

Table S1. Description of input parameters for *seamus\_run*

<u>Required input</u>	<u>Input type</u>	<u>Description</u>	<u>Default value</u>
simstart	integer	Year of simulation start, years before 1950	n/a
siminc	integer	Simulation timestep, years.	n/a
simend	integer	Year of simulation end, years before 1950	n/a
btinc	integer	Bioturbation timestep, years.	n/a
fpcm	integer	Specimens (all species) per centimetre of core.	n/a
realD14C	1 or 0	Include 'real' <sup>14</sup> C activity from calibration curve or simply calculate approximate <sup>14</sup> C activity according to half-life of <sup>14</sup> C. Value of 1 (Yes/Real) or 0 (No/Approximate).	n/a
blankbg	integer	<sup>14</sup> C blank value (in <sup>14</sup> C yr BP) for single specimens, i.e. that maximum <sup>14</sup> C age that any single specimens in the simulation can have.	
adpoints	m by 2 matrix	Age-depth relationship of sediment core, where column 1 is age (in ka) and column 2 is core depth (cm). At least two age-depth points are required. Simulation will interpolate/extrapolate when assigning values for specific timesteps.	n/a
bdpoints	m by 2 matrix	Temporal change in bioturbation depth. An n by 2 matrix, where column 1 is age (in ka) and column 2 is bioturbation depth (in cm). Simulation will interpolate/extrapolate when assigning values for specific timesteps.	n/a
savename	string	Save the output variables of the simulation to .mat file with this name.	n/a
<u>Optional input calls</u>			
'calcurve', string	string	The calibration curve to use to assign <sup>14</sup> C activities to single specimens. Must be in the standard IntCal .14c file format and be present in your Matlab search path (or, alternatively, include the file path in the string). A number of files are already bundled with SEAMUS.	'Marine13'
'speciesA', matrix	m by 2 matrix	Temporal abundance of Species A, where column 1 is age (in ka) and column 2 is abundance (a value between 0 and 1, indicating the fraction of the total sediment flux per timestep). Simulation will interpolate/extrapolate when assigning values for specific timesteps.	Constant abundance of 1
'speciesB', matrix	m by 2 matrix	As above, but for Species B. The sum of the fractions of Species A and Species B must be less than or equal to 1 for any given timestep.	Constant abundance of 0
'resageA', matrix	m by 2 matrix	Reservoir age of Species A, where column 1 is age (in ka) and column 2 is reservoir age (in <sup>14</sup> C yr). Simulation will interpolate/extrapolate when assigning values for specific timesteps.	Constant reservoir age of 0.
'resageB', matrix	m by 2 matrix	As above, but for Species B.	Constant reservoir age of 0.
'offsetA', matrix	m by 2 matrix	Cal age offset of Species A when assigning <sup>14</sup> C activity, where column 1 is age (in ka) and column 2 is cal age offset (in years). Simulation will interpolate/extrapolate when assigning values for specific timesteps.	Constant offset of 0.
'offsetB', matrix	m by 2 matrix	As above, but for Species B.	Constant offset of 0.
'carrierA', matrix	m by n matrix	Desired carrier signals for Species A, where column 1 is age (in ka), column 1+x is the x <sup>th</sup> carrier signal, etc. Simulation will interpolate when assigning values for specific timesteps, but not extrapolate.	none
'carrierB', matrix	m by n matrix	As above, but for Species B.	none
'do32bit', integer	1 or 0	Store arrays as 32-bit to save memory. 1 for yes, 0 for no.	0

Table S2. Output variables (all of the same length) from *seamus\_run*

<u>Output variable</u>	<u>Output type</u>	<u>Description</u>
depths	m by 1 matrix	Depth values for each unique single foraminifer (in cm).
depths_original	m by 1 matrix	Original depth values (non-bioturbated) for each unique single foraminifer.
cycles	m by 1 matrix	Number of bioturbation cycles for each unique single foraminifer.
types	m by 1 matrix	Species type of each unique single foraminifer (0 = Species A, 1 = Species B)
ages	m by 1 matrix	True age for each unique single foraminifer (in years before 1950).
foram14c	m by 1 matrix	<sup>14</sup> C age for each unique single foraminifer.
foramfmc	m by 1 matrix	<sup>14</sup> C activity, in fMC, for each unique single foraminifer.
carrierA	m by n matrix	Species A carrier signal value for each unique foraminifer (each column is a unique carrier). Tip: To isolate the carrierA signals associated with Species A specimens, use logical indexing: <code>carrierA(types==0, :)</code>
carrierB	m by n matrix	Species B carrier signal value for each unique foraminifer (each column is a unique carrier). Tip: To isolate the carrierB signals associated with Species B specimens, use logical indexing: <code>carrierB(types==1, :)</code>

Table S3. Input variables for *seamus\_pick*

<u>Required input</u>	<u>Input type</u>	<u>Description</u>	<u>Default value</u>
matfilein	string	String denoting the location of the .mat file generated by <i>seamus_run</i>	
matfileout	string	Save the output of <i>seamus_pick</i> to a .mat file of this name.	
Apickfordate	integer	Minimum number of whole Species A specimens to randomly pick for discrete depth samples (enter -1 to pick all available).	
Bpickfordate	integer	As above, but for Species B.	
calcurve	string	The calibration curve file to apply when <sup>14</sup> C calibrating the picked samples (e.g., 'Marine13'). The file must be present in the MatLab search path and conform to the IntCal '.14c' file format. A number of files are already bundled with SEAMUS.	
pickint	integer	The discrete depth interval (core slice) size to apply when picking (in cm).	
<b><u>Optional input calls</u></b>			
'Aresage', matrix	m by 3 matrix	Reservoir age to apply to downcore picked samples of Species A, where column 1 is depth (cm), column 2 is reservoir age (in <sup>14</sup> C years) column 3 is reservoir age uncertainty (in <sup>14</sup> C years). Simulation will interpolate/extrapolate when assigning values for specific core depths.	Constant reservoir age of 0.
'Bresage', matrix	m by 3 matrix	As above, but for Species B.	
'Abroken', matrix	m by 2 matrix	The fraction of broken specimens (excluded from the picking process) for subsamples from Species A. Column 1 is depth (cm) and column 2 is fraction broken (between 0 and 1). The corresponding fraction of the specimens with the highest number of bioturbation cycles will be considered as broken. Simulation will interpolate/extrapolate when assigning values for specific core depths.	Constant fraction broken of 0.
'Bbroken', matrix	m by 2 matrix	As above, but for Species B.	

Table S4. Output variables (all of the same length) from *seamus\_pick*

<u>Output variable</u>	<u>Output type</u>	<u>Description</u>
discdepth	m by 1 matrix	The mid-points of the discrete depth samples (in cm).
Adiscagemed	m by 1 matrix	The Species A median true ages for the discrete depth samples (in years).
Adiscagemean	m by 1 matrix	The Species A mean true ages for the discrete depth samples (in years).
AdiscAMSage	m by 1 matrix	The Species A laboratory <sup>14</sup> C ages for the discrete depth samples ( <sup>14</sup> C year).
AdiscAMSerr	m by 1 matrix	The Species A laboratory <sup>14</sup> C measurement errors for the discrete depth samples ( <sup>14</sup> C year).
Adisc14Cage	m by 1 matrix	The Species A mean <sup>14</sup> C age for the discrete depth samples ( <sup>14</sup> C year).
Adiscscalagemed	m by 1 matrix	The Species A median calibrated <sup>14</sup> C age for the discrete depth sample (in cm).
Adiscblank	m by 1 matrix	The number of Species A <sup>14</sup> C-blank whole specimens contained within each discrete depth sample (n foraminifera).
Adiscwhole	m by 1 matrix	The cut off point for whole specimens for each discrete depth sample (specimens with bioturbation cycles less than this number are considered to be whole).
Adisc Carmean	m by x matrix	Species A mean carrier signals, whereby each column corresponds to a carrier signal, and columns correspond to discrete depth samples in discdepth.
Adiscnforam	m by 1 matrix	Species A specimens picked for the discrete depth sample (n specimens). Should usually correspond to input value <i>Apickfordate</i> , unless there were not enough whole specimens available to pick to meet the minimum specified by the minimum sample size <i>Apickfordate</i> , in such case zero specimens will be picked. If <i>Apickfordate</i> is set at -1, <i>Adiscnforam</i> corresponds to the total amount of Species A whole specimens within the discrete depth sample.
Bdiscagemed	m by 1 matrix	As for Adiscagemed, but for Species B.
Bdiscagemean	m by 1 matrix	As for Adiscagemean, but for Species B.
BdiscAMSage	m by 1 matrix	As for AdiscAMSage, but for Species B.
BdiscAMSerr	m by 1 matrix	As for AdiscAMSerr, but for Species B.
Bdisc14Cage	m by 1 matrix	As for Adisc14Cage, but for Species B.
Bdiscscalagemed	m by 1 matrix	As for Adiscscalagemed, but for Species B.
Bdiscblank	m by 1 matrix	As for Adiscblank, but for Species B.
Bdiscwhole	m by 1 matrix	As for Adiscwhole, but for Species B.
Bdisc Carmean	m by x matrix	As for Adisc Carmean, but for Species B.
Bdiscnforam	m by 1 matrix	As for Adiscnforam, but for Species B.