

The Project

The Karr Model

Karr, Jonathan R., et al. "A whole-cell computational model predicts phenotype from genotype." *Cell* 150.2 (2012): 389-401.

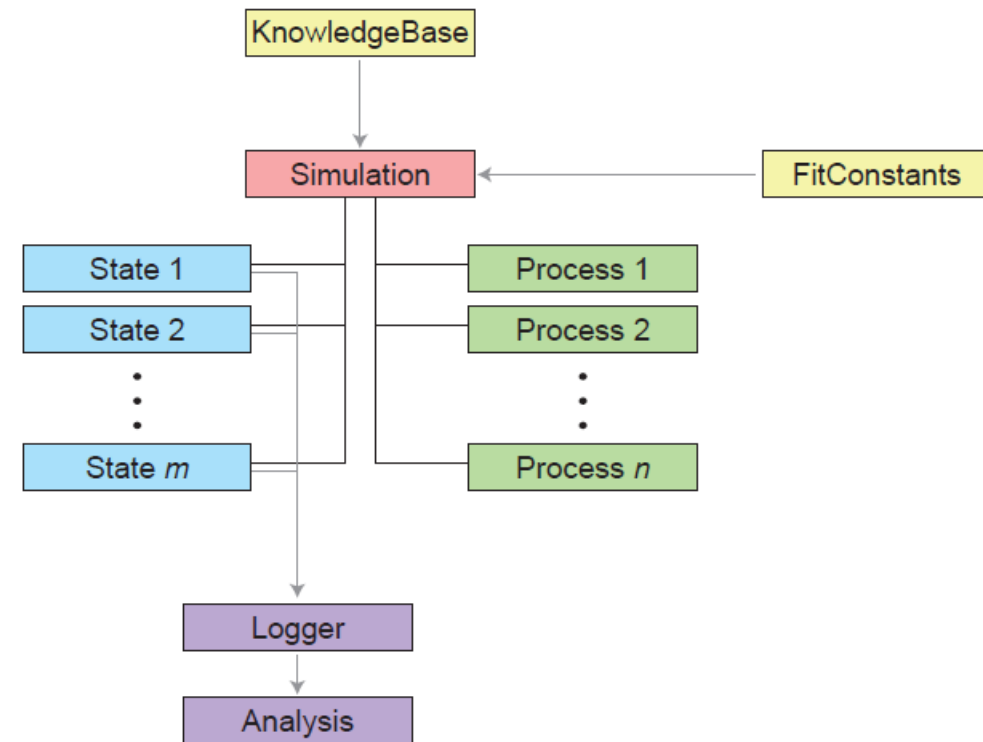
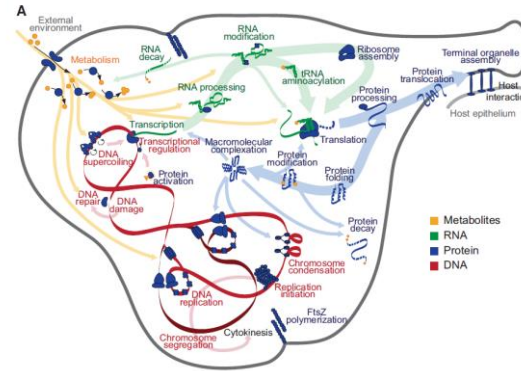
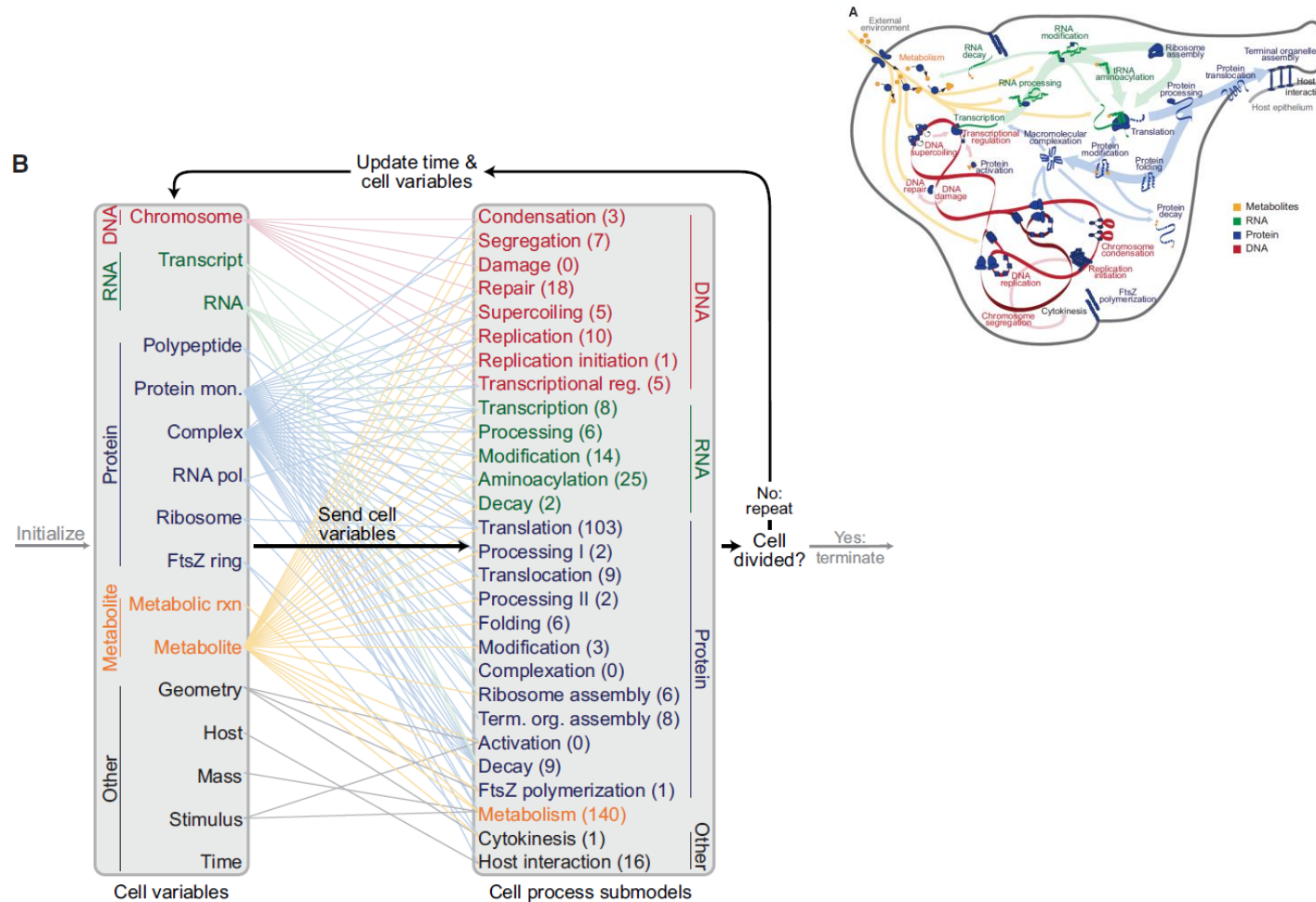


Figure 1. *M. genitalium* Whole-Cell Model Integrates 28 Submodels of Diverse Cellular Processes

Schematic S17. Whole-cell model architecture.

Our Model

General Classes

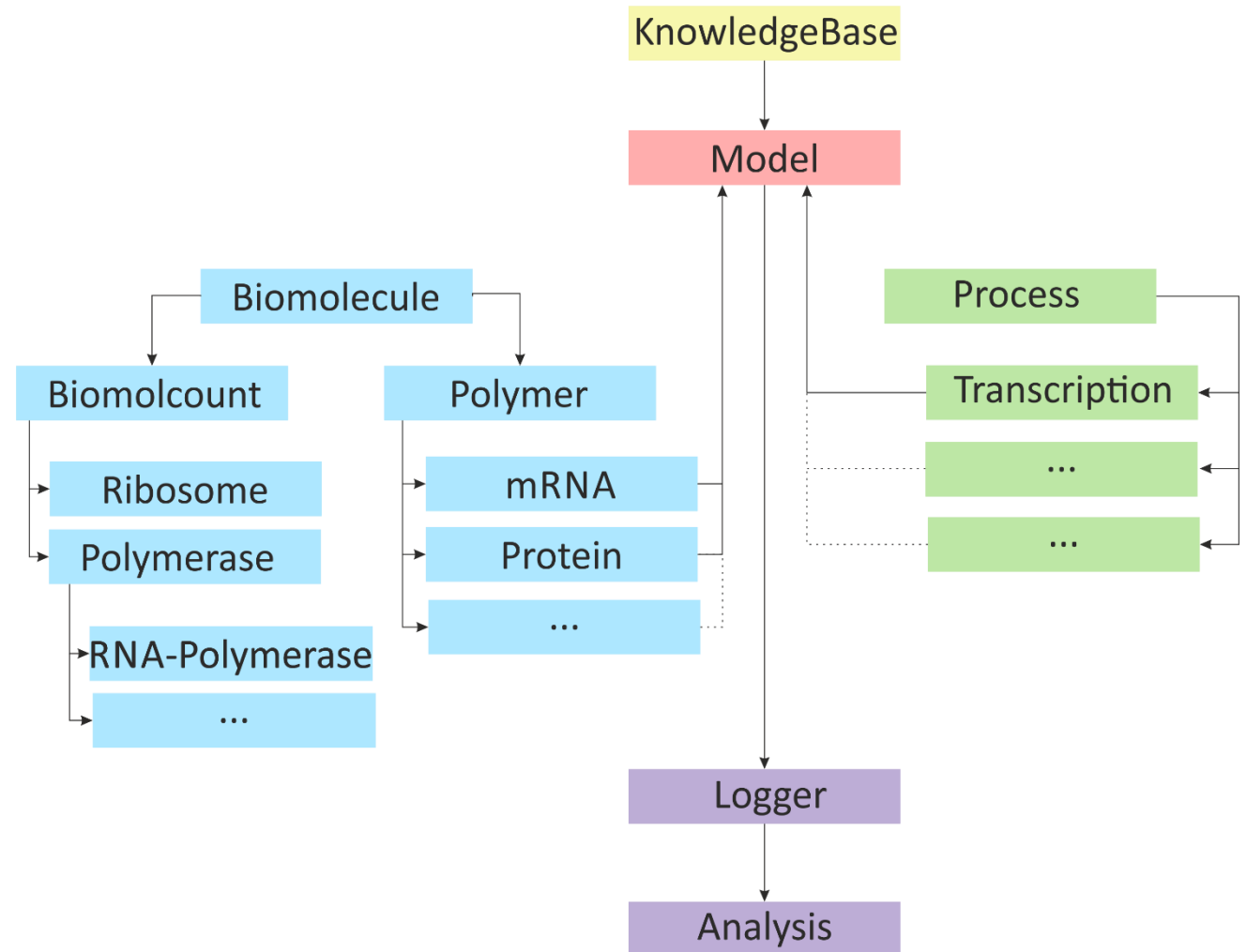
- holding general information

Count Classes

- Counting number of molecules

Property Classes

- Holding specific property of e.g. state or process



Our Model - Task and Groups

1. Read, Understand
2. Write, Improve

Group
Input Generator/Knowledgebase
Transcription
Replication
Translation
Visualisation
Metabolite
Logger/Output Generator

