Scientific Workflows Applied to the Coupling of a Continuum (Elmer v8.3) and a Discrete Element (HiDEM v1.0) Ice Dynamic Model

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Abstract. Scientific computing applications involving complex simulations and data-intensive processing are often composed of multiple tasks forming a workflow of computing jobs. Scientific communities running such applications on computing resources find it often cumbersome to manage and monitor the execution of these tasks and their associated data. These workflow implementations usually add overheads by introducing unnecessary I/O for coupling the involved models and in the worst case even lead to sub-optimal CPU utilisation; also running these workflow implementations in different environments requires significant adaptation efforts, thus hindering reproducibility of the underlying science. High-level scientific workflow management systems (WMS) can be used to automate and simplify complex task structures by providing tooling for the composition and execution of workflows even across distributed and heterogeneous computing environments. The WMS approach allows to focus on the underlying high-level workflow and to avoid low-level pitfalls that would lead to non-optimal resource usage while still having the workflow portable between different computing environments. As a case study, we apply the UNICORE workflow management system to enable the coupling of a glacier flow and calving models that contains many tasks and dependencies, ranging from pre-processing and data management to repetitive executions in heterogeneous high-performance computing (HPC) resource environments. Using the UNICORE workflow management system, the composition, management, and execution of the glacier modelling workflow becomes easier with respect to usage, monitoring, maintenance, re-usability, portability, and reproducibility in different environments and by different user groups. Last but not least, it helped to speed up the runs by reducing model coupling I/O overhead and it optimised CPU utilisation by avoiding idle CPU cores and running the involved models in a distributed way on those HPC cluster that fit best the characteristics of each model.

1 Introduction

The complexity of glaciological systems is in an increasing way reflected by the physical models used to describe the processes acting on different temporal and spatial scales. Addressing those complexities inevitably involves the combination of different sub-models into a single simulation that encompasses multiple tasks executed in a distributed computing facility. A particularly

good example for such a combination is the simulation of calving behaviour at the front of glaciers that combines continuum model and discrete element model simulations. These computational tasks are connected to each other to form a *scientific workflow:* the composition and execution of multiple data processing steps as defined by the requirements of the concerned scientific application.

Carrying out the discrete calving and ice flow modelling dynamically and as one workflow instance becomes very laborious without an automated mechanism. An analysis of such a workflow in more detail reveals that there are even more steps than just the two model elements mentioned above. These include, for instance, pre- and post-processing, job dependency management, job submission, monitoring, conditional invocations, and multi-site data management. These steps can be cumbersome for a user, for example if any step may produce an unexpected output, which can cause the whole workflow to fail, and may thus require to re-run the whole workflow. These issues often indicate that workflow implementation is sub-optimal because it requires coupling overhead (such as unnecessary I/O), or or because a high number of CPU cores is allocated, which suits the most CPU-intensive task to be executed, but leaves cores idle when other tasks are executed that are less CPU-intensive or do not scale well. A *Workflow Management System* (WMS) allows to automate and ease the workflow managements steps by means of abstraction, which not only increases usability, but also enhances portability to different computing platforms and thus reproducibility of the scientific model runs. In our case, it also allowed us to focus on performance aspects, thus enabling a reduction in coupling I/O overhead and an optimisation the CPU utilisation.

The main contribution of this article is to identify the workflow problems to be solved for coupling a glacier continuum model and a discrete element model in an optimised way, to elicit corresponding requirements that address – among others – portability, performance improvements, and CPU utilisation, and to implement an automated workflow based on the UNICORE (Streit et al., 2010) distributed computing middleware, in particular using the UNICORE workflow management system (Memon et al., 2007). We demonstrate this by combining ice flow modelling and discrete calving into a high-level easy-to-use and performance-optimised scientific workflow.

This article is structured as follows: Subsequent to this introduction, foundations on glacier calving modelling and on scientific workflows are provided in Section 2. The targeted glacier modelling use case is presented in Section 3, which describes a workflow baseline used for model coupling and the applications used for execution. It is then demonstrated how to create a good solution, by first identifying requirements to solve these problems (Section 4.1), followed by creating an improved matching workflow design (Section 4.2), and finally implementing the workflow (Section 4.3). The implemented workflow is evaluated in Section 5 from different perspectives, including a discussion of how the identified requirements from Section 4.1 have been fulfilled. Finally, a summary and an outlook conclude the article.

2 Foundations

2.1 Modelling and Simulating the Calving of a Glacier

The calving behaviour at the front of glaciers is still a largely unresolved topic in modern theoretical glaciology. The core of the problem is that ice as a material shows different behaviour, depending on the time scale on which the forces are applied (Greve

and Blatter, 2009). The everyday experience is that ice is a brittle solid body (e.g. breaking icicles). Such behaviour is observed if the reaction to a force is in the range of seconds to minutes. Theoretical glaciology up to recent years rather dealt with the long-term (i.e., beyond minutes to millennia) behaviour of glaciers and ice sheets, where ice shows the property of a strong non-linear, shear thinning fluid (Greve and Blatter, 2009). This leads to a description of long-term ice flow dynamics in classical

5 ice-sheet and glacier dynamics models (Gagliardini et al., 2013) in terms of thermo-mechanically coupled non-Newtonian Stokes flow continuum models.

In stark contrast to such a description, the process of cracking or calving (i.e., the complete failure of ice fronts) is an inherently discontinuous process, that – if addressed in a physically correct way – needs a completely different model approach. Models adopting a discontinuous approach have been developed throughout the recent years (e.g. Åström et al., 2013; Bassis

10 and Jacobs, 2013; Åström et al., 2014). These models describe the glacier as discrete particles connected by elastic beams that can be dissolved if a certain critical strain is exceeded, thus being able to mimic elastic as well as brittle behaviour of ice. The size of these model particles (in the range of metres), which need to resolve a whole glacier of several cubic kilometres, inherently demands large computational resources. In addition, the characteristic speeds of advancing cracks is close to the speed of sound, which, in combination with the small spatial resolution, imposes a maximum allowed timestep size of a

15 fraction of a second.

In other words, the combination of a discrete element and a continuum ice flow model is a temporal multi-scale problem, where the first basically describes an instant change of geometry or rheology for the latter. This means that both models need to be run in a sequential manner, with several repetitions. This defines a workflow of two model components that strongly differ in computational demand. In addition, these two model components have to effectively and efficiently exchange data – namely,

20 the new geometries either changed by flow deformation or by calving as well as damage caused by fraction.

2.2 Scientific Workflows

A scientific workflow can be defined as the composition and execution of multiple data processing steps as required by a scientific computing application, i.e. e-Science. Such a workflow captures a series of analytical steps of computational experiments to "aid the scientific discovery process through the combination of scientific data management, analysis, simulation,

25 and visualisation" (Barker and van Hemert, 2008). Conceptually, scientific workflows can be considered (and are typically visualized) as graphs consisting of nodes representing individual tasks and constructs, and edges representing different types of associations between nodes, such as sequential or conditional execution.

Carrying out the discrete calving and ice flow model simulations becomes very complex as two (or even more) parallel *High-Performance Computing* (HPC) applications are involved, especially if there are tasks in the workflow that consist of

30 pre- and post-processing phases, and require multi-site and iterative job and data management functions. The overall scenario may easily become unmanageable, and the workflow management might be prone to errors, failures, poor reproducibility, and sub-optimal HPC resource usage.

Such a workflow scenario will be even more challenging when some parts are launched on heterogeneous resource management systems equipped with different file systems, different data transfer mechanisms, and different job submission systems.

In our case, for example, two different HPC clusters with different characteristics are simultaneously used, one for the ice flow modelling and another one for the discrete element (i.e., calving) modelling executions.

These workflow challenges can be addressed by a *Workflow Management System* (WMS) that is capable of managing the complex dependencies of many job steps with multiple conditional and nested constructs. Several scientific WMSs have been developed to automate complex applications from multi-disciplinary backgrounds. Ferreira da Silva et al. (2017) comprehensively categorized different workflow management systems according to the type of execution scenario and capabilities they offer, and also identified their specialised scientific domain. WMSs are widely used to facilitate complex scientific scenarios, among them Pegasus (Deelman et al., 2015), Kepler (Ludäscher et al., 2006) and Taverna (Oinn et al., 2006), to name just a few. These WMSs are also used for specialised scenarios and cater to a specific group of users who interact with HPC resources.

Our scenario from the domain of glaciology using HPC technology includes a complex workflow graph, and is therefore not easily manageable for users having only little expertise concerning HPC environments. Hence it is important to implement the glacier modelling use case with a WMS that offers a rich graphical front-end and simultaneously offers seamless execution and monitoring of involved applications. Considering that, the glacio-coupling use case is automated through our standards-based workflow management system (Memon et al., 2007) that is a part of the *Uniform Interface to Computing Resources* (UNICORE) (Streit et al., 2010) distributed computing middleware. It is specifically designed to support HPC applications deployed in a massively parallel environment. As described later in Section 4.3, our WMS for UNICORE provides a rich graphical interface for the composition, management and monitoring of scientific workflows by users with different levels of system expertise.

3 Use Case: Kronebreen Glacier Simulation

Coupling a continuum ice flow model and a particle-based calving model of the Kronebreen glacier provides a well-suited case study for the application of a WMS. More details on the scientific background of such a coupling and on models description are presented in (Vallot et al., 2018). In that study, a series of key processes (ice flow, surface and subglacial hydrology, ocean water mixing, undercutting at the front and finally ice calving in the ocean) were simulated by different models in an offline coupling. The aim was to show the feasibility of the coupling by comparing observations and historical data to simulation results and to identify the resulting interactions through this global approach. In this article, we introduce a full coupling that can be used for prognostic simulations. To simplify the problem we only use two models: the ice flow model (Elmer/Ice) and the discrete particle model (HiDEM). In the following, we describe the involved software executables and the underlying workflow.

3.1 Conceptual Scheme

Kronebreen is a tidewater glacier (ice flowing directly into the ocean) that is one of the fastest-flowing glaciers of the Svalbard archipelago. After a period of stability, it started to retreat in 2011 and continued since then. This glacier has been extensively studied (e.g. Kääb et al., 2005; Luckman et al., 2015; Nuth et al., 2012; van Pelt and Kohler, 2015; Schellenberger et al., 2015;

Vallot et al., 2017), partly due to its situation close to a research station and its interesting behaviour in terms of sliding and calving. For that reason, it is a good candidate for the present study. The aim is to reproduce both continuous (ice flow) and discrete (calving) processes using a *Finite Element Model* (FEM) and a first-principle ice fracture model, respectively.

3.2 Applications: Meshing Tools, Continuum and Discrete Ice Dynamics Model

Within our application, we use the continuum model Elmer/Ice (Gagliardini et al., 2013), and for the discrete calving model, the *Helsinki Discrete Element Model* (HiDEM) (Åström et al., 2013). Both codes can be run on large parallel HPC platforms. Implied by the physics that have to be addressed and by the modelling tools, the workflow contains three main applications that are part of the use case implementation:

1. **Meshing: Gmsh** (Geuzaine and Remacle, 2009) is the applied meshing tool used to provide the updated mesh for the continuum ice flow model run. It creates an updated footprint mesh in the horizontal plane that further is extruded and reshaped using the bedrock as well as free surface elevation to form the three-dimensional computing mesh for the ice dynamic simulation. Gmsh is an open source versatile and scriptable meshing tool that perfectly matches the demands of being deployed within a workflow like this one. Gmsh applies a bottom-up geometry and meshing strategy, starting from outline points of the glacier, building a closed loop of its outline and further creating a planar surface that is being meshed in two dimensions.

2. **Continuum Modelling: Elmer/Ice** (Gagliardini et al., 2013) is the open source ice sheet model used to compute the long-term dynamics of the glacier. Elmer/Ice is based on the multi-physics package Elmer (Råback et al., 2018), an open source Finite Element code developed by CSC – IT Center for Science Ltd. Elmer/Ice is able to utilize parallel processing, applying the *Message Passing Interface* (MPI) paradigm (Message Passing Interface Forum, 2012) that uses messages to exchange data between nodes of a distributed parallel processing environment, and – for certain solver implementations – OpenMP (Dagum and Menon, 1998) for shared-memory parallel processing using multi-threading. Elmer also provides the `ElmerGrid` executable that can be used to convert the mesh created by Gmsh and at the same time perform a domain decomposition on the footprint, using the Metis library. The solver executable `ElmerSolver` has a built-in feature to internally extrude the given footprint mesh into layered columns of prisms and impose the given surface and bedrock elevation to form the volume of the glacier. Elmer is built on a shared library concept, meaning all solver modules are loaded during runtime. This enables the easy deployment of user-written functions and solvers through an API.

3. **Discrete Modelling: HiDEM** (Helsinki Discrete Element Model) (Åström et al., 2013) is a discrete element model that represents the glacier as mass-points connected by massless beams that are allowed to break if exceeding a given threshold. An additionally applied repelling potential based on distance guarantees a non-intersection of compressed loose particles. Solving Newton's equation on such a setup, it is possible to realistically reproduce the behaviour of fracturing. The downside of this approach is the high demand of computational power, as the several cubic kilometres large glacier is discretised in pieces of a few tens of cubic metres. Furthermore, the time scales for the simulation are

PLAN VIEW   SIDE VIEW
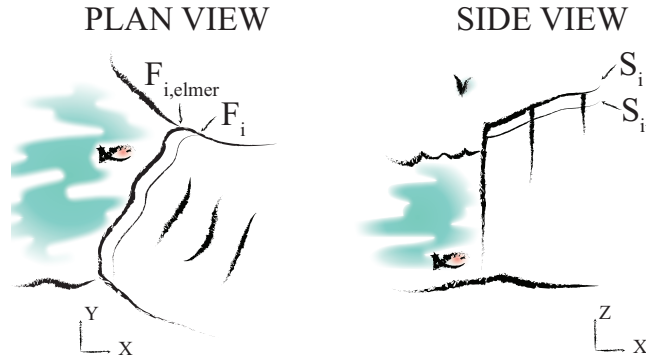
Figure 1. Conceptual plan and side view of an Elmer/Ice transient run. The initial front F_i and surface S_i are evolved to a new position of the front $F_{i,elmer}$ and a new surface elevation S_{i+1}.

imposed by the ratio of the speed of sound to the typical length of the discretised particles, which falls clearly below seconds. Hence, despite the fact that the code is utilizing massive parallel computing using the MPI paradigm, only a few minutes to hours of physical time can be computed even on a huge HPC cluster. HiDEM receives the initial geometry from Elmer/Ice, in form of gridded data over a limited area at the tongue of the glacier, and also receives the basal friction coefficient distribution computed within the continuum ice flow model.

3.3 Initial Base Workflow

The continuum ice flow model and the discrete calving model need to be coupled, thus leading to a scientific workflow. A baseline version of the workflow was initially realised by a Bash shell script that calls the above executables as well as additional Python helper code, and performs all the needed management operations using shell script commands. The underlying workflow is as follows:

Step 1: Generate the Mesh for Elmer/Ice

At $t = t_i$, the front position F_i and the contour $Cont$ are given as input to create the mesh M_i. This determines the domain of the glacier for the ice flow model Elmer/Ice. A Python script invokes the meshing executable `gmsh` to build the mesh from the contour and the front position, and invokes ElmerGrid (Råback, 2015) to convert it into Elmer format. In this particular application, the mesh is then split into 16 partitions. This step runs as a single-threaded application, as with respect to resource requirements, mesh generation is not very CPU-intensive (serial, i.e. 1 CPU core), but it consumes some storage space.

Step 2: Ice Flow Modelling and Conversion to HiDEM Domain

The continuum ice flow model is executed using the `ElmerSolver` application which is an MPI-based implementation and part of the Elmer application suite. The number of time steps (N_t) depends on the studied glacier and process as well as the

spatial resolution. Here, we simulate $N_t = 11$ days in one run, which – using a time-step size of one day – corresponds to the update frequency of remote sensing satellite data which was used for model validation.

As the basal boundary condition (BC), we assume a no-penetration condition with no basal melting nor accumulation and a basal friction law of any type (currently a Weertman friction law). The upper BC is defined as a stress-free surface and is

5 able to evolve during the simulation following an advection equation forced by a surface mass balance. As the BC in contact with the ocean, the normal component of the stress vector is equal to the hydrostatic water pressure exerted by the ocean where ice is below sea level. The front is also able to evolve, using a Lagrangian scheme (i.e., mesh velocity equal to ice flow velocity corrected by melting). The temperature profile in the ice and lateral BC are prescribed but can be changed easily. The ice is flowing as a non-linear isotropic viscous fluid following Glen's flow law (Cuffey and Paterson, 2010) and the Stokes

10 equations for an incompressible fluid are solved over the ice volume. Elmer/Ice executes a solver input file, SIF_i, with the above-mentioned parameters.

After the simulation, the glacier has a new position of the front $F_{i,elmer}$, a new surface elevation S_{i+1} (see Fig. 1) and a map of basal friction coefficients (determined by a linear sliding law). These form the output of Elmer/Ice and input to HiDEM. Elmer/Ice can be sped up by parallel processing, but is not as CPU-intensive as HiDEM, hence only 16 CPU cores are used for

15 a relatively small glacier, like Kronebreen, in this part of the workflow.

The output format of Elmer/Ice does not match the input format of HiDEM, and HiDEM does not need to process the whole glacier, but only the front that is relevant for calving. Hence, a conversion step runs a set of helper scripts ("Elmer to HiDEM") implemented in Python. This step is performing a conversion of the output of `ElmerSolver` to the HiDEM grid ($10\,\mathrm{m} \times 10\,\mathrm{m}$ in our case) that is used for the calving front of the glacier. Elevations are offset so that the minimum bed elevation is equal to

20 0. It also includes places with no ice where the surface elevation is equal to the bed elevation. This conversion step creates a text input file for HiDEM, Pin_i, with coordinates, surface, bed and basal friction coefficient. This conversion is performed on a single CPU.

Step 3: Discrete Particle Modelling and Conversion to Elmer/Ice Domain

The converted output from Elmer/Ice is passed to HiDEM. The implementation of HiDEM requires an MPI environment

25 (560 cores running the MPI processes in our case), because in comparison to the other steps, it consumes the biggest share of CPU hours due to the high spatial and temporal resolution. In order to avoid excess computations, HiDEM scales down the obtained friction parameters it receives from Elmer/Ice (in our case using the factor 10^{-4}) so as to increase the sliding speeds and thereby reduce the physical time (in our case 100 s) needed to evaluate the resulting fractures. This can be justified because the distribution of the friction parameters and hence the instantaneous fracture pattern does not change, and the time scales of

30 ice flow (represented by the continuum model) and fracturing are separate anyhow. A new front position, F_{i+1}, is modelled after the simulation. Because of the high spatial resolution, the involved text files are rather large.

Once a HiDEM run is completed, the next step is to re-convert this data set to the Elmer/Ice format, so that the next iteration of the coupled glaciology models' workflow can begin. Again, a Python script ("HiDEM to Elmer") is used to convert the HiDEM output into a format that can be read by Gmsh and ElmerGrid. For this purpose, the new front position F_{i+1} (after

calving) and surface elevation S_{i+1} are re-introduced into Step 1 at $t = t_{i+1}$. Again, the conversion is performed in serial execution. After this step, the workflow is begins again, starting from Step 1.

4 Workflow

4.1 Requirements Analysis

5   The problem analysis of the initial shell script-based workflow led to a set of requirements that aim at improving the workflow with respect to usability, adaptability, maintainability, portability, robustness, resource usage (I/O and CPU), and overall runtime. Based on the weaknesses of the initial workflow implementation, we focused in particular on reducing the overhead associated with the initial coupling approach by improving overall runtime, optimising the CPU resource usage and coupling-related I/O, as well as the factors stated in the beginning on enabling a uniform access to widen the scientific community

10 adoption of this glaciology workflow.

The requirements elicitation phase yielded the following requirements, which led to an improved design and implementation of the workflow (a summary of the requirements is provided in Table 1 together with a description of the UNICORE-based implementation.):

R1: Readability and Understandability To continuously develop, maintain, and disseminate a scientific application for

15 collaboration requires the implementation to have a clean, clearly modularized and error-free code. Since our case study consists of many independent applications related to each workflow task, it is important that the identified tasks are well-segregated and do not overlap each other. A well-segregated workflow not only helps the application developer to further enhance the application, but also to distribute the code in order to collaborate with a larger scientific community.

R2: Sequential Pipeline The execution of jobs in the workflow should be orchestrated in a sequential manner such that one

20 job step should not commence unless all previous steps are completed. This requirement envisages the whole scenario as a sequence of jobs that should connect all the involved applications in a batch system-agnostic manner.

R3: Dynamic Data Injection The data injection for any workflow job should be transparent and easy to express. This requirement refers to the provisioning of data sets to individual workflow steps: Before a job is started, the required data needs to be available. Furthermore, dynamic data injection allows to import data from various sources using different protocols. A

25 data-transfer-agnostic access is an add-on to this requirement.

R4: Minimise Coupling I/O The cost of data sharing across the jobs of the workflow steps becomes high when the data is unnecessarily replicated across each of the job steps. This increases the used storage space and negatively impacts the overall workflow footprint in terms of resource consumption, in particular with respect to I/O performance. Therefore, an adequate data sharing mechanism that minimises the coupling-related I/O of all the tasks should be available, which allows at the same time a

30 simplified integration of data at application runtime. It will also facilitate optimal storage resource usage (e.g. of a parallel file system) in the target system. This is of particular importance when dealing with two different HPC clusters running different steps of the workflow, where data needs to be exchanged between the HPC clusters.

R5: Minimise CPU Resource Consumption The continuum ice flow model (Elmer/Ice) is less CPU resource-intensive than the calving model (HiDEM). This is due to very different spatial and temporal resolutions but also the models themselves, which require different amounts of computational resources (16 cores for the continuous ice flow model, but 560 cores for the discrete particle model). Getting access to CPU time on a small HPC cluster is typically easier than on big clusters, hence the workflow shall support the possibility to run these two significantly different steps on two different computing resources, thus reducing the amount of CPU and queueing time needed on the larger cluster. If the executions are running on heterogeneous clusters, a layer of abstraction is needed that encapsulates the intricacies of different resource management systems (see R11). If the executions are running on the same cluster, it needs to be avoided that more cores are allocated than actually used (e.g. do not allocate 560 cores for running a 16 core Elmer/Ice job or even for executing a serial data conversion script).

R6: Parametric Execution In our case study, most of the job steps need to be executed in an iterative way. Every new iteration takes input from a plain ASCII text file, called `n_list.txt`, that records the surface velocity data of some days of ice flow simulation. The requirement is to take the input data from the file and use it as a parameter for the iteration of the tasks. It means that the parameter value is shared by all the tasks involved. Furthermore, the iteration should not exceed a certain threshold.

R7: Workflow Composition and Visual Editing It will be more robust for users to have a graphical interface that allows them to visually program and manage scientific workflows. In the glacier modelling scenario there are six main steps, each with different shell scripts and resource configurations, therefore a *Graphical User Interface* (GUI) can be very useful for visual editing, composition and automation of all the steps.

R8: Workflow Tracing and Monitoring It should be possible to trace and monitor the whole workflow, including its sub-elements such as individual jobs. The extensive process of calving simulation may have to be aborted at some stage due to data or parameter anomalies. Therefore, it must be possible to interrupt the workflow at any point. Apart from that, real-time status of the jobs managed by the workflow should be provided.

R9: Workflow Reproducibility The workflow needs to support reproducing results both by the original researchers and by third parties. If the created workflow is carefully designed and validated against any errors, it can be exported for re-use by a larger community. This includes not only exposing that workflow to a wider community on the same computational resource, but also running it in a completely different hardware or software environment (re-usability, adaptability, portability, and maintainability).

R10: Secure Access The workflow management system should be capable of providing an interface to let users run scientific workflows in a secure manner. This implies that adequate authentication and authorization need to be in place. This requirement further mandates the workflow system to be compatible with back-end computing clusters and existing production computing infrastructures.

R11: Execution Platform Independence This requirement supports a scenario which allows scientists to submit computations without knowledge of the parallel execution environment installed at the target computing resource. In our case, there are at least two different MPI execution environments involved, and thus two different MPI implementations. Another aspect is to

abstract from the batch system used for job submission to the HPC cluster(s). The intended middleware abstraction should not require a user to know the target environment that is providing the actual execution.

R12: Data and Variable Configuration Configuring required data elements such as workflow-centric input and output locations, and shared applications' environment variables or constants across many job steps can reduce much workflow man-
5 agement and development overhead. This may allow carrying out the design, execution, and debugging phases of many tasks in a more efficient manner. Therefore, in terms of overall usability and application maintenance, this requirement is considered important for realising the complex structure of connected tasks.

Any solution that addresses this set of requirements will make the scientific workflow usable for a wider set of communities working in Glaciology.

10 ## 4.2 Workflow Design

Using the initial shell script-based workflow as a starting point and taking the requirements R1–R12 into account, this section discusses the design of the glacio-coupling workflow implementation. Figure 2 shows the workflow composition.

The data conversion tasks, such as "Elmer to HiDEM" and "HiDEM to Elmer" existed in the initial workflow implementation as part of the respective ElmerSolver and HiDEM jobs. As the latter are both resource-intensive (i.e., they run on multiple
15 cores), while the data conversion tasks are serial and require less resources, it is inappropriate to reserve (and thus waste) parallel resources for the serial data conversion. The separation of tasks in the workflow's design enables them to use only a single core, which is sufficient for their serial execution.

The step "shared preprocessing" is introduced as an additional task to manage the initialisation phase of the workflow. It mainly provides the involved applications with the required initial input data sets and prepares shared output directories
20 where the subsequent individual workflow steps accumulate intermediate and final results. In this step, the shared workflow variables are also initialized, and the required intermediate working directories are created. Without input and output storage management and shared variables, our workflow implementation would stall. Therefore, this step is a necessary prerequisite for all further iterations.

4.3 Workflow Implementation

25 This section describes the workflow implementation and its realisation through *Uniform Interface to Computing Resources* (UNICORE) (which includes a workflow engine). The UNICORE middleware is not only used for the developement and automation, but for the processing and management of the entire workflow on deployed HPC resources. We have contributed to the creation of both UNICORE in general (Memon et al., 2007) and the workflow engine in particular (Memon et al., 2013b). This section briefly details the UNICORE foundations, the workflow implementation and it concludes with resource setup and
30 interaction.
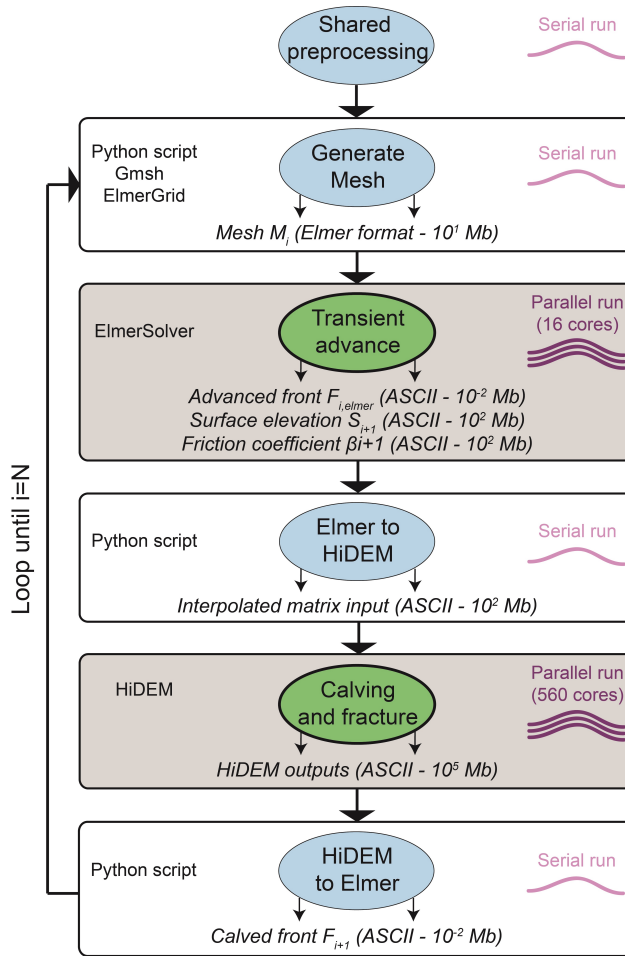
Figure 2. Whole workflow with blocks representing steps.

4.3.1 UNICORE Foundations

UNICORE (Streit et al., 2010) is a distributed computing middleware that provides abstractions for job submission and management on different kinds of job scheduling systems. Hence, jobs can be submitted to a cluster without needing to know about the job scheduling system internally used by that cluster. The abstraction is achieved through a unified set of interfaces that enable scientists to submit computation jobs without considering any intricacies of the underlying batch system. UNICORE takes care of automatic translation of job requests to multiple target resource environments.

UNICORE provides a workflow system based on the *Service Oriented Architecture* (SOA), i.e., all the main functional interfaces of the workflow system are exposed as web services. Figure 3 gives a holistic view of UNICORE's multi-layered architecture that is composed of Client, Server, and Target System tiers. The Client tier has two main variants, the *UNICORE*
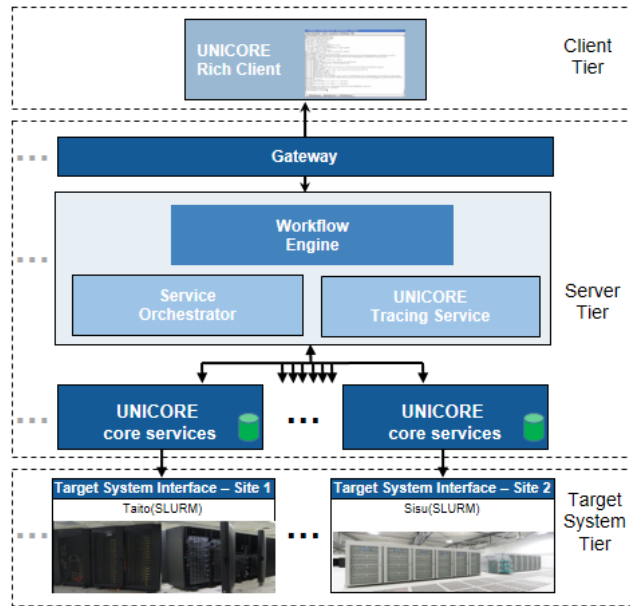
Figure 3. Multi-tiered UNICORE architecture.

Command-line Client (UCC) and *UNICORE Rich Client* (URC). However, other third party client applications such as scientific gateways, science portals and client APIs can also be integrated, if they comply with the provided server-side interfaces.

To address the goal of usability, we put emphasis on the URC, which is an Eclipse-based (Eclipse Foundation, 2013) client application implemented in Java. It provides users with a wide range of functionalities such as workflow management and
5   monitoring, data down- and upload to a remote cluster, a GUI for workflow editing and resource and environment selection panels. An example screenshot of the URC workbench is shown in Fig. 4. For more details about the URC we refer to (Demuth et al., 2010).

4.3.2   Workflow Realisation using UNICORE

Considering the complexity of the compute and data aspects, satisfying our requirements R1–R12 would take tremendous
10   effort if no abstractions and high-level concepts (such as those provided by UNICORE) were used. We therefore employ the UNICORE workflow management system to automate the workflow of our use case in a high-level way.

To improve usability, the new, improved workflow was designed using the visual editor provided by the URC. The editor allows scientists to visually drag and drop different task types for different application types that may be enclosed in conditional structures. The supported task types are simplified, and small Bash shell scripts containing customized or generic applications
15   can be executed remotely on user-specified resources.
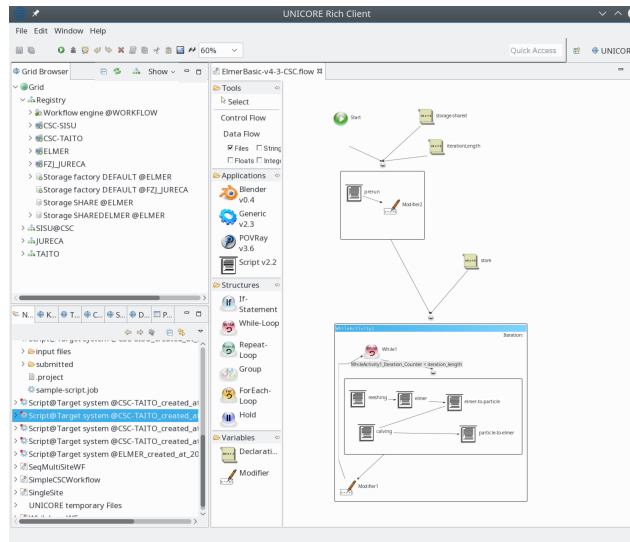
Figure 4. The UNICORE Rich Client workbench.

Figure 5 shows the sequence of the workflow tasks defined for our glacier modelling case study. The major steps described in Section 3.3 can be directly mapped to the tasks defined at the URC level. However, there is an additional step required for arranging any intermediate input and output data sets. The concrete tasks defined at the URC tier are:

1. prerun: This initial task declares global constants for all the workflow instances and also creates a central output directory
5   that is shared across the jobs participating in an instance of the workflow. It also sets an initial input that contains the total number of iterations.

2. meshing: This task generates the mesh for Elmer/Ice by running the Gmsh and ElmerGrid tools sequentially using a set of input files. ElmerGrid is a mesh generator that takes as input a mesh from Gmsh to generate the output mesh to be used in the following step by Elmer/Ice.

10   3. elmer: In this task, the finite element modelling is executed. In order to achieve that, the parallel `ElmerSolver` application is invoked. This application is based on MPI/OpenMPI standards and thus typically runs in HPC environments.

4. elmer-to-particle: A Python script that transforms the Elmer/Ice output produced by the previous step to create a format required for the HiDEM application.

5. calving: This task performs discrete element modelling by running the HiDEM application. This step consumes much
15   more resources than any other task of the workflow.

6. particle-to-elmer: A Python script transforming the output of the output of the calving job into the format used by task 2, (re-)meshing for Elmer/Ice.
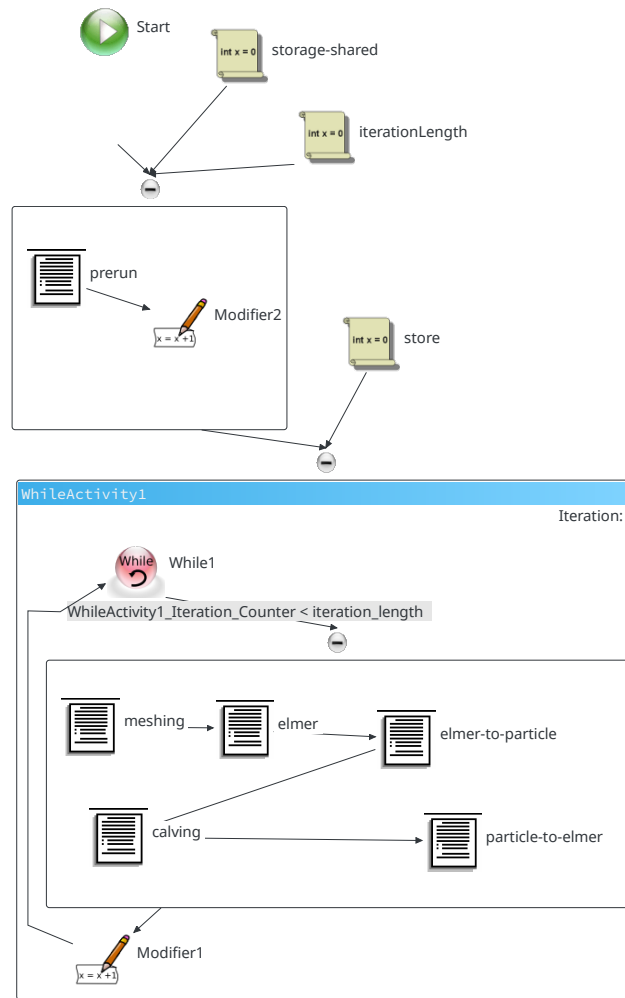
Figure 5. Graphical workflow snippet from the URC workbench.

In addition to the task definitions, a shared variable is required that contains the workflow output location that is to be used across all the tasks. This is the only variable meant to be customized for a different user: In case another user wants to run the same workflow on the same set of resources, e.g. the same HPC cluster, then this single value has to be adjusted to the preferred file storage location.

5   Prior to the workflow execution by URC, the user has to: 1) configure on which target site each task runs; 2) specify the extent of computing resources it requires; 3) provide a list of input and output files involved. Once the tasks are prepared, the workflow can be submitted for execution on (remote) HPC clusters. During the workflow execution phase, the sequence of running tasks will follow the workflow graph specified by the user.

```
1
2 particle-to-elmer:
3     # creating task-specific folders
4     python $JOBWD/input/Python_particle/ParticleToElmer.py $nb $JOBWD
5     # accumulate output and move to the main workflow output
6
7 common code:
8     if [ $currentctr -gt 1 ]; then
9         nrbefore=`sed -n -e "$((COUNTER))p" $JOBWD/input/n_list.bak`
10        nb_before=`awk '{print $1}' <<< $nrbefore`
11        firstIteration=false
12    fi
```

Listing 1. Excerpt of the particle-to-elmer tasks, and the common script snippets implemented in URC

Listing 1 shows two code snippets from the URC environment: First snippet shows the kernel of the particle-to-elmer task, which simply invokes the Python executable. Batch system-specific components are added by the WMS (lines 2–5); and second, the common code section (lines 7–12) that fetches the value of the last iteration required to process the data of the current iteration. This common code snippet must be present in all the workflow steps (including the iteration blocks) except

5   the prerun step. Practically, this is just a syntactic overhead, and considered negligible when the number of affected steps is small.

4.3.3   Resource Setup and Interaction Scenario

Our new and improved workflow requires the deployment of separate UNICORE server and client instances. The server-side deployment spans two production clusters at CSC in Finland, namely the *Taito* cluster for smaller jobs such as Elmer/Ice and

10 the bigger *Sisu* cluster for massively parallel jobs such as HiDEM. On both sites, the UNICORE instances were separately deployed. These sites already have SLURM as a resource management system available, but with different hardware configurations: *Taito* has heterogeneous node groups with varying capabilities and CPU layouts (Intel's Haswell and Sandy Bridge processors), whereas *Sisu* has a symmetric configuration with all the nodes providing same number of processing, data and memory resources. Furthermore, as some sort of master, a shared UNICORE workflow management and a resource broker

15 instance have been deployed on a cloud computing instance running at the Jülich Supercomputing Centre (JSC) in Germany.

The resources at CSC needed to have the respective applications installed to support the complete workflow execution, i.e. on *Taito*, the Elmer suite with the Elmer/Ice glaciology extension was installed, whereas the particle calving application (HiDEM) was provided on *Sisu*. In addition to these executables, a Python environment had to be available on both systems for running the Elmer-to-Particle (and vice versa) conversion scripts.

20 The workflow development and remote execution is managed by the user through the *UNICORE Rich Client* (URC). It is thus required to have the URC installed on the user side. To obtain access to the remote UNICORE sites at CSC, the user has to
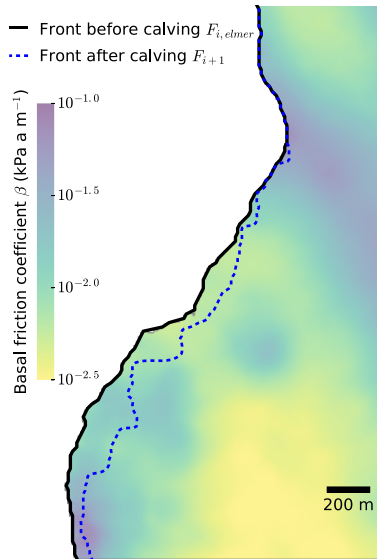
Figure 6. Basal friction coefficient, β and new position of the front F_{i+1} after calving from the HiDEM simulation generated through the UNICORE-based implementation.

acquire X.509 credentials and trusted certificates of the server instances. By using these credentials, the user can interact with all the UNICORE server instances of the infrastructure that she has access to.

After the credentials are set up, the user has to add sites that shall be used for the workflow execution. For this, only a single location of the discovery service called Registry is provided. If the user's identity is known to the Registry instance and all

5 the concerned compute sites, then these sites will be available for execution. Following the discovery service inclusion, the workflow development and management can be performed easily.

Figure 6 shows the output of the calving task that is the last step of each workflow iteration. Without the UNICORE-based implementation, it was difficult to manage the overall makespan of this step and in general the whole workflow. After transforming it using the UNICORE system, the management became easier and seamless as the calving tasks are only invoked

10 when the preceding phases (such as coupling and data conversion) and iterations were completed successfully, i.e. when they could provide reasonable input to the computationally expensive HiDEM executable.

5 Discussion

This section discusses the most vital elements of the glacio-coupling case study to show that the main goal was achieved, i.e. a coupling of two different models dynamically and simplified access to distributed HPC resources.

15 In the implementation using UNICORE, we use the same application environment and dataset as before the introduction of a WMS. Therefore, this discussion does not cover the application performance and scalability, but rather the overall workflow effectiveness, robustness, and usability.

Table 1. Summary of requirements and how the new workflow implementation addresses them.

	Description	UNICORE-based Realisation
R1	Readability and usability	URC workflow management and interface
R2	Sequential pipeline	Workflow management and enactment
R3	Dynamic data injection	Automatic data import and export
R4	Data sharing across job steps	UNICORE's data management services
R5	Resource-agnostic access	UNICORE's job management services
R6	Parametric execution	Composite constructs and loops
R7	Workflow composition and visual editing	URC workflow editor and widgets
R8	Workflow tracing and monitoring	UNICORE's workflow tracing and management services
R9	Workflow reproducibility	URC's project export wizard
R10	Secure access	PKI, X.509, and mutual authentication
R11	Execution environment independence	Job incarnation through XNJS and *Target System Interface* (TSI)
R12	Data and variable configuration	Middleware-supported variable resolution

5.1 Fulfilment of Requirements

In this section, we show how the requirements presented in Section 4.1 have been fulfilled through the use of the UNICORE workflow management system. Table 1 lists each of the requirements and explains briefly its realisation in the UNICORE-based version. The details are as follows:

5 Requirements *R1 – Readability and usability* and *R7 – Workflow composition and visual editing* are addressed through the URC client as it comes with a rich workflow editor that allows simplified composition and association of workflow tasks in a user-friendly manner.

The UNICORE WMS provides sequential access by enforcing a barrier on a workflow task that is about to be processed until its preceding task completes successfully. This supports requirement *R2 – Sequential pipeline*.

10 The workflow's data management is considered to be an essential requirement for any data-intensive application. It is typically either a remote data transfer or data movement within the file system used by that computational resource. The workflow management system should not bother the user with this. In our case, the UNICORE atomic services take care of any data movement to a third-party data space or a local cluster; the user is only expected to specify the source and target file locations. After the workflow has been submitted, the required data transfers are carried out by the UNICORE middleware. This

15 functionality supports requirements *R3 – Dynamic data injection* and *R4 – Minimise Coupling I/O*.

For the glacier modelling workflow, the UNICORE-based implementation executes Steps 2-6 of the workflow in a WHILE loop until a certain number of observations has been reached. As the observations are stored in a file, they need to be processed and the values need to be loaded to UNICORE's WHILE loop variable store. Each time the workflow instance is created and submitted, the loop construct loads the file called `n_list.txt` and takes each observation from that file to run the underlying

20 steps in a parametric way. This feature supports requirement *R6 – Parametric execution*.

The UNICORE-based glacio-coupling workflow is using the computing resources deployed on CSC's *Sisu* and *Taito* clusters. If a future user of this application intends to deploy and run the workflow in a different resource and application environment or with a different number of cores, this will be possible with minimal effort: The UNICORE atomic services provide a layer of abstraction over execution environments and batch systems, which fulfills requirements *R11 – Execution platform independence* and *R5 – Minimise CPU Resource Consumption*. The latter requirement is also fulfilled by splitting the previously monolithic job submission into separate job submissions, thus allowing to specify exactly the number of cores needed for each jobs and preventing idle CPU cores that are reserved but in fact never used.

In case another user is interested in using the UNICORE-based implementation, URC provides a feature to export the workflow in a reproducible format to be re-usable by other users. This supports requirement *R9 – Workflow reproducibility* (more details on workflow reproducibility are discussed later in Section 5.8).

The URC interface allows users to specify any application-, data- and environment-specific variables, scoped either to one task or a group of tasks. To enhance and simplify our new workflow implementation, a number of workflow-wide and application-specific variables were used. During workflow runtime, they are resolved without needing any user intervention. This addresses requirement *R12 – Data and variable configuration*.

Requirement *R10 – Secure access* is essential since the workflow will have access to large and precious compute resources, for which the UNICORE-based deployment ensures secure interaction between the user and all the services she communicates with, such as workflow executions and access to storage and data. Users accessing any remote UNICORE-based services are required to possess X.509 credentials in order to use these services.

Finally, to compose, manage and monitor workflow submissions interactively, URC provides a separate visual interface to edit or create individual workflow tasks or monitor running workflows and the involved jobs. This supports requirement *R8 – Workflow tracing and monitoring*.

5.2 Middleware Deployment Overhead

While UNICORE is powerful and enabled the optimisation of our workflow, having that additional layer may introduce some overhead: the provider of the computational resources has to ensure the availability of UNICORE server-side. Maintaining a server-side deployment needs a dedicated server that manages workflow jobs. On the other hand, the URC is easy to use due to its GUI and does not have any significant installation overhead – it is Java-based and thus easily usable on any hardware platform. However, every URC user needs to maintain a credential store and personal X.509 certificates.

5.3 Modularization

The UNICORE-based implementation using URC allows us to cleanly separate the tasks in a modular way, which enables us to individually monitor and manage tasks even while they are in the execution phase. The complete workflow management can be performed interactively and visually through the URC's GUI. Our experience is that using the URC is less error-prone than the purely shell-script-based approach.

5.4 Data Transfer and Management

UNICORE significantly eases data handling: For example, during the UNICORE-based workflow development and testing phase we ran one application instance in Germany (JSC) the other in Finland (CSC) with respective Elmer/Ice and HiDEM deployments, i.e. the worklow execution was distributed and the associated data had to be transferred back and forth between both sites. With the shell-script-based implementation, we found the inter-task input and output (I/O) of the workflow not easily manageable and prone to multiple data transfer errors during the data staging phase. In contrast, the UNICORE-based approach takes care of the data movement automatically, in which only the input and output files and their physical or logical addresses have to be declared in the beginning. The I/O is automatically managed by UNICORE as the WMS reaches the specific task with data staging declarations. Similarly, the shell-based approach including manual I/O statements is more susceptible to file staging failures, and potentially increases the time span to reach the workflow usage phase.

5.5 Efficient Resource Utilization

Using our improved workflow allowed us to optimise CPU utilisation of running the models and data conversion and to speed up the I/O needed for model coupling.

The ratio of needed computational resources between HiDEM and Elmer/Ice is about 10:1. Hence, when running the same workflow as a single job submission (allocating the number of CPU cores needed for HiDEM), 90 percent of the CPU cores in the Elmer/Ice stage would go idle, which would lead to extremely bad performance (not in terms of wall-clock time, but efficiency). In a similar manner, the data conversion steps in the workflow are less compute-intensive, and if attached to any of the Elmer or HiDEM job submission, could be very inefficient in terms of resource utilization. One might argue that this could also be improved through batch job scripts, but this would be challenging as those scripts would have to be tailored to a specific computing platform (SLURM, PBS, etc.). This issue is avoided by using UNICORE, which enables even different computing platforms to be combined into a single workflow.

Our workflow approach minimises the I/O consumption by using UNICORE's internal workflow storage management services, which provision data (in the scope of a single infrastructure) to the next task without creating any explicit copy of the data set. Yet, UNICORE is flexible enough to support also distributed scenarios, by automatically transferring in a secure way data across geographically distributed workflow tasks – as described previously, when we were using resources both at JSC in Germany and at CSC in Finland. The glacio-coupling use case intensively uses UNICORE's managed workflow storage that organizes the individual workflow instances and their output data. In a resource-conservative environment, where the secondary storage, though not costly, is limited and regulated on the basis of site-constrained user quotas, the workflow-wide storage services proved to be adequate while supporting the complex data management requirements.

Usage of shared variables spanning all workflow tasks is essential to the glacio-coupling workflow implementation. In the UNICORE-based approach, the $prerun$ job encapsulates the creation of shared variables for managing a workflow-wide structure useful for arranging the input and output data in a single location. This is realised through a single job that runs on the cluster's login node and in a batch system-agnostic manner.

5.6 Extendable Workflow Structure

In practice, enhancements or addition of new scientific methods to an existing workflow are inevitable. In the UNICORE-based workflow implementation, in contrast, the editing and validation of the individual workflow tasks or the whole structure can easily be performed. This process happens before the whole workflow is submitted for execution on HPC resources. Furthermore, if there are any enhancements to be performed after the workflow request is submitted, the running workflow instance can even be put on hold for intermittent script updates and restarted later.

The glacio-coupling model uses Elmer/Ice and HiDEM to analyse the complete scenario in the form of one structured recipe. Our approach adds flexibility through the fact that the used models are interchangeable. This means that if there are other glaciological models than Elmer/Ice or HiDEM to be used, they can easily be integrated into the existing workflow structure. Therefore, other ice sheet modelling communities can benefit from the implemented glacio-coupling workflow template and couple their models with much less technical effort. Similarly, the workflow can be extended with new script tasks or control constructs (conditional or iterative composites) from any part of the workflow structure, according to the scenario requirements. For instance, let us assume that we want to introduce some additional tasks, e.g. on a different HPC resource than the one already implied here.

5.7 Resource Management Agnostic Access

UNICORE-based job submission does not require a hard-coded approach, as it provides users with a seamless interface for varying resource management systems (e.g. SLURM, LSF etc.). The underlying server-side UNICORE services automatically take care of the job submission commands' translation to the target batch system on behalf of the user. However, while this middleware abstraction offers user-friendliness, it also means that, due to the abstraction, some batch system-specific low-level technical features that might be useful for the application are truncated. This is because the middleware layer hides them for the sake of a unified, less complex and consistent user experience. In case any batch system-specific features are necessary, workflow tasks could still be partially re-programmed to use custom features. In our case study, we needed only standard job submission features, so no custom batch system-specific functions were required.

5.8 Reproducibility and Re-use

As in every field of science, it is necessary that other scientists (but also the original scientist) are able to reproduce and validate the glaciological results we obtained. It is however not trivial to ensure this in particular if the resource environment has changed, e.g. when using a different or updated HPC cluster or batch system.

In the UNICORE-based implementation (where the batch system translation is automated as described in Section 5.7 and hard-coded, system-dependent paths can be easily avoided), this scenario is much simplified for the end users, as for them just the UNICORE workflow needs to be exported into a re-usable workflow (using an XML format). The exported version can easily be imported by any other UNICORE system. The only requirement is that the imported workflow tasks' resource requirements and the shared workflow variables have to be re-aligned to the new environment (that might, e.g., have a lower

number of CPU cores). If the cluster environment stays the same, but only the user changes, there is not even any need to re-configure target resource requirements, but only shared workflow variables concerning the storage of user-specific data, e.g. the location of the datasets to be used as input needs to be adjusted. In addition to reproducing experiments, the high-level UNICORE workflows can also easily be extended (cf. Section 5.6) by other scientists from the glaciology community to adapt them to their needs.

6   Related Work

There is a wide variety of work and research on scientific workflows that couple different computing-intensive applications in many disciplines. However, new research fields often pop up, recently e.g. data-intensive applications such as machine learning, data mining, or statistical analysis. As a consequence, the WMS technologies are often evolved to fit the needs of specific user communities or hardware resources, which makes them too distinct to share across systems or a broad set of user communities (Ferreira da Silva et al., 2017).

One known example is Taverna (Wolstencroft et al., 2013), which in principle is a general WMS, but is significantly driven by bio-informatics communities with the need for *High-Throughput Computing* (HTC)-driven "-omics" analyses (proteomics, transcriptomics, etc.) and thus lacks distinct support of cutting-edge HPC systems such as those used in our case study. At the same time one can observe that HPC systems quickly evolve with an ever new set of features that need to be adopted to ensure good performance of the applications, thus motivating the use of the UNICORE WMS that is specifically designed for HPC environments and constantly maintained and tuned to new HPC system designs.

Having a closer look in the Earth science domain, another field of related work are scientific gateways such as the Southern California Earthquake Center (SCEC) Earthworks portal that inherently adopts the WMS system Pegasus (Deelman et al., 2015) and DAGMan (Frey, 2003) in order to run on systems provided by the US infrastructure Extreme Science and Engineering Discovery Environment (XSEDE). Pegasus itself is just one component on top of DAGMan that in turn is based on the HTCondor middleware for HTC, which in our review did not meet the full capabilities required for HPC in general and the large supercomputers used in our study in particular.

Given the nature of the scientific gateway of the Earthworks portal and its focus on specifically only supporting earthquake science applications, it is not possible to re-use the system for our research in glaciological models and the above-described coupling approaches using European HPC systems.

Reviewing related work further leads to consideration of older WMS systems such as VisTrails (Callahan et al., 2006). Work has been done there in the past to work with emerging HPC systems, but maintenance is typically lacking today. There are also adaptations of VisTrails to specific environments such as the NASA Earth Exchange (NEX) collaboration platform, as described by Zhang et al. (2013).

To the best of our knowledge, there is no general WMS that is both mostly used with distinct workflow features (as outlined above) in the Earth science domain, and is also applicable to cutting-edge HPC systems, as required in our study to perform the efficient calculations.

7 Conclusions

Scientific workflows automate and enable complex scientific computational scenarios, which include data-intensive scenarios, parametric executions, and interactive simulations. In this article, a glacier ice flow and calving model have been combined into a single high-level scientific workflow. The ice flow is solved using Elmer/Ice, a glaciological extension to the *Finite Element Model* (FEM) code Elmer, whereas calving was simulated by the discrete element code *Helsinki Discrete Element Model* (HiDEM).

We created a workflow implementation based on the state-of-the-art UNICORE middleware suite. The workflow can easily be composed on a high and abstract level through the *UNICORE Rich Client* (URC)'s visual workflow editor. The workflow developed this way can be submitted in a fire-and-forget pattern to HPC clusters, while real-time monitoring is also possible. Such a versatile GUI-type environment that allows for automated error reporting and handling clearly gives an operational advantage. It helps to reduce time needed to debug setups prior to production and helps to deal more effectively with unexpected problems during the production phase. For this case study, the production deployment of UNICORE instances on CSC's clusters *Taito* and *Sisu* has been used.

We evaluated our workflow implementation from different points of view, such as streamlining coupling-related I/O, improving CPU utilisation, workflow extensions, usability, and portability in order to foster reproducibility. Unnecessary file copying was removed, thus speeding up I/O and as such the whole workflow. The abstracted workflow eased to allocate only as many CPU cores as needed for each step, thus avoiding idle cores and making them available for other jobs. The UNICORE-based workflow implementation can be exported to an abstract machine-readable format, so that other users interested in reproducing results can easily re-run the simulation without any change on a different platform and still obtain the same outputs generated by our experiment, or they can re-use the workflow to adapt and apply it to new datasets. Furthermore, this UNICORE-based workflow can be easily changed by simply updating the existing tasks, given they are properly configured with respect to the needed target resources. The workflow can also be easily extended due to the inherent high-level of abstraction.

While we demonstrated the workflow management system approach based on the glacier modelling case study, we believe that the requirements that we derived from our use case are in fact applicable to many other Earth Science modelling applications, and even to further scientific disciplines that involve distributed HPC resources. Hence, our UNICORE-based approach appears promising also for other e-Science cases. The high-level workflow approach allows to focus on critical workflow-related aspects such as optimised coupling-related I/O, improved CPU utilisation, and reproducibility.

With regard to future work, it would be possible to create a portal that provides even simpler access to our glaciology workflow. This might include a web-based interface where a scientist simply has to upload her credentials for using an HPC cluster, upload or point to the dataset to be used, configure some simulation-specific parameters, and finally press a button to start the workflow on one or multiple HPC clusters.

As the UNICORE workflow management system is independent from any scientific domain, we encourage other disciplines to transform and automate their e-Science steps into automated workflows. We have successfully demonstrated this

already for applications in remote sensing (Memon et al., 2018) and for interpretation of analytical ultracentrifugation experiments (Memon et al., 2013a).

Code availability. Elmer and Elmer/Ice sources are freely available at https://github.com/ElmerCSC/elmerfem. The initial coupling (shell) scripts can be obtained by directly contacting the author. HiDEM sources can be openly accessed via https://doi.org/10.5281/zenodo.1252379. All the UNICORE packages are available at http://unicore.eu. The UNICORE-based glacier model coupling workflow that can be used as template and associated Bash helper scripts are available via http://doi.org/10.23728/b2share.f10fd88bcce240fb9c8c4149c130a0d5.

To access and run the workflow, the UNICORE sites and the workflow services, and the application packages and the coupling scripts have to be installed. The intended users need to have appropriate and valid X.509 credentials, because *UNICORE Rich Client* (URC) requires them to present the credentials while accessing the workflow services.

Author contributions. SM has developed the overall workflow design, prototyping, development and realisation, which also includes the workflow deployment and administration. He has also streamlined the glacier modelling use case scripts and application deployment on CSC clusters. DV contributed the scientific problem that motivated the construction of this workflow. She has also developed the coupling script, and provided significant contributions during the workflow development, testing and deployment phases. TZ is heavily involved in the Elmer/Ice project and provided his support in the integration and deployment of Elmer/Ice. JÅ is the main author of HiDEM. HN provided input on workflow foundations, conclusions, and also worked on streamlining the manuscript. In addition, he was in charge of the application to NeIC Dellingr for CPU time on CSC clusters. MR has provided related work in highlighting scientific workflows and Earth science modelling. MB has contributed to the system architecture from the software engineering perspective.

Competing interests. The authors declare that they have no conflict of interest.

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