

# INTRODUCING DATA PROVENANCE AND ERROR HANDLING FOR NGS WORKFLOWS WITHIN THE MOLGENIS COMPUTATIONAL FRAMEWORK

H. V. Byelas, M. Dijkstra and M. A. Swertz

*Genomics Coordination Center, Department of Genetics, University Medical Center Groningen  
Groningen, The Netherlands  
Bioinformatics Center, University of Groningen, Groningen, The Netherlands*

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**Abstract:** Running bioinformatics analyses in a distributed computational environment and monitoring their executions has become a huge challenge due to the size of data and complexity of analysis workflows. Some attempts have been made to combine computational and data management in a single solution using the MOLGENIS software generator. However, it was not clear how to explicitly specify output data for a particular research, evaluate its quality or possibly repeat the analysis depending on results. We present here a new version of a MOLGENIS computational framework for bioinformatics, which reflects lessons learnt and new requirements from end users. We have improved our initial solution in two ways. First, we propose a new data model, which describes a workflow as a graph in a relational database, where nodes are analysis operations and edges are transactions between them. Inputs and outputs of the workflow nodes are explicitly specified. Second, we have extended the executional logic to trace data, show how final results were created and how to handle errors in the distributed environment. We illustrate system applications on several analysis workflows for next generation sequencing.

## 1 INTRODUCTION

In recent years, we have approached several genome wide associations and expression quantitative trait loci studies (Y. Li and R. Jansen, 2010), (Li and Swertz, 2009), (Fu and Swertz, 2007), (J. Fu and R. Jansen, 2007). Every of these analyses involves large numbers of shell or R scripts that have to be run in parallel on large compute clusters or grids. Recently, we were designated as data coordination center for next generation sequencing projects, most notably the Genome of the Netherlands project (GoNL) (BBMRI-NL bioinformatics team, 2010). The GoNL project is a Dutch National initiative funded by the Dutch Biobanking consortium BBMRI-NL to establish a HapMap of the Dutch population by sequencing 750 Dutch individuals at 12x depth in 250 parent/child trios using Illumina HiSeq 2000 sequencing. In the first phase of the project, a major computational challenge was to run thousands of analysis pipelines on 45TB of input data, each consisting of tens of protocols (scripts), to output 90TB of alignment of the DNA reads to the reference genome and

calls of Single Nucleotide Polymorphism (SNPs) in this aligned data set (analogous to the pipelines described in the 1000 Genomes project (1000 Genomes Project Consortium, 2010)). Besides a computational challenge, tracking all input and produced biomaterials adds a data management component to the problem, *i.e.* flowcells, lanes, samples, DNA libraries, trios, QC reports, raw fq.gz files, alignment BAM files and variant calling VCF files.

Starting all pipelines manually becomes very time consuming for such a large and computationally intensive research, *e.g.* each sample has been measured in three lanes on average, resulting in 2250 lanes total needing alignment requiring 15 analysis steps totaling each a runtime of 50 hours of computation on four cpu cores. Furthermore, conducting the data management, which includes keeping track of what computational protocols are used to produce particular research results, separately from computational management makes it error prone.

In the first version of the MOLGENIS (Swertz and Jansen, 2007), (M. Swertz and R. Jansen, 2007) computational framework - MCF (H. Byelas and M.

Swertz, 2011), we aimed to combine computational and data management in a single system. However, several important functionalities were left out of the initial solution. These included easy tracing of the data produced and run-time error handling during workflow execution. By error handling, we mean scenarios which can be applied if some data is missing or quality indications for results are low.

In the new version of the MCF, our main goal is to help a user to understand how the complex analyses were accomplished and what computational processes were used. In this paper, we describe the design and implementation challenges to specifying data provenance and handling errors during workflow execution. In particular, we present our solution for the NGS workflows used in the GoNL project.

This paper is structured as follows. Section 2 reviews related work in the context of data provenance and error handling in other workflow management systems. Section 3 describes the new model in details. Section 4 reviews the system design in rough lines. Section 5 details the new functional logic of the system for error handling for generic pipelines and, in particular - for the NGS pipeline and gives examples of generated user interfaces. Section 6 discusses our experience with using the system in practice. Section 7 concludes the paper.

## 2 RELATED WORK

Extensive overviews of data provenance approaches and techniques are given in (Glavic and Dittrich, 2007) and (Simmhan and Gannon, 2005). We did not set out to develop a new theoretical model for data provenance, rather, we are interested in using a lightweight data provenance approach for the specific bioinformatics domain. In our scenario, several individual researchers involved in the same project would like to collaborate on analysing data. Here, data sources, intermediate and final analysis results and computational processes are often shared between researchers to speed up the analysis. Consequently, data and process oriented provenance should be combined in one solution. Without proper data annotation, the analysis results can easily be overwritten or duplicated when the analysis is re-run on the same data with other parameters, in other execution settings or just at an other time. We are interested in methods to avoid such situations.

J. Yu *et al.* present a taxonomy of workflow management systems in their work (Yu and Buyya, 2005). Data provenance is modelled and implemented in various ways in different data warehouses and workflow

management systems. In the Taverna 2.0 workflow system (Oinn and Greenwood, 2005), the semantics of workflows is modelled using so-called traces (Sroka and Goble, 2010), which record sequences of events. These events can be of three types: input events, representing values on input ports, atomic executions and output events, *i.e.* values on output ports. The model is implemented in the system using the file-based database. Taverna can remember workflow runs and only saves the results to file system after running a workflow with different inputs. Users have the possibility to switch data provenance options off, which can give a performance benefit and reduce a disk-space usage. By default, Taverna stores the input values, intermediate values and the results of workflow runs in memory. When Taverna is closed the values are lost. In-memory storage can also be switched off for workflows where passed data is large. In Kepler (Altintas and Berkley, 2004), ordered trees are used to represent data products of workflows (M. K. Anand and T. McPhillips, 2009). These trees are stored in trace files using the XML format. Kepler allows browsing and navigation in the history of execution traces by querying trace files. Queries can become large and complex to produce scientifically meaningful results. Kepler also enables outputs of one run to be used as inputs of another. The specific bioinformatics management systems Galaxy (Blankenberg and Taylor, 2007) tracks metadata to ensure reproducibility of analyses. However, it is not sufficient to capture the intent of analysis. Galaxy is not really integrated with any data management system. All the results produced by all analysis runs are saved in a disk storage, which considerably increases the storage requirements for large analyses. Furthermore, Galaxy considers a workflow as a black box and if errors occur during execution, they will be received as the end result of the analysis.

Keeping in mind features of the workflow systems we are aware of, it emerges that even data provenance is present to some extent in all of them. However, an automatic error handling is missing. Adding error handling can save a lot of time for computationally intensive analyses, where a re-run of an individual analysis operation *ad hoc* instead of re-running the whole workflow later would save a lot of time and efforts. It can be difficult to find a good quality indications of the successful completion of operations. These indicators should be present in the model to specify recovery scenarios. Comparing our developments to the above workflow systems, we aimed to create a specific solution for a particular bioinformatics analysis (*i.e.* NGS workflows). However, we want to introduce more advanced error handling into the system. In our

case, the set of possible failures is definite, hence, it is possible to overlay all of them. This is discussed in detail below.

### 3 INTEGRATED METADATA MODEL

Before talking about the integrated model for data and computational management, we briefly review the main requirements for the system. First, it is important to provide less technically involved bioinformaticians with simple interfaces to specify the workflow of commands they need, while scaling up to hundreds of jobs to get the terabytes of genetic data processed. Furthermore, the meta model should efficiently specify data provenance and workflow execution logic. Second, it should be possible to monitor workflow execution and the data products produced in these workflows in one seamless solution. Third, it is crucial to spread executions among the available resources to shorten the analysis time, thereby improving system productivity. Finally, research results and quality control scores must be efficiently represented for final users. The results should be considered as part of the biological entity that is the target of study (e.g. samples, lanes and trios in GoNL; cohorts, individuals, markers, probes, and phenotypes in QTL studies). In our scenarios, actual data results are stored on remote disks, where computations took place, only data quality indications are recorded in the database for monitoring.

MOLGENIS is a software toolkit to rapidly generate rich biology software platforms from database and user interface models which each are described in the XML format. We currently use the eXtensible meta data model for Genotypes And Phenotypes (XGAP) as main model which already covers an extensive list of biological experiments (Genomics Coordination Center, Groningen, 2011), (M. Swertz and R. Jansen, 2010). This core of the model is reused for many projects and is now being further developed for other domains in collaboration with NL-NBIC, BBMRI-NL, EU-GEN2PHEN, EU-BioSHARE, and EU-PANACEA consortia and consists of a number of modules. However, each experiment/biotechnology can have its own specific extension of the shared model. Here, we discuss only the specific data model extension used for NGS experiments (MOLGENIS NGS) combined with the computational data model extension (MOLGENIS Compute), which is generic for any computational application generated using MOLGENIS.

The design of the NGS model (Fig. 1) is based

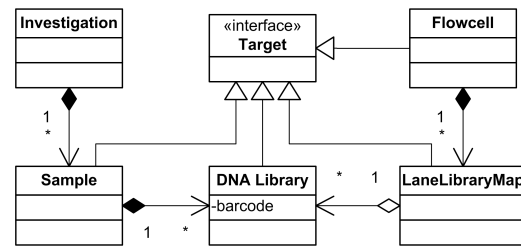


Figure 1: Core of the NGS model.

on the laboratory process when using Illumina HiSeq 2000 which produces the input data for our analysis workflows. It starts in a "wet lab", where a set of samples (*Sample* elements) are taken from individual(s). These samples are involved in one or more analysis projects, which are the *Investigation* elements. *Samples* are split into *DNA Libraries*, optionally using barcodes. These libraries are then analysed in *Flowcells* in various orders, where currently eight lanes of one flowcell can be filled with several libraries of samples. Information about mapping libraries to flowcell lanes and corresponding result analysis data is the input "worksheet" for NGS analysis workflows. In addition to the input from the "wet lab" data, we introduce the *Target* interface into the model to enable us to later uniformly refer to these subjects from different analyses. The *Target* interface is present in the generic MOLGENIS model. All NGS analysis targets implement it.

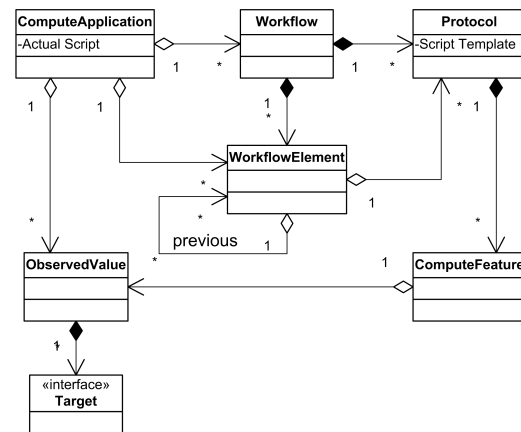


Figure 2: Core of the compute model.

The simplified compute model is presented in Figure 2. The *Workflow* element represents the whole analysis. *Workflow* consists of *WorkflowElements*. *WorkflowElements* know their forerunners (dependencies). In this way, a workflow graph is built up, where *WorkflowElements* are the nodes of the graph and edges are the transactions between them. Every node performs an operation, which is specified in a *Protocol* element. Our system aims to support specifying of

any external analysis tool, which can be invoked from a command line or be run as an executable script (e.g. a shell or R-script). Each *Protocol* contains a script template. The use of templates is described in Section 5.1. *Protocol* can have a number of *ComputeFeatures*. In the user interface, every *ComputeFeature* becomes a field to enter an analysis parameter. Some analysis parameters can be predefined as having a default and stored in the database, or can be marked to be technical so not for view by the end-user but only the protocol designer. The *ComputeApplication* elements record application of *Workflows* and *Protocols* during the analysis, i.e., what actual analysis scripts (filled in templates) were actually run. *ComputeApplication* records for each *ComputeFeature* what parameters or data files were used (input) and what files or variables were produced (output) using *ObservedValue* element to link *ComputeFeature*, *Targets* and *Protocol*.

To conclude, the *Target* interface is the link between the data management for the NGS analysis and for computation management, i.e., the subclasses *Sample* and *Lane* are typical targets of compute protocol applications. The implementation of this model into an integrated software solution is the topic of the next section.

## 4 FRAMEWORK ARCHITECTURE

Since, the system design has not been changed extensively from the first version of MOLGENIS compute (H. Byelas and M. Swertz, 2011), we only present it briefly here. In our developments, we concentrated on the functionality requested and that most appreciated by the end system users. We have two types of users:

- bioinformaticians, who design and edit analysis workflows;
- biologists, who run analyses and examine results.

### 4.1 System Design

The visual representation of the system architecture (Figure 3) has been changed accordingly to the new use-case scenarios and functionality.

We have learnt in practice, that bioinformaticians want to have a simple way to import/export the workflows and NGS data into the system, where, later, they can edit some elements of it. We support two ways to import workflows. First, it is an import of a workflow described as an Excel file in the MOLGENIS standard format. Here, each Excel sheet represents

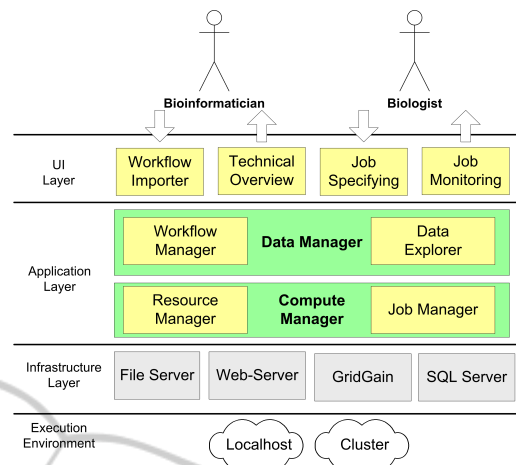


Figure 3: Generic architecture for MOLGENIS compute applications.

a database table with workflows data, i.e., one Excel sheet can list the properties of *Workflows*, *Protocols*, *ComputeFeatures* and so on. Second, it is a single tool import from the Galaxy (Blankenberg and Taylor, 2007) XML tool description file. Here, a single tool operation becomes the whole analysis workflow. Additionally, for NGS data, we support importing a 'worksheet' listing all *Flowcells*, *Lane*, *Sample* and *emphLibrary* properties from one Excel file that we received from the "wet lab". Another functionality, we found important for bioinformaticians, is to be able to overview the system performance and to receive technical reports about workflow executions, e.g., how many workflows completed/failed, execution times, CPU load, failure frequency.

Biologists' requirements are straightforward. They want to be able to start an analysis pipeline in a user friendly way by selecting analysis targets in batch, setting batch level and individual level parameters, pushing a button to generate scripts and submit those to the compute back-end, monitor its execution progress and finally see workflow results locally. In our scenario, results include log files from analysis tools, the output files of the analysis procedure and quality control scores. Hence, we concentrated our developments on two user interfaces for biologists to enter analysis parameters and monitor analysis execution.

Both biologists and bioinformaticians can browse and edit the NGS database. If a biologist is more interested in reviewing results, a bioinformatician is more interested in editing workflow, which is nothing more than editing database records. These functionalities are standard for MOLGENIS-based systems. Executing workflows includes starting resources to execute them and sending analysis scripts for execution.

It is implemented in the Compute Manager module (Fig.4).

## 4.2 System Topology

We also refined the system topology (Fig.4) specifically for the NGS analysis. Now, all analysis scripts run in one place, e.g. in the Millipede cluster in Groningen (Millipede Cluster Team, Groningen, 2010). This solution was taken to avoid transferring large files in the network. The input file sizes for the GoNL project are about 6-9 GB and the intermediate workflow results grow up to 60 GB per Lane, totalling 45TB of input data and 450TB of intermediate data. In the future, we are planning to re-introduce a grid solution into the system, addressing then the need for optimised large data management in grid environments. All statistics are stored in the MOLGENIS database, based on MySQL, next to the cluster. Users have an access to the database through a MOLGENIS-generated user interface (see Section 5.4) running on the Tomcat web server.

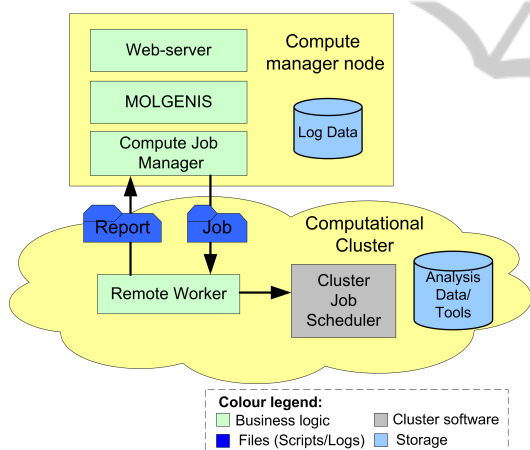


Figure 4: System topology for NGS analyses.

All analysis scripts are generated in the database and transported from *Job Manager* to the cluster. The communication and data transfer are implemented using the GridGain development platform (Ivanov, 2010) and the Ganymed SSH-2 library for Java (Swiss Federal Institute of Technology, 2006). In the implementation using GridGain (shown in Fig.4), the remote *Worker* receives jobs and forward them to the cluster PBS scheduler and monitors their execution. When an analysis operation is finished, *Worker* transfers specified log files into the MOLGENIS database. In the implementation using Ganymed SSH-2, *Job Manager* sends jobs directly to the cluster PBS scheduler via a secure channel to the frontend cluster node. This increases the load on the frontend node and can

cause a problem when cluster is heavily used by other users. Hence, the GridGain solution is preferable for a large-scale analysis and better tested so far. All analysis tools used in workflows are pre-installed in the cluster.

## 5 DATA PROVENANCE AND ERROR HANDLING

### 5.1 Using String Templates to Specify Analysis Products

All run scripts and log information about analysis runs are stored in the MOLGENIS database. The exact location of files produced during an analysis is known only after a user has entered all input parameters in the user interface and actual analysis script have been generated. However, we would like to have a way to pre-define file locations in the database. For this, we use the Freemarker template processor that we use to define *ComputeProtocol* scripts to pre-format output locations. The use of templates for specifying input/outputs of operation allows us to trace data. An example of a script template of the *Protocol X* is listing below.

```

${tooldir}/${bwa} aln
${resdir}/${genome}/indices/${index}
${datadir}/${bwa-in} -t ${cores}
-f ${bwa-out}
    
```

Variables in curly brackets will be replaced with actual values during template processing. Some variables are predefined in a database, others are received from a user interface. Furthermore, some variables can consist of a combination of others: we call these *complex* variables. They are, in turn, also constructed using templates. In this template, *bwa-in* and *bwa-out* are variables, which specify input and output files for the analysis operation. The template for *bwa-out* is shown below:

```

${outdir}/${sample}/${id}.${index}.sai
    
```

Here, the *complex* variable consists of four *simple* variables, which are placed in curly brackets. In our data model (Section 3), *bwa-in* and *bwa-out* are *ComputeFeatures* of the *Protocol X*. After applying *Protocol X*, they will receive actual values. For example, *bwa-out* can be given the value:

```

results/run01/bwa/sample01/bwa01.sai
    
```

This value of *ComputeFeatures* *bwa-out* is recorded in a database as an *ObservedValue*. Hence, we know the locations of output results of analysis

operations. Typical analysis tools, in particular, tools we are using in the NGS workflow (e.g. GATK (The Genome Analysis Toolkit, 2011), FastQC (FastQC, 2011)), produce several outputs of two types: these are the actual analysis output and log files about analysis execution. Besides log files from analysis tools, cluster PBS software writes script command line error/outputs to the cluster file system. We consider these files as technical information about the analysis execution. We add information about analysis run time, machine on which analysis took place and sizes of data output files to the log file as well. All this technical information is transferred back to the MOLGENIS database. Now, we can construct a summary about workflow execution and a user can review it online without searching for it in the cluster storage.

### 5.2 Generic Error Handling for Analysis Workflows

In general, the content of the log files and actual existence of output files on the cluster are good indications for successful analysis execution. First we will discuss the problem indications and resolving strategies we are considering for a generic workflow. We propose two error indicators, which are unexpected output size and output absence. We mark them as UNEXP. and ABSENT, respectively. Here, by an expected size, we mean file sizes in bytes. Usually, it is possible to estimate an approximate size range for output files in terms of MBs or GBs, for example, the range between 500 MB and 2 GB. In bioinformatics analyses, this number often depends on the size of an input dataset.

Our recovery strategies also include two operations. The first is to set an error indicator to a database and continue analysis (INDIC.). The second is to repeat an analysis operation one or more times (REPEAT) until a correct result is achieved, which is a kind of a backward error recovery. In the case of repeated failures (e.g.  $n > 3$ ), the analysis should be stopped. Recovery operations are applied if any kind of output, the analysis data or log files, are absent.

		Analysis data		
		Status	OK	UNEXP.
Log files	OK	OK	INDIC.	REPEAT
	UNEXP.	INDIC.	REPEAT	REPEAT
	ABSENT	INDIC.	REPEAT	REPEAT

Figure 5: Generic error/recovery matrix.

The proposed matrix of error indications and re-

covery operations for generic workflows is shown in Figure 5. We extended the Compute model (Section 3) with a *RecoveryOperation* element to incorporate this matrix into the system logic. We also added two fields to the *ComputeFeature* element: these are the type of output and the expected file size range (see Fig. 6). *ComputeFeature* that specifies an output type, can have values *data* or *log*. For example, the expected size of the error log file produced by the cluster software, if a script ran successfully, is zero bytes. Hence, if the size is larger, we indicate it in the *ObservedValue* object and transfer the contents of the log file to the database.

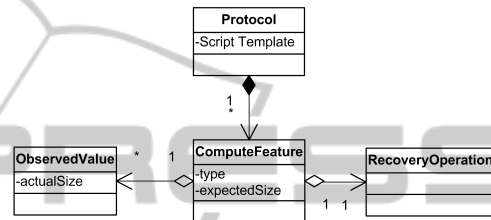


Figure 6: Introducing error-handling into compute model.

Additionally, we found the operation execution time being a practical indicator. We always indicate *ComputeApplications* in our NGS workflow, if their execution take less than 30 seconds. Certainly, more advanced error handling can be applied for particular cases, when we have more knowledge about the analysis operations and the correlations between their input and output data. This situation for the NGS analysis is described in the next section.

### 5.3 Error Handling for the NGS Workflow

The NGS analysis workflows are highly computationally intensive. For instance, our NGS lane analysis workflow takes more than 50 hours to run on a machine with 4 3GHz AMD Opteron cores. Having thousands of lanes to analyse for the GoNL project, we would not like to rely only on the context of the log files. We know that the number of DNA sequence reads is constant from input workflow files to final results of the analysis. The number of reads in sequence data files can be calculated using the Genome Analysis Toolkit (GATK (The Genome Analysis Toolkit, 2011)). Checking this pre-/postcondition before/after workflow operations guarantees correct completion of the analysis. Now, we can leave out reading log files for error handling and, instead of it, we just take into account the number of DNA reads in analysis files.

It simplifies the error handling logic (see Fig. 7), but adds some extra computational overhead to the

Analysis data			
Status	OK	UNEXP.	ABSENT
	OK	REPEAT	REPEAT

Figure 7: Error-handling matrix for the NGS workflows.

analysis (*i.e.* a counting reads operation, which takes about half an hour for datasets we are considering in our project). Hence, it is important to select right points in the workflow logic, where to perform advanced conditional checks. How results of the workflow execution are shown to users is discussed in the next section.

### 5.4 Implementation of User Interfaces

MOLGENIS-generated web interfaces are used for diverse bioinformatics applications. Because of this automated procedure the style of user interfaces is uniform easing learning the system. For the NGS analysis, a user have an access to several generated interfaces to overview lanes, flowcells *etc.* for analysis, edit different elements of workflows, and view progress and analysis results.

In practice, after importing a workflow to a MOLGENIS database, a user commonly can edit

- a sequence of workflow elements,
- analysis script templates or their inputs/outputs,
- default values of parameters.

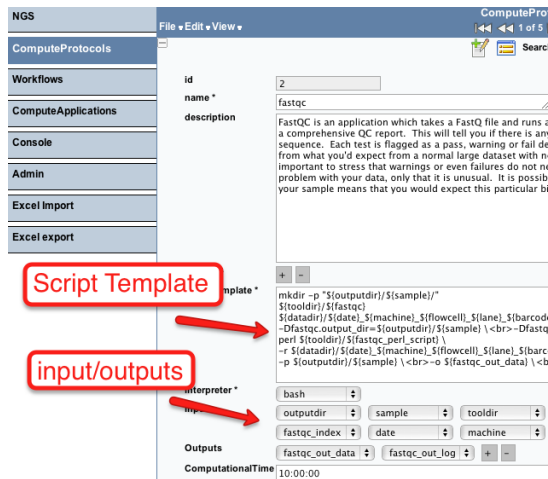


Figure 8: Generated web user interface for editing an analysis element.

An example of the generated user interface for *ComputeProtocol* is shown in Figure 8. Here, users can edit the listing of a template and specify inputs/outputs, which they are interested in. It is com-

mon that an analysis workflow will contain a few typos in templates or wrong paths to analysis tools, especially when new protocols/tools are added or when the system is deployed in a new environment. Hence, a bioinformatician uses this interface mostly during the workflow testing. Interfaces to edit a sequence of workflow elements and default parameters look similar to the one presented in Figure 8.

We show a progress of a workflow using a simple coloured table. The table displays the names of analysis steps and a number of *ComputeApplications* in steps, which are running in parallel. Colours indicate the status of a step.

Figure 9 shows the workflow progress table with the running NGS alignment analysis. This workflow consists of 15 steps and, 19 *ComputeApplications*, which are generated from 12 different *ComputeProtocols*. In some steps, *ComputeApplications* are running in parallel.

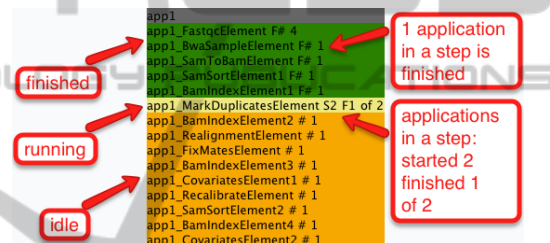


Figure 9: Workflow monitoring.

In Figure 9, a number of steps is finished, one is currently running and some are waiting in a queue. In the step currently running, one *ComputeApplication* is already finished, but the *JobManager* (see Fig. 3) is waiting for the second *ComputeApplication* to be finished before starting the next step.

Even if we are using one table per workflow, this visualisation does not scale well to show many running pipelines efficiently. Furthermore, it is not really informative, if a user wants to see dependencies or execution times of workflow elements in a workflow in a single image. Some ideas on how to improve current workflow visualisation are discussed in Section 6.

Another important functionality is to have an overview of the results of analyses when it is finished. As it is mentioned in Section 5.1, we store all run scripts and log information about runs in a database as *ComputeApplications*. Figure 10 shows an example of a single analysis operation execution. Here, a user can see an actual script, which has been run, and the logs about its execution. In this example, the error log is empty, indicating the successful completion of the operation. A user can navigate from *ComputeApplication* to its *ObservedValues* to see parameters of the analysis.

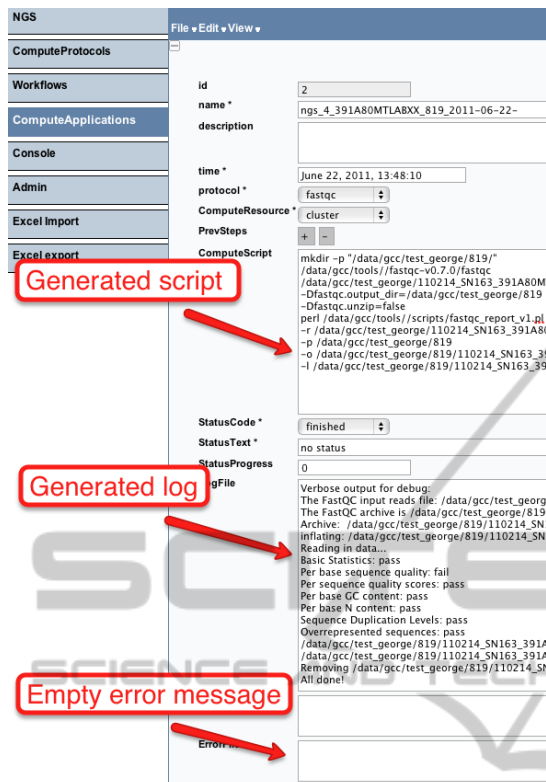


Figure 10: Viewing analysis results in the user interface.

To summarise, we enable a user to navigate through different user interfaces and review all details about the analysis and its targets online. Making a statistical summary about the analyses run is also possible, but this completely depends on particular user needs and wishes and we do not standardise it.

## 6 DISCUSSION

The main results and findings obtained during this research can be considered in three areas.

*Specifying an analysis:* We have tried to combine the NGS data model with the generic model for computational management. This leads us to the specific solution to support only NGS analysis workflows. We narrowed the possible structural design of the workflow. For example, we left out conditional execution of workflow elements and iteration over several parameters of a workflow element. This was done, because we do not need these complex mechanisms in workflows we consider necessary for NGS. We have also not included dependencies of analysis operations on resources, such as analysis tools, in the model. We aimed to use a less complex workflow model, that covers practical problems for NGS analyses.

*Monitoring analysis execution and error handling:* Defining one explicit pre-/post-condition, *i.e.* a number of DNA sequence reads, which guarantees the correct completion of the operation, allows us to easily introduce error handling into the system implementation for NGS (see Fig. 7). Theoretically, it is possible to define such indications for any generic analysis operations. However, it can be time-consuming to find different criteria and implement it, especially, if the number of analysis operation is large and their nature is different. The implementation basically includes implementing a log/error file parser, which should interpret outputs from analysis tools. These tasks are not complex, but depend directly on a number and complexity of tools and their expected outputs. Still, our recovery matrix in Figure 5 is easy to implement for generic workflows and use in the distributed execution environment.

We show a progress of a workflow in a coloured table (Fig. 9). A number of interesting aspects, such as a workflow graph structure, execution times of individual workflow operations, actual machines where executions take place and applying error-handling applications, are missing in the current progress representation. We are planning to incorporate these aspects in a future version, where the workflow will be visualised as a graph of analysis operations. A pop-up window with detailed information about each operation will be shown, when a user navigates through a workflow graph with a mouse.

*Presenting analysis results:* Even if we save all logs produced by analysis tools to a database, the information would not always be informative for an average user. Users can be familiar with running complete workflows and interested in the final analysis results. Adding simple indicators to the logging information, such as execution times, sizes of output files *etc.*, raises the quality of logging reports. Furthermore, it helps to foresee what computational resources will be needed to run an analysis, in terms of computational time and storage capacity.

Having all the information about analyses means, more views on data can be constructed to show a biological target and the analyses applied to it. The generated user interface is fully customisable, so that it can be adjusted for user preferences. Some information can be hidden in a user interface, which makes a view on the data more compact and easier to comprehend.

## 7 CONCLUSIONS

We demonstrated a data model to record analysis



provenance and a data model to record NGS analyses. We reported implementation of this model and extension of the existing compute framework to accommodate the large scale of analysis in the MOLGENIS open source software (Genomics Coordination Center, Groningen, 2011). Currently we are using these models for both GoNL and in-house analyses. Based on these results, we are convinced that newly established NGS centres can benefit from this work when setting up data management and analysis infrastructure, optionally using the MOLGENIS framework to speed up customisations where needed.

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