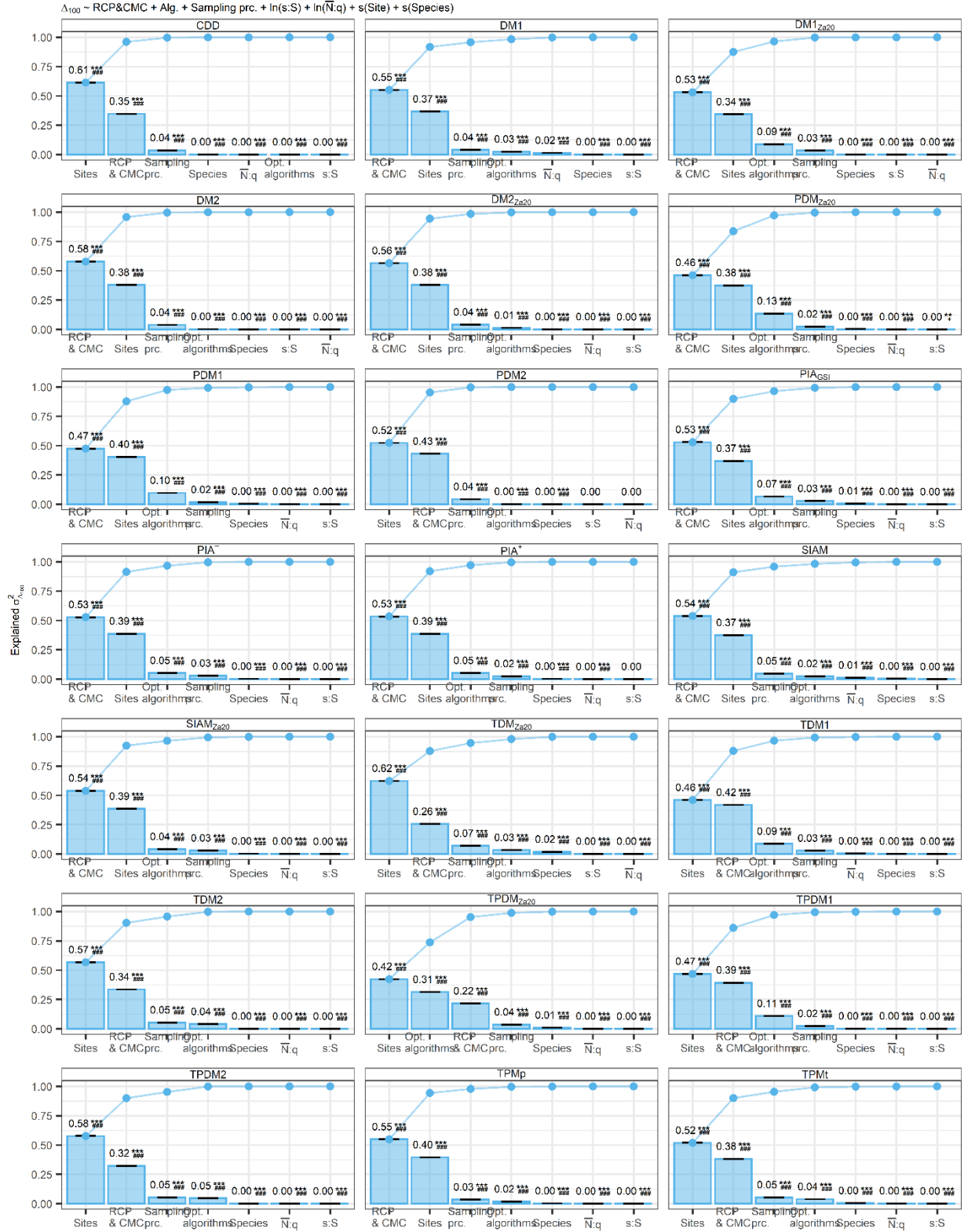


Figure S7. Estimated influence of the climate projection scenarios (i.e. representative concentration pathways, RCP, and climate model chains, CMC), optimization algorithms, and calibration samples on the 100-year shifts (Δ_{100}) of autumn phenology at site level derived from species-specific models and projected within sample. (See Figure S6 for description.)

33/42

Table S27. Relative variance in the 100-shifts of autumn phenology (influence) explained by the evaluated factors per model, when projected with site-specific models.

Projections according to site-specific phenology models
 $\Delta_{100} \sim \text{RCP\&CMC} + \text{Alg.} + \text{Sampling prc.} + \ln(\text{Nq}) + \text{s(Site)} + \text{s(Species)}$

Phenology model CDD

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|--------------------------|--------------------------|
| RCP & CMC | 0.5622 (0.5622 – 0.5622) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5622 |
| Sites | 0.4370 (0.4370 – 0.4370) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9992 |
| Species | 5e-04 (5e-04 – 5e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9997 |
| Opt. algorithms | 2e-04 (2e-04 – 2e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| Nq | 1e-04 (1e-04 – 1e-04) | 2.91e-284 – 2.91e-284 | 1/1.0e+280 – 1/1.0e+280 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 3.58e-05 – 3.58e-05 | 1/752 – 1/752 | 1.0000 |

Adj. R^2 : ~0.91 ; Dev. expl.: 5× 0.91 ; n_{SAM} : 5× 1,848,885

Phenology model DM1

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|--------------------------|--------------------------|
| RCP & CMC | 0.5649 (0.5647 – 0.5653) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5649 |
| Sites | 0.3493 (0.3490 – 0.3497) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9143 |
| Nq | 0.0503 (0.0503 – 0.0504) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9646 |
| Opt. algorithms | 0.0310 (0.0309 – 0.0311) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9956 |
| Species | 0.0044 (0.0043 – 0.0044) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 3.35e-14 – 2.29e-12 | 1/2.5e+11 – 1/4.2e+09 | 1.0000 |

Adj. R^2 : ~0.60 ; Dev. expl.: ~0.60 ; n_{SAM} : 5× 2,546,981

Phenology model DM1_{Z20}

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|--------------------------|--------------------------|
| RCP & CMC | 0.5023 (0.5023 – 0.5023) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5023 |
| Sites | 0.3698 (0.3698 – 0.3698) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8721 |
| Opt. algorithms | 0.1274 (0.1274 – 0.1274) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 |
| Species | 4e-04 (4e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| Nq | 1e-04 (1e-04 – 1e-04) | 2.05e-97 – 2.05e-97 | 1/5.3e+93 – 1/5.3e+93 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 2.19e-09 – 2.19e-09 | 1/6.0e+06 – 1/6.0e+06 | 1.0000 |

Adj. R^2 : 5× 0.67 ; Dev. expl.: 5× 0.67 ; n_{SAM} : 5× 2,394,651

Phenology model SiAM

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|--------------------------|--------------------------|
| RCP & CMC | 0.6669 (0.6667 – 0.6674) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6669 |
| Sites | 0.3029 (0.3024 – 0.3032) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9699 |
| Opt. algorithms | 0.0217 (0.0216 – 0.0219) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9916 |
| Nq | 0.0047 (0.0046 – 0.0047) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9963 |
| Species | 0.0037 (0.0036 – 0.0037) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 0.0939 – 0.7223 | 1/1.5 – 1/1.0 | 0.9999 |

Adj. R^2 : ~0.59 ; Dev. expl.: ~0.59 ; n_{SAM} : 5× 2,562,002

Phenology model TDM1

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|--------------------------|--------------------------|
| Sites | 0.5839 (0.5839 – 0.5839) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5839 |
| RCP & CMC | 0.4000 (0.4000 – 0.4000) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9839 |
| Opt. algorithms | 0.0157 (0.0157 – 0.0157) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| Species | 3e-04 (3e-04 – 3e-04) | 1.06e-110 – 1.06e-110 | 1/8.5e+106 – 1/8.5e+106 | 0.9999 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 2.62e-05 – 2.62e-05 | 1/995 – 1/995 | 0.9999 |
| Nq | 0.0000 (0.0000 – 0.0000) | 7.18e-05 – 7.18e-05 | 1/404 – 1/404 | 0.9999 |

Adj. R^2 : 5× 0.64 ; Dev. expl.: 5× 0.64 ; n_{SAM} : 5× 928,136

Phenology model PDM1

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|--------------------------|--------------------------|
| Sites | 0.5540 (0.5540 – 0.5540) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5540 |
| RCP & CMC | 0.4145 (0.4145 – 0.4145) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9685 |
| Opt. algorithms | 0.0289 (0.0289 – 0.0289) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9974 |
| Species | 0.0025 (0.0025 – 0.0025) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 2.62e-04 – 2.62e-04 | 1/130 – 1/130 | 0.9999 |
| Nq | 0.0000 (0.0000 – 0.0000) | 1.91e-12 – 1.91e-12 | 1/5.0e+09 – 1/5.0e+09 | 0.9999 |

Adj. R^2 : ~0.55 ; Dev. expl.: 5× 0.55 ; n_{SAM} : 5× 1,299,403

Phenology model TPDM1

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|--------------------------|--------------------------|
| Sites | 0.5779 (0.5779 – 0.5779) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5779 |
| RCP & CMC | 0.3441 (0.3441 – 0.3441) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9220 |
| Opt. algorithms | 0.0773 (0.0773 – 0.0773) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9993 |
| Species | 7e-04 (7e-04 – 7e-04) | 1.10e-198 – 1.10e-198 | 1/4.1e+194 – 1/4.1e+194 | 1.0000 |
| Nq | 0.0000 (0.0000 – 0.0000) | 0.7699 – 0.7699 | 1/1.0 – 1/1.0 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 0.0420 – 0.0420 | 1/2.4 – 1/2.4 | 1.0000 |

Adj. R^2 : 5× 0.51 ; Dev. expl.: 5× 0.51 ; n_{SAM} : 5× 1,248,201

Phenology model DM2

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|--------------------------|--------------------------|
| RCP & CMC | 0.7579 (0.7576 – 0.7584) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.7579 |
| Sites | 0.2390 (0.2385 – 0.2394) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9969 |
| Opt. algorithms | 0.0017 (0.0017 – 0.0017) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9986 |
| Species | 0.0014 (0.0013 – 0.0014) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 1.55e-07 – 0.0021 | 1/1.1e+05 – 1/22 | 1.0000 |
| Nq | 0.0000 (0.0000 – 0.0000) | 2.54e-36 – 1.27e-24 | 1/1.2e+33 – 1/3.6e+21 | 1.0000 |

Adj. R^2 : ~0.73 ; Dev. expl.: ~0.73 ; n_{SAM} : 5× 2,573,626

Table S27. Continued.

Phenology model DM2_{Zu20}

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-------------------------|--------------------------|
| RCP & CMC | 0.6911 (0.6911 – 0.6911) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6911 |
| Sites | 0.2862 (0.2862 – 0.2862) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9773 |
| Opt. algorithms | 0.0219 (0.0219 – 0.0219) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9992 |
| Species | 7e-04 (7e-04 – 7e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 0.1758 – 0.1758 | 1/1.1 – 1/1.1 | 0.9999 |
| N;q | 0.0000 (0.0000 – 0.0000) | 8.02e-25 – 8.02e-25 | 1/5.6e+21 – 1/5.6e+21 | 0.9999 |

Adj. R²: 5× 0.77 ; Dev. expl.: 5× 0.77 ; η_{GAM} : 5× 2,446,041

Phenology model TDM2

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| Sites | 0.5106 (0.5106 – 0.5106) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5106 |
| RCP & CMC | 0.4633 (0.4633 – 0.4633) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9739 |
| Opt. algorithms | 0.0254 (0.0254 – 0.0254) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9993 |
| Species | 6e-04 (6e-04 – 6e-04) | 3.10e-178 – 3.10e-178 | 1/1.7e+172 – 1/1.7e+172 | 0.9999 |
| N;q | 1e-04 (1e-04 – 1e-04) | 1.41e-26 – 1.41e-26 | 1/3.0e+23 – 1/3.0e+23 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 9.91e-08 – 9.91e-08 | 1/1.7e+05 – 1/1.7e+05 | 1.0000 |

Adj. R²: 5× 0.56 ; Dev. expl.: 5× 0.56 ; η_{GAM} : 5× 1,065,011

Phenology model PDM2

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-------------------------|--------------------------|
| Sites | 0.4978 (0.4978 – 0.4978) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4978 |
| RCP & CMC | 0.4905 (0.4905 – 0.4905) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9883 |
| Opt. algorithms | 0.0114 (0.0114 – 0.0114) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9997 |
| Species | 3e-04 (3e-04 – 3e-04) | 6.92e-67 – 6.92e-67 | 1/2.3e+63 – 1/2.3e+63 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 0.0622 – 0.0622 | 1/1.9 – 1/1.9 | 1.0000 |
| N;q | 0.0000 (0.0000 – 0.0000) | 0.7431 – 0.7431 | 1/1.0 – 1/1.0 | 1.0000 |

Adj. R²: 5× 0.42 ; Dev. expl.: ~0.42 ; η_{GAM} : 5× 1,470,561

Phenology model TPDM2

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| Sites | 0.5650 (0.5650 – 0.5650) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5650 |
| RCP & CMC | 0.3849 (0.3849 – 0.3849) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9499 |
| Opt. algorithms | 0.0493 (0.0493 – 0.0493) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9992 |
| N;q | 5e-04 (5e-04 – 5e-04) | 9.52e-117 – 9.52e-117 | 1/9.2e+112 – 1/9.2e+112 | 0.9997 |
| Species | 3e-04 (3e-04 – 3e-04) | 1.70e-71 – 1.70e-71 | 1/8.7e+67 – 1/8.7e+67 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 6.63e-07 – 6.63e-07 | 1/2.8e+04 – 1/2.8e+04 | 1.0000 |

Adj. R²: 5× 0.42 ; Dev. expl.: ~0.42 ; η_{GAM} : 5× 1,445,150

Phenology model TPMt

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-------------------------|--------------------------|
| RCP & CMC | 0.5433 (0.5433 – 0.5433) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5433 |
| Sites | 0.4482 (0.4482 – 0.4482) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9915 |
| Opt. algorithms | 0.0081 (0.0081 – 0.0081) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| Species | 5e-04 (5e-04 – 5e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0001 |
| N;q | 0.0000 (0.0000 – 0.0000) | 8.21e-50 – 8.21e-50 | 1/2.7e+46 – 1/2.7e+46 | 1.0001 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 0.0025 – 0.0025 | 1/20 – 1/20 | 1.0001 |

Adj. R²: 5× 0.72 ; Dev. expl.: 5× 0.72 ; η_{GAM} : 5× 2,025,657

Phenology model TPMp

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.6105 (0.6105 – 0.6105) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6105 |
| Sites | 0.3625 (0.3625 – 0.3625) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9730 |
| Opt. algorithms | 0.0252 (0.0252 – 0.0252) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9982 |
| Species | 0.0015 (0.0015 – 0.0015) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9997 |
| N;q | 2e-04 (2e-04 – 2e-04) | 3.74e-137 – 3.74e-137 | 1/2.0e+133 – 1/2.0e+133 | 0.9999 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 2.82e-05 – 2.82e-05 | 1/929 – 1/929 | 0.9999 |

Adj. R²: 5× 0.62 ; Dev. expl.: 5× 0.62 ; η_{GAM} : 5× 1,995,369Phenology model SIAM_{Zu20}

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.5733 (0.5733 – 0.5733) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5733 |
| Sites | 0.3954 (0.3954 – 0.3954) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9687 |
| Opt. algorithms | 0.0311 (0.0311 – 0.0311) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| Species | 1e-04 (1e-04 – 1e-04) | 1.53e-127 – 1.53e-127 | 1/5.3e+123 – 1/5.3e+123 | 0.9999 |
| N;q | 0.0000 (0.0000 – 0.0000) | 1.14e-22 – 1.14e-22 | 1/4.4e+19 – 1/4.4e+19 | 0.9999 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 1.97e-04 – 1.97e-04 | 1/167 – 1/167 | 0.9999 |

Adj. R²: 5× 0.61 ; Dev. expl.: ~0.61 ; η_{GAM} : 5× 2,506,004Phenology model TDM_{Zu20}

| Factor | Influence | P value | <u>BF_{all}</u> | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-------------------------|--------------------------|
| Sites | 0.5023 (0.5023 – 0.5023) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5023 |
| RCP & CMC | 0.3498 (0.3498 – 0.3498) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8521 |
| Opt. algorithms | 0.1450 (0.1450 – 0.1450) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9971 |
| Species | 0.0028 (0.0028 – 0.0028) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 4.32e-04 – 4.32e-04 | 1/84 – 1/84 | 0.9999 |
| N;q | 0.0000 (0.0000 – 0.0000) | 8.20e-09 – 8.20e-09 | 1/1.7e+06 – 1/1.7e+06 | 0.9999 |

Adj. R²: 5× 0.42 ; Dev. expl.: 5× 0.42 ; η_{GAM} : 5× 1,928,981

Table S27. Continued.Phenology model PDM_{7x20}

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.4105 (0.4105 – 0.4105) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4105 |
| Sites | 0.3608 (0.3608 – 0.3608) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.7713 |
| Opt. algorithms | 0.2271 (0.2271 – 0.2271) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9984 |
| Species | 0.0016 (0.0016 – 0.0016) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| N;q | 0.0000 (0.0000 – 0.0000) | 0.8424 – 0.8424 | 1/1.0 – 1/1.0 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 0.0353 – 0.0353 | 1/2.6 – 1/2.6 | 1.0000 |

Adj. R²: ~0.51 ; Dev. expl.: 5× 0.51 ; n_{GAM}: 5× 2,332,142Phenology model TPDM_{7x20}

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.3871 (0.3871 – 0.3871) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.3871 |
| RCP & CMC | 0.3323 (0.3323 – 0.3323) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.7194 |
| Opt. algorithms | 0.2787 (0.2787 – 0.2787) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9981 |
| Species | 0.0019 (0.0019 – 0.0019) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 4.85e-09 – 4.85e-09 | 1/2.8e+06 – 1/2.8e+06 | 1.0000 |
| N;q | 0.0000 (0.0000 – 0.0000) | 2.76e-18 – 2.76e-18 | 1/2.3e+15 – 1/2.3e+15 | 1.0000 |

Adj. R²: ~0.52 ; Dev. expl.: ~0.52 ; n_{GAM}: 5× 1,731,414Phenology model PIA_{SS}

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.5435 (0.5435 – 0.5435) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5435 |
| Sites | 0.4039 (0.4039 – 0.4039) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9474 |
| Opt. algorithms | 0.0515 (0.0515 – 0.0515) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9989 |
| Species | 0.0010 (0.0010 – 0.0010) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| N;q | 1e-04 (1e-04 – 1e-04) | 1.72e-60 – 1.72e-60 | 1/1.0e+57 – 1/1.0e+57 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 1.00e-22 – 1.00e-22 | 1/5.0e+19 – 1/5.0e+19 | 1.0000 |

Adj. R²: 5× 0.63 ; Dev. expl.: 5× 0.63 ; n_{GAM}: 5× 2,226,607Phenology model PIA⁺

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.5143 (0.5143 – 0.5143) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5143 |
| Sites | 0.4359 (0.4359 – 0.4359) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9502 |
| Opt. algorithms | 0.0493 (0.0493 – 0.0493) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 |
| Species | 4e-04 (4e-04 – 4e-04) | 2.28e-301 – 2.28e-301 | 1/1.3e+297 – 1/1.3e+297 | 0.9999 |
| N;q | 1e-04 (1e-04 – 1e-04) | 5.26e-60 – 5.26e-60 | 1/3.4e+56 – 1/3.4e+56 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 1.61e-09 – 1.61e-09 | 1/8.0e+06 – 1/8.0e+06 | 1.0000 |

Adj. R²: 5× 0.59 ; Dev. expl.: 5× 0.59 ; n_{GAM}: 5× 2,325,867Phenology model PIA⁺

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.5207 (0.5207 – 0.5207) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5207 |
| Sites | 0.4237 (0.4237 – 0.4237) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9444 |
| Opt. algorithms | 0.0547 (0.0547 – 0.0547) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9991 |
| Species | 9e-04 (9e-04 – 9e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| Sampling prc. | 0.0000 (0.0000 – 0.0000) | 8.93e-11 – 8.93e-11 | 1/1.3e+08 – 1/1.3e+08 | 1.0000 |
| N;q | 0.0000 (0.0000 – 0.0000) | 1.58e-17 – 1.58e-17 | 1/4.2e+14 – 1/4.2e+14 | 1.0000 |

Adj. R²: ~0.59 ; Dev. expl.: 5× 0.59 ; n_{GAM}: 5× 2,272,116*Note:* See Table S22 for further details.

Table S28. Relative variance in the 100-shifts of autumn phenology (influence) explained by the evaluated factors per model, when projected with species-specific models within sample.

Projections according to species-specific phenology models and within sample

$$\Delta_{100} \sim \text{RCP \& CMC} + \text{Alg.} + \text{Sampling prc.} + \ln(s:S) + \ln(\bar{N}:q) + s(\text{Site}) + s(\text{Species})$$

Phenology model CDD

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| Sites | 0.6135 (0.6132 – 0.6138) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6135 |
| RCP & CMC | 0.3474 (0.3472 – 0.3477) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9609 |
| Sampling prc. | 0.0363 (0.0363 – 0.0364) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9973 |
| Species | 0.0017 (0.0017 – 0.0018) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9990 |
| $\bar{N}:q$ | 7e-04 (7e-04 – 7e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9997 |
| Opt. algorithms | 3e-04 (3e-04 – 3e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| s:S | 0.0000 (0.0000 – 0.0000) | 4.05e-284 – 6.42e-249 | 1/7.8e+279 – 1/5.8e+244 | 1.0000 |

Adj. R^2 : -0.91 ; Dev. expl.: -0.91 ; n_{SAM} : 5× 2,500,000

Phenology model DM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.5514 (0.5507 – 0.5520) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5514 |
| Sites | 0.3666 (0.3661 – 0.3671) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9181 |
| Sampling prc. | 0.0403 (0.0401 – 0.0405) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9584 |
| Opt. algorithms | 0.0251 (0.0249 – 0.0253) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9835 |
| $\bar{N}:q$ | 0.0150 (0.0150 – 0.0151) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9985 |
| Species | 0.0014 (0.0013 – 0.0015) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| s:S | 1e-04 (1e-04 – 1e-04) | 3.16e-204 – 4.52e-166 | 1/1.5e+200 – 1/1.3e+162 | 1.0000 |

Adj. R^2 : -0.79 ; Dev. expl.: -0.79 ; n_{SAM} : 5× 2,600,000

Phenology model DM1₂₀₀

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.5316 (0.5314 – 0.5319) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5316 |
| Sites | 0.3438 (0.3436 – 0.3439) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8754 |
| Opt. algorithms | 0.0888 (0.0886 – 0.0891) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9642 |
| Sampling prc. | 0.0340 (0.0339 – 0.0341) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9981 |
| Species | 0.0014 (0.0014 – 0.0014) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 |
| s:S | 2e-04 (2e-04 – 2e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9997 |
| $\bar{N}:q$ | 2e-04 (2e-04 – 2e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |

Adj. R^2 : -0.78 ; Dev. expl.: -0.78 ; n_{SAM} : 5× 2,600,000

Phenology model SIAM

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|----------------------|------------------------|--------------------------|
| RCP & CMC | 0.5377 (0.5366 – 0.5385) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5377 |
| Sites | 0.3737 (0.3731 – 0.3748) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9115 |
| Sampling prc. | 0.0481 (0.0479 – 0.0482) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9596 |
| Opt. algorithms | 0.0237 (0.0236 – 0.0239) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9833 |
| $\bar{N}:q$ | 0.0119 (0.0119 – 0.0120) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9953 |
| Species | 0.0045 (0.0045 – 0.0046) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| s:S | 2e-04 (2e-04 – 2e-04) | 0.00e+00 – 7.95e-287 | 1/1.0e+09 – 1/3.9e+282 | 1.0000 |

Adj. R^2 : -0.72 ; Dev. expl.: -0.72 ; n_{SAM} : 5× 2,600,000

Phenology model TDM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.4602 (0.4599 – 0.4608) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4602 |
| RCP & CMC | 0.4186 (0.4184 – 0.4189) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8788 |
| Opt. algorithms | 0.0869 (0.0866 – 0.0873) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9657 |
| Sampling prc. | 0.0274 (0.0273 – 0.0274) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9931 |
| $\bar{N}:q$ | 0.0040 (0.0039 – 0.0040) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9971 |
| Species | 0.0024 (0.0023 – 0.0024) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 |
| s:S | 5e-04 (5e-04 – 6e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |

Adj. R^2 : -0.74 ; Dev. expl.: -0.74 ; n_{SAM} : 5× 2,506,152

Phenology model PDM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.4742 (0.4738 – 0.4747) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4742 |
| Sites | 0.4041 (0.4037 – 0.4044) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8763 |
| Opt. algorithms | 0.0967 (0.0966 – 0.0969) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9750 |
| Sampling prc. | 0.0178 (0.0177 – 0.0178) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9928 |
| Species | 0.0041 (0.0041 – 0.0041) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9969 |
| $\bar{N}:q$ | 0.0022 (0.0022 – 0.0022) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9991 |
| s:S | 8e-04 (8e-04 – 9e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |

Adj. R^2 : -0.73 ; Dev. expl.: -0.73 ; n_{SAM} : 5× 2,502,881

Phenology model TPDM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.4679 (0.4676 – 0.4683) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4679 |
| RCP & CMC | 0.3938 (0.3931 – 0.3941) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8616 |
| Opt. algorithms | 0.1093 (0.1091 – 0.1095) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9709 |
| Sampling prc. | 0.0238 (0.0237 – 0.0240) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9948 |
| Species | 0.0026 (0.0026 – 0.0026) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9974 |
| $\bar{N}:q$ | 0.0021 (0.0021 – 0.0021) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 |
| s:S | 6e-04 (5e-04 – 6e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |

Adj. R^2 : -0.68 ; Dev. expl.: -0.68 ; n_{SAM} : 5× 2,509,147

Phenology model DM2

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|-----------------|--------------------------|----------------------|-----------------------|--------------------------|
| RCP & CMC | 0.5783 (0.5778 – 0.5790) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5783 |
| Sites | 0.3792 (0.3785 – 0.3796) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9575 |
| Sampling prc. | 0.0384 (0.0383 – 0.0385) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9980 |
| Opt. algorithms | 0.0030 (0.0030 – 0.0031) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9990 |
| Species | 0.0010 (9e-04 – 0.0010) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| s:S | 1e-04 (1e-04 – 1e-04) | 0.00e+00 – 1.48e-322 | 1/1.0e+09 – 1/inf | 1.0001 |
| $\bar{N}:q$ | 0.0000 (0.0000 – 0.0000) | 3.81e-10 – 1.67e-05 | 1/3.2e+07 – 1/1.5e+03 | 1.0001 |

Adj. R^2 : -0.88 ; Dev. expl.: -0.88 ; n_{SAM} : 5× 2,600,000

Table S28. Continued.

Phenology model DM2_{Ta20}

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.5648 (0.5644 – 0.5652) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5648 |
| Sites | 0.3793 (0.3789 – 0.3796) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9441 |
| Sampling prc. | 0.0407 (0.0406 – 0.0409) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9848 |
| Opt. algorithms | 0.0135 (0.0135 – 0.0136) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9984 |
| Species | 0.0013 (0.0012 – 0.0013) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| N _q | 3e-04 (3e-04 – 3e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| s:S | 1e-04 (1e-04 – 1e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |

Adj. R²: ~0.89 ; Dev. expl.: ~0.89 ; n_{GM}: 5 × 2,600,000

Phenology model TDM2

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.5673 (0.5670 – 0.5676) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5673 |
| RCP & CMC | 0.3363 (0.3360 – 0.3366) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9035 |
| Sampling prc. | 0.0541 (0.0540 – 0.0542) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9576 |
| Opt. algorithms | 0.0404 (0.0403 – 0.0405) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9981 |
| Species | 0.0013 (0.0013 – 0.0013) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9994 |
| N _q | 4e-04 (4e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| s:S | 2e-04 (2e-04 – 3e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |

Adj. R²: ~0.74 ; Dev. expl.: ~0.74 ; n_{GM}: 5 × 2,592,274

Phenology model PDM2

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.5234 (0.5232 – 0.5237) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5234 |
| RCP & CMC | 0.4305 (0.4301 – 0.4307) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9539 |
| Sampling prc. | 0.0430 (0.0429 – 0.0431) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9969 |
| Opt. algorithms | 0.0023 (0.0023 – 0.0024) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9992 |
| Species | 8e-04 (8e-04 – 8e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| s:S | 0.0000 (0.0000 – 0.0000) | 0.2966 – 0.9101 | 1/1.0 – 1/1.0 | 1.0000 |
| N _q | 0.0000 (0.0000 – 0.0000) | 0.0139 – 0.8063 | 1/5.1 – 1/1.0 | 1.0000 |

Adj. R²: ~0.77 ; Dev. expl.: ~0.77 ; n_{GM}: 5 × 2,600,000

Phenology model TPDM2

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.5771 (0.5765 – 0.5773) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5771 |
| RCP & CMC | 0.3223 (0.3221 – 0.3226) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8994 |
| Sampling prc. | 0.0534 (0.0533 – 0.0535) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9528 |
| Opt. algorithms | 0.0460 (0.0458 – 0.0462) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9988 |
| Species | 8e-04 (8e-04 – 9e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| N _q | 3e-04 (3e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| s:S | 0.0000 (0.0000 – 0.0000) | 1.13e-30 – 2.79e-24 | 1/3.2e+27 – 1/1.7e+21 | 0.9999 |

Adj. R²: ~0.69 ; Dev. expl.: ~0.69 ; n_{GM}: 5 × 2,587,444

Phenology model TPMt

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.5187 (0.5184 – 0.5191) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5187 |
| RCP & CMC | 0.3820 (0.3817 – 0.3822) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9006 |
| Sampling prc. | 0.0539 (0.0539 – 0.0540) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9546 |
| Opt. algorithms | 0.0380 (0.0378 – 0.0381) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9925 |
| Species | 0.0048 (0.0048 – 0.0048) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9973 |
| N _q | 0.0020 (0.0020 – 0.0020) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9993 |
| s:S | 6e-04 (6e-04 – 6e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |

Adj. R²: ~0.75 ; Dev. expl.: ~0.75 ; n_{GM}: 5 × 2,568,997

Phenology model TPMp

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.5485 (0.5478 – 0.5490) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5485 |
| Sites | 0.3952 (0.3946 – 0.3960) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9437 |
| Sampling prc. | 0.0347 (0.0346 – 0.0348) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9784 |
| Opt. algorithms | 0.0181 (0.0180 – 0.0181) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9964 |
| Species | 0.0029 (0.0029 – 0.0030) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9994 |
| N _q | 6e-04 (6e-04 – 6e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| s:S | 1e-04 (1e-04 – 1e-04) | 7.65e-123 – 1.20e-105 | 1/1.1e+119 – 1/8.3e+101 | 1.0001 |

Adj. R²: ~0.75 ; Dev. expl.: ~0.75 ; n_{GM}: 5 × 2,600,000

Phenology model SIAM_{Ta20}

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.5385 (0.5378 – 0.5391) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5385 |
| Sites | 0.3854 (0.3849 – 0.3860) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9239 |
| Opt. algorithms | 0.0417 (0.0416 – 0.0418) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9656 |
| Sampling prc. | 0.0290 (0.0289 – 0.0291) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9947 |
| Species | 0.0035 (0.0035 – 0.0036) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9982 |
| N _q | 0.0016 (0.0016 – 0.0017) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| s:S | 2e-04 (2e-04 – 2e-04) | 9.06e-268 – 3.33e-251 | 1/3.8e+263 – 1/1.1e+247 | 1.0000 |

Adj. R²: ~0.70 ; Dev. expl.: ~0.70 ; n_{GM}: 5 × 2,600,000

Phenology model TDM_{Ta20}

| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.6226 (0.6218 – 0.6235) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6226 |
| RCP & CMC | 0.2552 (0.2543 – 0.2560) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8778 |
| Sampling prc. | 0.0689 (0.0687 – 0.0692) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9467 |
| Opt. algorithms | 0.0335 (0.0333 – 0.0338) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9802 |
| Species | 0.0183 (0.0182 – 0.0185) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9985 |
| s:S | 8e-04 (8e-04 – 8e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9993 |
| N _q | 6e-04 (6e-04 – 7e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |

Adj. R²: ~0.52 ; Dev. expl.: ~0.52 ; n_{GM}: 5 × 2,600,000

Table S28. Continued.Phenology model PDM_{JA20}

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.4621 (0.4613 – 0.4629) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4621 |
| Sites | 0.3754 (0.3749 – 0.3758) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8375 |
| Opt. algorithms | 0.1349 (0.1346 – 0.1354) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9723 |
| Sampling prc. | 0.0239 (0.0238 – 0.0241) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9963 |
| Species | 0.0033 (0.0033 – 0.0034) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| \bar{N}_q | 4e-04 (4e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| s:S | 0.0000 (0.0000 – 0.0000) | 3.14e-08 – 0.0092 | 1/4.9e+05 – 1/6.9 | 1.0000 |

Adj. R²: ~0.67 ; Dev. expl.: ~0.67 ; n_{GM}: 5 × 2,600,000Phenology model TPDM_{JA20}

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| Sites | 0.4237 (0.4229 – 0.4245) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4237 |
| Opt. algorithms | 0.3135 (0.3129 – 0.3139) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.7372 |
| RCP & CMC | 0.2154 (0.2150 – 0.2158) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9526 |
| Sampling prc. | 0.0362 (0.0361 – 0.0364) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9888 |
| Species | 0.0099 (0.0098 – 0.0101) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9987 |
| \bar{N}_q | 8e-04 (8e-04 – 8e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 |
| s:S | 5e-04 (5e-04 – 5e-04) | 2.96e-310 – 2.53e-285 | 1/9.5e+305 – 1/1.2e+281 | 1.0000 |

Adj. R²: ~0.50 ; Dev. expl.: ~0.50 ; n_{GM}: 5 × 2,600,000Phenology model PIA_{GS}

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|----------------------|-----------------------|--------------------------|
| RCP & CMC | 0.5296 (0.5289 – 0.5301) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5296 |
| Sites | 0.3693 (0.3688 – 0.3699) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8988 |
| Opt. algorithms | 0.0665 (0.0664 – 0.0666) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9653 |
| Sampling prc. | 0.0280 (0.0279 – 0.0282) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9933 |
| Species | 0.0061 (0.0061 – 0.0061) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9994 |
| \bar{N}_q | 5e-04 (5e-04 – 6e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| s:S | 1e-04 (1e-04 – 1e-04) | 1.81e-101 – 1.48e-87 | 1/5.7e+97 – 1/8.1e+83 | 1.0000 |

Adj. R²: ~0.71 ; Dev. expl.: ~0.71 ; n_{GM}: 5 × 2,600,000Phenology model PIA⁺

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.5344 (0.5337 – 0.5350) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5344 |
| Sites | 0.3857 (0.3851 – 0.3863) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9201 |
| Opt. algorithms | 0.0520 (0.0518 – 0.0522) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9721 |
| Sampling prc. | 0.0247 (0.0246 – 0.0248) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9967 |
| Species | 0.0032 (0.0032 – 0.0032) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| \bar{N}_q | 1e-04 (1e-04 – 1e-04) | 6.30e-161 – 2.06e-139 | 1/1.0e+157 – 1/3.6e+135 | 1.0000 |
| s:S | 0.0000 (0.0000 – 0.0000) | 1.10e-07 – 0.1911 | 1/1.5e+05 – 1/1.1 | 1.0000 |

Adj. R²: ~0.70 ; Dev. expl.: ~0.70 ; n_{GM}: 5 × 2,600,000Phenology model PIA⁺

| Factor | Influence | P value | BF_{all} | Cumulated mean influence |
|-----------------|--------------------------|----------------------|------------------------|--------------------------|
| RCP & CMC | 0.5278 (0.5268 – 0.5288) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5278 |
| Sites | 0.3867 (0.3858 – 0.3878) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9145 |
| Opt. algorithms | 0.0523 (0.0522 – 0.0524) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9668 |
| Sampling prc. | 0.0292 (0.0291 – 0.0293) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9960 |
| Species | 0.0034 (0.0033 – 0.0034) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9994 |
| \bar{N}_q | 4e-04 (4e-04 – 5e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| s:S | 2e-04 (2e-04 – 2e-04) | 0.00e+00 – 6.38e-297 | 1/1.0e+09 – 1/4.7e+292 | 1.0000 |

Adj. R²: ~0.71 ; Dev. expl.: ~0.71 ; n_{GM}: 5 × 2,600,000*Note:* See Table S22 for further details.

Table S29. Relative variance in the 100-shifts of autumn phenology (influence) explained by the evaluated factors per model, when projected with species-specific models within population.

Projections according to species-specific phenology models and within population

 $\Delta_{100} \sim \text{RCP \& CMC} + \text{Alg.} + \text{Sampling prc.} + \ln(\text{s:S}) + \ln(\bar{\text{N}}_q) + \text{s(Site)} + \text{s(Species)}$

Phenology model CDD

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|-----------------------|-------------------------|--------------------------|
| Sites | 0.6208 (0.6205 – 0.6212) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6208 |
| RCP & CMC | 0.3134 (0.3130 – 0.3138) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9342 |
| Sampling prc. | 0.0639 (0.0638 – 0.0641) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9981 |
| Species | 0.0017 (0.0017 – 0.0017) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| s:S | 1e-04 (1e-04 – 1e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| $\bar{\text{N}}_q$ | 0.0000 (0.0000 – 0.0000) | 3.00e-07 – 0.0259 | 1/5.9e+04 – 1/3.3 | 0.9999 |
| Opt. algorithms | 0.0000 (0.0000 – 0.0000) | 1.71e-189 – 1.15e-153 | 1/3.0e+185 – 1/5.7e+149 | 0.9999 |

Adj. R^2 : ~0.89 ; Dev. expl.: ~0.89 ; n_{OAM} : 5× 2,500,000

Phenology model DM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.4468 (0.4453 – 0.4479) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4468 |
| Sites | 0.4453 (0.4444 – 0.4463) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8921 |
| Sampling prc. | 0.0706 (0.0700 – 0.0710) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9627 |
| Opt. algorithms | 0.0196 (0.0194 – 0.0197) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9823 |
| $\bar{\text{N}}_q$ | 0.0155 (0.0154 – 0.0156) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9978 |
| Species | 0.0018 (0.0017 – 0.0018) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| s:S | 5e-04 (4e-04 – 5e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0001 |

Adj. R^2 : ~0.72 ; Dev. expl.: ~0.72 ; n_{OAM} : 5× 2,600,000Phenology model DM1_{2x20}

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.4410 (0.4404 – 0.4413) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4410 |
| Sites | 0.4194 (0.4190 – 0.4201) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8604 |
| Opt. algorithms | 0.0759 (0.0759 – 0.0760) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9363 |
| Sampling prc. | 0.0616 (0.0615 – 0.0618) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9979 |
| Species | 0.0011 (0.0011 – 0.0012) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9991 |
| s:S | 8e-04 (8e-04 – 8e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| $\bar{\text{N}}_q$ | 1e-04 (1e-04 – 2e-04) | 4.92e-235 – 1.28e-195 | 1/8.2e+230 – 1/3.9e+191 | 1.0000 |

Adj. R^2 : ~0.72 ; Dev. expl.: ~0.72 ; n_{OAM} : 5× 2,600,000

Phenology model SIAM

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.4657 (0.4653 – 0.4665) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4657 |
| Sites | 0.4459 (0.4453 – 0.4465) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9117 |
| Sampling prc. | 0.0652 (0.0649 – 0.0655) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9768 |
| Opt. algorithms | 0.0180 (0.0179 – 0.0182) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9949 |
| $\bar{\text{N}}_q$ | 0.0027 (0.0027 – 0.0028) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9976 |
| Species | 0.0021 (0.0020 – 0.0021) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| s:S | 4e-04 (4e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |

Adj. R^2 : ~0.67 ; Dev. expl.: ~0.67 ; n_{OAM} : 5× 2,600,000

Phenology model TDM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.5094 (0.5089 – 0.5099) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5094 |
| RCP & CMC | 0.3812 (0.3802 – 0.3821) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8906 |
| Opt. algorithms | 0.0711 (0.0704 – 0.0716) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9617 |
| Sampling prc. | 0.0332 (0.0331 – 0.0334) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9949 |
| Species | 0.0029 (0.0028 – 0.0030) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9978 |
| s:S | 0.0022 (0.0022 – 0.0022) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| $\bar{\text{N}}_q$ | 1e-04 (1e-04 – 1e-04) | 4.45e-81 – 1.30e-62 | 1/2.9e+77 – 1/1.3e+59 | 1.0001 |

Adj. R^2 : ~0.59 ; Dev. expl.: ~0.59 ; n_{OAM} : 5× 2,569,633

Phenology model PDM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|---------------------|-----------------------|--------------------------|
| RCP & CMC | 0.4590 (0.4583 – 0.4595) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4590 |
| Sites | 0.4396 (0.4387 – 0.4400) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8985 |
| Opt. algorithms | 0.0722 (0.0719 – 0.0726) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9707 |
| Sampling prc. | 0.0256 (0.0256 – 0.0257) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9964 |
| Species | 0.0035 (0.0035 – 0.0036) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| $\bar{\text{N}}_q$ | 0.0000 (0.0000 – 1e-04) | 5.59e-54 – 6.88e-38 | 1/3.6e+50 – 1/4.2e+34 | 0.9999 |
| s:S | 0.0000 (0.0000 – 0.0000) | 2.81e-13 – 2.36e-06 | 1/3.2e+10 – 1/8.6e+03 | 0.9999 |

Adj. R^2 : ~0.65 ; Dev. expl.: ~0.65 ; n_{OAM} : 5× 2,538,957

Phenology model TPDM1

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|---------------------|-----------------------|--------------------------|
| Sites | 0.4972 (0.4969 – 0.4976) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4972 |
| RCP & CMC | 0.3723 (0.3722 – 0.3725) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8695 |
| Opt. algorithms | 0.0919 (0.0916 – 0.0924) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9615 |
| Sampling prc. | 0.0321 (0.0319 – 0.0324) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9936 |
| Species | 0.0038 (0.0038 – 0.0040) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9974 |
| s:S | 0.0025 (0.0025 – 0.0025) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| $\bar{\text{N}}_q$ | 0.0000 (0.0000 – 0.0000) | 5.59e-05 – 0.5805 | 1/505 – 1/1.0 | 0.9999 |

Adj. R^2 : ~0.55 ; Dev. expl.: ~0.55 ; n_{OAM} : 5× 2,600,000

Phenology model DM2

| Factor | Influence | P value | BF_{01} | Cumulated mean influence |
|--------------------|--------------------------|-----------------------|-------------------------|--------------------------|
| RCP & CMC | 0.4919 (0.4915 – 0.4928) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4919 |
| Sites | 0.4376 (0.4367 – 0.4381) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9295 |
| Sampling prc. | 0.0667 (0.0666 – 0.0669) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9962 |
| Opt. algorithms | 0.0022 (0.0022 – 0.0023) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9985 |
| Species | 0.0014 (0.0013 – 0.0014) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| s:S | 1e-04 (1e-04 – 1e-04) | 2.52e-290 – 3.84e-263 | 1/1.2e+286 – 1/9.1e+258 | 0.9999 |
| $\bar{\text{N}}_q$ | 1e-04 (1e-04 – 1e-04) | 3.29e-232 – 7.47e-215 | 1/1.2e+228 – 1/6.0e+210 | 1.0000 |

Adj. R^2 : ~0.83 ; Dev. expl.: ~0.83 ; n_{OAM} : 5× 2,600,000

Table S29. Continued.

| Phenology model DM _{2x20} | | | | | Phenology model TDM2 | | | | |
|---|--------------------------|-----------------------|-------------------------|--------------------------|---|--------------------------|-----------------------|-------------------------|--------------------------|
| Factor | Influence | P value | BF ₀₁ | Cumulated mean influence | Factor | Influence | P value | BF ₀₁ | Cumulated mean influence |
| RCP & CMC | 0.4871 (0.4865 – 0.4877) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4871 | Sites | 0.5760 (0.5753 – 0.5767) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5760 |
| Sites | 0.4304 (0.4296 – 0.4310) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9175 | RCP & CMC | 0.3016 (0.3007 – 0.3022) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8775 |
| Sampling prc. | 0.0682 (0.0680 – 0.0684) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9857 | Sampling prc. | 0.0869 (0.0867 – 0.0873) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9645 |
| Opt. algorithms | 0.0126 (0.0125 – 0.0127) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9983 | Opt. algorithms | 0.0334 (0.0332 – 0.0335) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9979 |
| Species | 0.0012 (0.0012 – 0.0012) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 | Species | 0.0017 (0.0016 – 0.0017) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9995 |
| N _q | 4e-04 (3e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 | s:S | 4e-04 (3e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| s:S | 1e-04 (1e-04 – 1e-04) | 5.35e-216 – 5.07e-190 | 1/8.4e+211 – 1/1.0e+186 | 1.0000 | N _q | 1e-04 (1e-04 – 1e-04) | 8.90e-169 – 4.21e-145 | 1/6.7e+164 – 1/1.7e+141 | 1.0000 |
| Adj. R ² : ~0.84 ; Dev. expl.: ~0.84 ; n _{0AM} : 5× 2,600,000 | | | | | Adj. R ² : ~0.72 ; Dev. expl.: ~0.72 ; n _{0AM} : 5× 2,600,000 | | | | |
| Phenology model PDM2 | | | | | Phenology model TPDM2 | | | | |
| Factor | Influence | P value | BF ₀₁ | Cumulated mean influence | Factor | Influence | P value | BF ₀₁ | Cumulated mean influence |
| Sites | 0.5402 (0.5391 – 0.5415) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5402 | Sites | 0.5823 (0.5818 – 0.5824) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5823 |
| RCP & CMC | 0.3864 (0.3854 – 0.3874) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9266 | RCP & CMC | 0.3030 (0.3026 – 0.3035) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8853 |
| Sampling prc. | 0.0707 (0.0704 – 0.0709) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9973 | Sampling prc. | 0.0842 (0.0837 – 0.0844) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9695 |
| Opt. algorithms | 0.0013 (0.0013 – 0.0014) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9986 | Opt. algorithms | 0.0281 (0.0280 – 0.0283) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9976 |
| Species | 0.0010 (9e-04 – 0.0010) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 | Species | 0.0020 (0.0020 – 0.0021) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9996 |
| N _q | 4e-04 (4e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 | N _q | 4e-04 (3e-04 – 4e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| s:S | 0.0000 (0.0000 – 0.0000) | 3.98e-30 – 1.03e-20 | 1/9.3e+26 – 1/5.3e+17 | 1.0000 | s:S | 0.0000 (0.0000 – 0.0000) | 1.54e-21 – 4.57e-12 | 1/3.4e+18 – 1/2.2e+09 | 1.0000 |
| Adj. R ² : ~0.74 ; Dev. expl.: ~0.74 ; n _{0AM} : 5× 2,600,000 | | | | | Adj. R ² : ~0.68 ; Dev. expl.: ~0.68 ; n _{0AM} : 5× 2,600,000 | | | | |
| Phenology model TPMt | | | | | Phenology model TPMp | | | | |
| Factor | Influence | P value | BF ₀₁ | Cumulated mean influence | Factor | Influence | P value | BF ₀₁ | Cumulated mean influence |
| Sites | 0.5092 (0.5088 – 0.5101) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5092 | Sites | 0.4630 (0.4622 – 0.4639) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4630 |
| RCP & CMC | 0.3840 (0.3829 – 0.3846) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8932 | RCP & CMC | 0.4513 (0.4503 – 0.4524) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9143 |
| Sampling prc. | 0.0808 (0.0805 – 0.0811) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9740 | Sampling prc. | 0.0689 (0.0684 – 0.0692) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9832 |
| Opt. algorithms | 0.0213 (0.0212 – 0.0214) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9953 | Opt. algorithms | 0.0126 (0.0125 – 0.0127) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9958 |
| Species | 0.0031 (0.0030 – 0.0031) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9983 | Species | 0.0033 (0.0032 – 0.0033) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9990 |
| s:S | 0.0015 (0.0015 – 0.0016) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 | s:S | 9e-04 (9e-04 – 9e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| N _q | 1e-04 (1e-04 – 1e-04) | 2.11e-165 – 5.40e-133 | 1/2.9e+161 – 1/1.4e+129 | 1.0000 | N _q | 1e-04 (1e-04 – 1e-04) | 3.50e-184 – 1.62e-162 | 1/1.5e+180 – 1/3.8e+158 | 1.0000 |
| Adj. R ² : ~0.71 ; Dev. expl.: ~0.71 ; n _{0AM} : 5× 2,600,000 | | | | | Adj. R ² : ~0.70 ; Dev. expl.: ~0.70 ; n _{0AM} : 5× 2,600,000 | | | | |
| Phenology model SIAM _{2x20} | | | | | Phenology model TDM _{2x20} | | | | |
| Factor | Influence | P value | BF ₀₁ | Cumulated mean influence | Factor | Influence | P value | BF ₀₁ | Cumulated mean influence |
| RCP & CMC | 0.4645 (0.4640 – 0.4663) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4645 | Sites | 0.5802 (0.5788 – 0.5824) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.5802 |
| Sites | 0.4491 (0.4476 – 0.4499) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9137 | RCP & CMC | 0.2557 (0.2531 – 0.2566) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8359 |
| Sampling prc. | 0.0509 (0.0507 – 0.0511) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9646 | Sampling prc. | 0.1134 (0.1127 – 0.1137) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9493 |
| Opt. algorithms | 0.0332 (0.0330 – 0.0333) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9978 | Opt. algorithms | 0.0356 (0.0353 – 0.0358) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9849 |
| Species | 0.0017 (0.0016 – 0.0017) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9994 | Species | 0.0127 (0.0126 – 0.0130) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9977 |
| N _q | 5e-04 (4e-04 – 5e-04) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 | s:S | 0.0013 (0.0013 – 0.0014) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9990 |
| s:S | 1e-04 (1e-04 – 1e-04) | 4.89e-105 – 2.09e-80 | 1/2.0e+101 – 1/6.3e+76 | 1.0000 | N _q | 0.0011 (0.0010 – 0.0011) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| Adj. R ² : ~0.65 ; Dev. expl.: ~0.65 ; n _{0AM} : 5× 2,600,000 | | | | | Adj. R ² : ~0.53 ; Dev. expl.: ~0.53 ; n _{0AM} : 5× 2,600,000 | | | | |

Table S29. Continued.

| Phenology model PDM _{7d20} | | | | | Phenology model TPDM _{7d20} | | | | |
|-------------------------------------|--------------------------|-----------------------|------------------------|--------------------------|--------------------------------------|--------------------------|-----------------------|-------------------------|--------------------------|
| Factor | Influence | P value | BF _{all} | Cumulated mean influence | Factor | Influence | P value | BF _{all} | Cumulated mean influence |
| Sites | 0.4320 (0.4309 – 0.4330) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4320 | Sites | 0.4391 (0.4382 – 0.4409) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4391 |
| RCP & CMC | 0.3749 (0.3744 – 0.3755) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8068 | RCP & CMC | 0.2441 (0.2428 – 0.2450) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.6832 |
| Opt. algorithms | 0.1428 (0.1422 – 0.1435) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9496 | Opt. algorithms | 0.2406 (0.2403 – 0.2408) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9238 |
| Sampling prc. | 0.0468 (0.0466 – 0.0470) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9964 | Sampling prc. | 0.0652 (0.0649 – 0.0655) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9890 |
| Species | 0.0034 (0.0034 – 0.0035) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 | Species | 0.0092 (0.0091 – 0.0092) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9982 |
| N _q | 1e-04 (1e-04 – 1e-04) | 3.95e-126 – 1.33e-103 | 1/2.1e+122 – 1/7.6e+99 | 0.9999 | s:S | 0.0016 (0.0015 – 0.0016) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9998 |
| s:S | 0.0000 (0.0000 – 1e-04) | 1.26e-56 – 1.50e-39 | 1/1.5e+53 – 1/1.8e+36 | 1.0000 | N _q | 3e-04 (3e-04 – 3e-04) | 6.58e-175 – 8.39e-158 | 1/8.7e+170 – 1/7.7e+153 | 1.0001 |

Adj. R²: ~0.62 ; Dev. expl.: ~0.63 ; n_{GAM}: 5 × 2,600,000Adj. R²: ~0.51 ; Dev. expl.: ~0.51 ; n_{GAM}: 5 × 2,600,000

| Phenology model PIA _{GSI} | | | | | Phenology model PIA ⁺ | | | | |
|------------------------------------|--------------------------|---------------------|-----------------------|--------------------------|----------------------------------|--------------------------|---------------------|-----------------------|--------------------------|
| Factor | Influence | P value | BF _{all} | Cumulated mean influence | Factor | Influence | P value | BF _{all} | Cumulated mean influence |
| RCP & CMC | 0.4538 (0.4532 – 0.4544) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4538 | Sites | 0.4555 (0.4540 – 0.4566) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4555 |
| Sites | 0.4329 (0.4323 – 0.4334) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8866 | RCP & CMC | 0.4445 (0.4436 – 0.4460) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9000 |
| Opt. algorithms | 0.0579 (0.0577 – 0.0580) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9445 | Sampling prc. | 0.0500 (0.0498 – 0.0505) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9500 |
| Sampling prc. | 0.0494 (0.0493 – 0.0496) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9939 | Opt. algorithms | 0.0436 (0.0434 – 0.0437) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9936 |
| Species | 0.0051 (0.0050 – 0.0051) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9990 | Species | 0.0037 (0.0036 – 0.0037) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9973 |
| s:S | 0.0010 (9e-04 – 0.0010) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 | s:S | 0.0027 (0.0027 – 0.0027) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 1.0000 |
| N _q | 0.0000 (0.0000 – 1e-04) | 1.77e-70 – 3.23e-50 | 1/8.6e+66 – 1/6.7e+46 | 1.0000 | N _q | 0.0000 (0.0000 – 0.0000) | 0.0026 – 0.1617 | 1/19 – 1/1.2 | 1.0000 |

Adj. R²: ~0.67 ; Dev. expl.: ~0.67 ; n_{GAM}: 5 × 2,600,000Adj. R²: ~0.65 ; Dev. expl.: ~0.65 ; n_{GAM}: 5 × 2,600,000

| Phenology model PIA ⁺ | | | | |
|----------------------------------|--------------------------|---------------------|-----------------------|--------------------------|
| Factor | Influence | P value | BF _{all} | Cumulated mean influence |
| Sites | 0.4524 (0.4517 – 0.4535) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.4524 |
| RCP & CMC | 0.4461 (0.4450 – 0.4467) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.8985 |
| Sampling prc. | 0.0535 (0.0533 – 0.0537) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9520 |
| Opt. algorithms | 0.0432 (0.0431 – 0.0434) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9952 |
| Species | 0.0030 (0.0029 – 0.0030) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9982 |
| s:S | 0.0017 (0.0016 – 0.0018) | 0.00e+00 – 0.00e+00 | 1/1.0e+09 – 1/1.0e+09 | 0.9999 |
| N _q | 0.0000 (0.0000 – 1e-04) | 5.12e-60 – 2.32e-41 | 1/3.5e+56 – 1/1.1e+38 | 1.0000 |

Adj. R²: ~0.66 ; Dev. expl.: ~0.66 ; n_{GAM}: 5 × 2,600,000*Note:* See Table S22 for further details.