Opportunities for Automated Workflow and Planning with Robot Scientists

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A natural extension of the trend of increased involvement in science is the concept of a Robot Scientist [King et al. (2004),King et al. (2009)]. A Robot Scientist automatically: originates hypotheses to explain observations, devises experiments to test these hypotheses, physically runs the experiments using laboratory robotics, interprets the results to change the probability of hypotheses, and then repeats the cycle (Figure 1). Robot Scientists can autonomously execute high-throughput hypothesis led research. In addition to automating experimentation Robot Scientists are well suited to recording scientific knowledge: as the experiments are conceived and executed automatically by computer, it is possible to completely capture and digitally curate all aspects of the scientific process [King et al. (2009)]).

The first Robot Scientists are Adam and Eve (Figure 2). The advances that distinguish Adam and Eve from other complex laboratory systems (such as high-throughput drug-screening pipelines, and X-ray crystallography crystal-screening systems) are their AI software, their many complex internal cycles, and their ability to execute individually planned cycles of experiments in high- throughput. Adam was designed to plan and execute microbiological experiments. Adam was fully automated and there is no essential requirement for a technician, except to periodically add laboratory consumables and remove waste. Adam was the first machine demonstrated to have autonomously discovered novel scientific knowledge [King et al. (2009)]. Eve is designed to automate drug discovery.

There are many opportunities to improve Adam and Eve using automated workflows and planning. Below I describe some of these opportunities in Adam. The target of

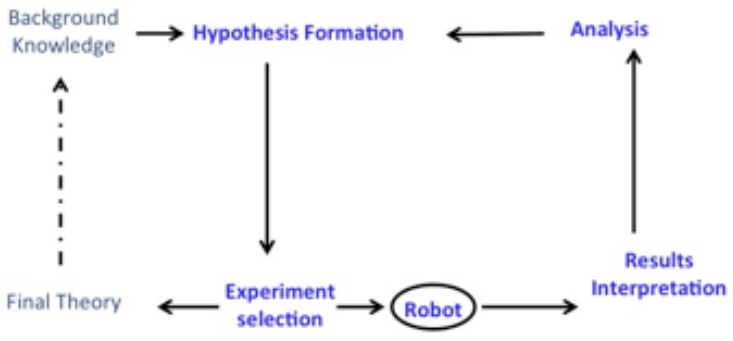

Fig. 1. Robot Scientist workflow, blue.

Fig. 2. Picture of Eve.

Adams investigation were locally orphan enzymes. These enzymes catalyse biochemical reactions known to be in yeast, but for which the coding genes are unknown. Adam used bioinformatic methods to abduce genes that could encode these orphan enzymes - hypotheses. However, there are many orphan enzymes, and we manually (and greedily) selected the enzymes for Eve to investigate that we estimated to be most experimentally tractable based on availability of metabolites. This strategy was not necessarily the best. It would be better automate and integrate such problem selection tasks using planning.

In developing Adam a large amount of effort was put into developing the software to control the laboratory automation (robotics). But currently Adam dont use any workflows, with only some planning to fit investigations onto plates, and there remain many opportunities to improve Eve using workflows and planning technology. A key practical difficulty in applying workflows and planning is the lack of a good standard operating systems for laboratory automation.

Another area where there are many opportunities to improve Adam using automated workflows and planning is in experiment interpretation. The function of most genes in S. cerevisiae that when deleted results in qualitative effects (such as no growth) have already been discovered. The remaining genes result only in quantitatively effects when deleted, e.g. they may have slower growth (bradytrophs), faster growth, higher/lower biomass yield, etc. This required Eve to measure small quantitative difference, which in turn required application of statistical experiment design and use of machine learning methods to determine which results were repeatable. To implement these methods Adam used ad hoc scripts. Workflows and planning technology would have been better: more efficient and enabling better annotation.

References

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