Extraction and Representation of *in silico* Biological Methods from the Literature

Geraint Duck Email: duckg@cs.man.ac.uk Web: http://www.cs.man.ac.uk/~duckg/

Supervisors: Robert Stevens, Goran Nenadic and David Robertson

Research Group: Text Mining (TM)

The current shift towards *in silico* biological experimentation is making deciding on the "best" method for an experiment challenging for current researchers. We hypothesise that each field can be characterised by the methods employed providing a way of exploring potential methods for a given task. For *in silico* experiments, we define databases and tools as the key elements of a method.

Introduction

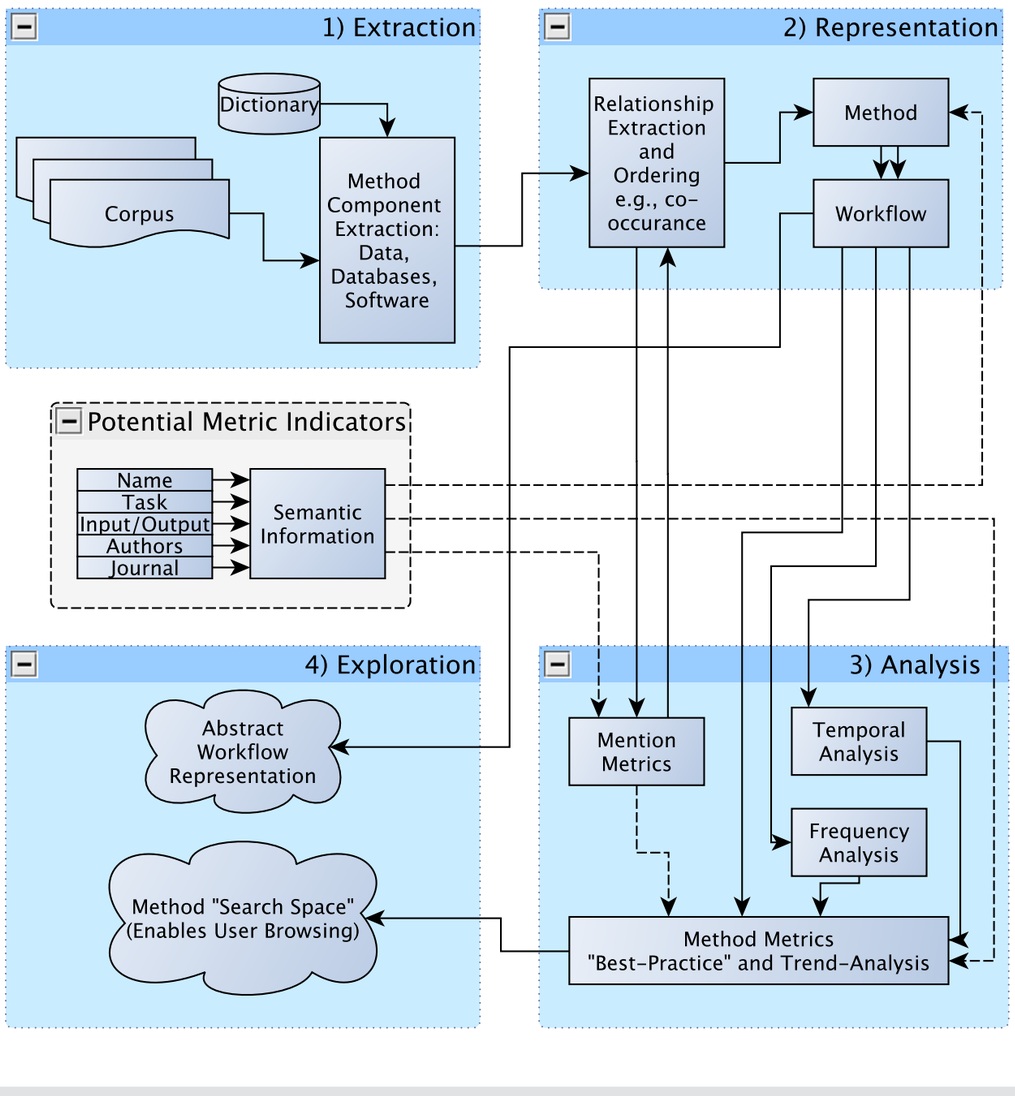
- Methods enable research and new knowledge
- They answer: What? Why? Where? How? When?
- Define "Current Approach" and "Best Practice"
- Issues of Reproducibility and Replication
- Our Focus: Bioinformatics and Computation Biology

Aim and Hypothesis

- Aim: To design, develop and evaluate a framework for literature extraction and representation of method
- Hypothesis: We can extract *in silico* biological methods from literature assisting method selection

Method

Figure 1: Method Overview



Discussion

- Preliminary analysis has highlighted some of the challenges of this task (e.g., see Figure 2)
- These challenges arise due to the volatile nature of the fields we are investigating making a solely dictionary based approach insufficient
- Once resolved, we will analyse database and tool usage throughout the literature

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Extraction Example

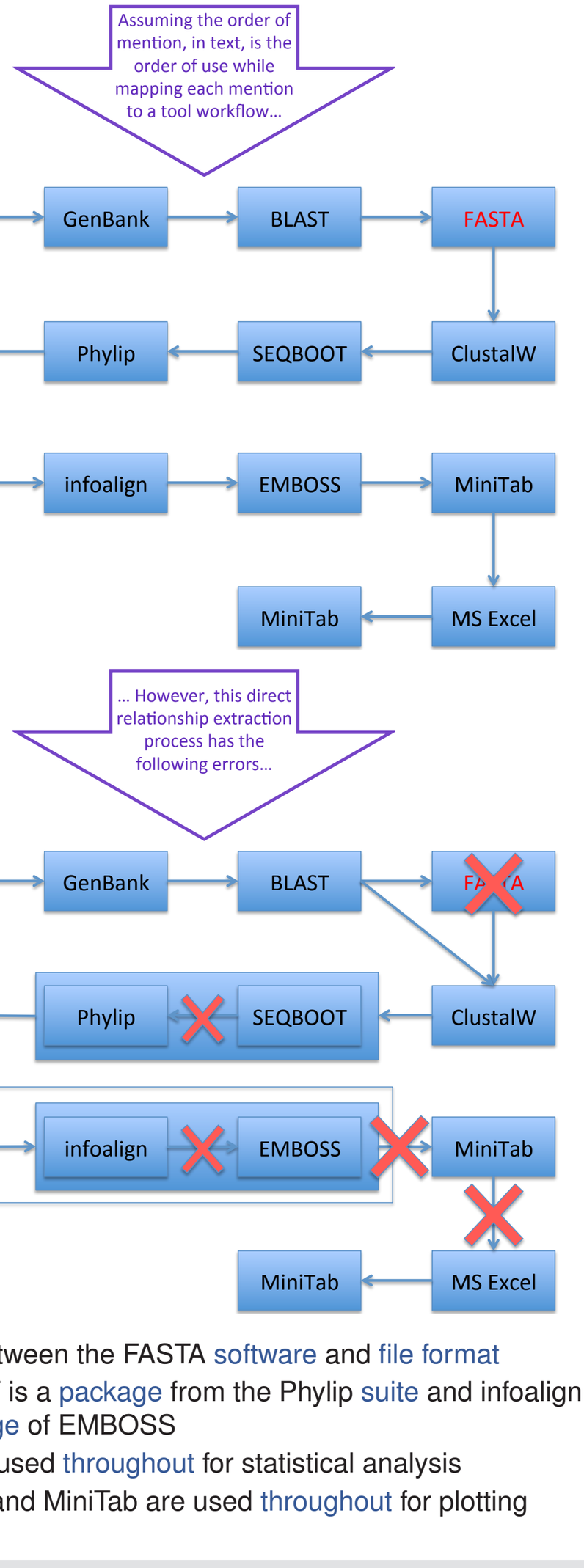
Figure 2: Example Extraction Workflow Process; Lagerström et al. (2006)

... all sequences were aligned ... using ... ***BLAT*** 3.0 ... in which case the ***GenBank*** sequence was used...

... divided ... by ***BLAST*** searches ... were combined into a *FASTA* file and aligned using ... ***ClustalW*** 1.82 ... The alignment was bootstrapped ... using ***SEQBOOT*** from the ... ***Phylip*** 3.6 package ... *[excerpt removed]*

... branch lengths were estimated in ***TreePuzzle*** using the following parameters ...

... constructed and scored automatically using a *bash-script* that utilized ***ClustalW*** as alignment engine and ***infoalign*** from the ***EMBOSS*** 2.8.0 package for scoring, ... All statistical analysis was performed using ***MiniTab***. Graphs were plotted using ***Microsoft Excel*** and ***MiniTab***.



Issues:

- Conflict between the FASTA software and file format
- SEQBOOT is a package from the Phylip suite and infoalign is a package of EMBOSS
- MiniTab is used throughout for statistical analysis
- MS Excel and MiniTab are used throughout for plotting graphs