Cytokinesis group

Submodels `FtsZPolymerization` and `Cytokinesis`

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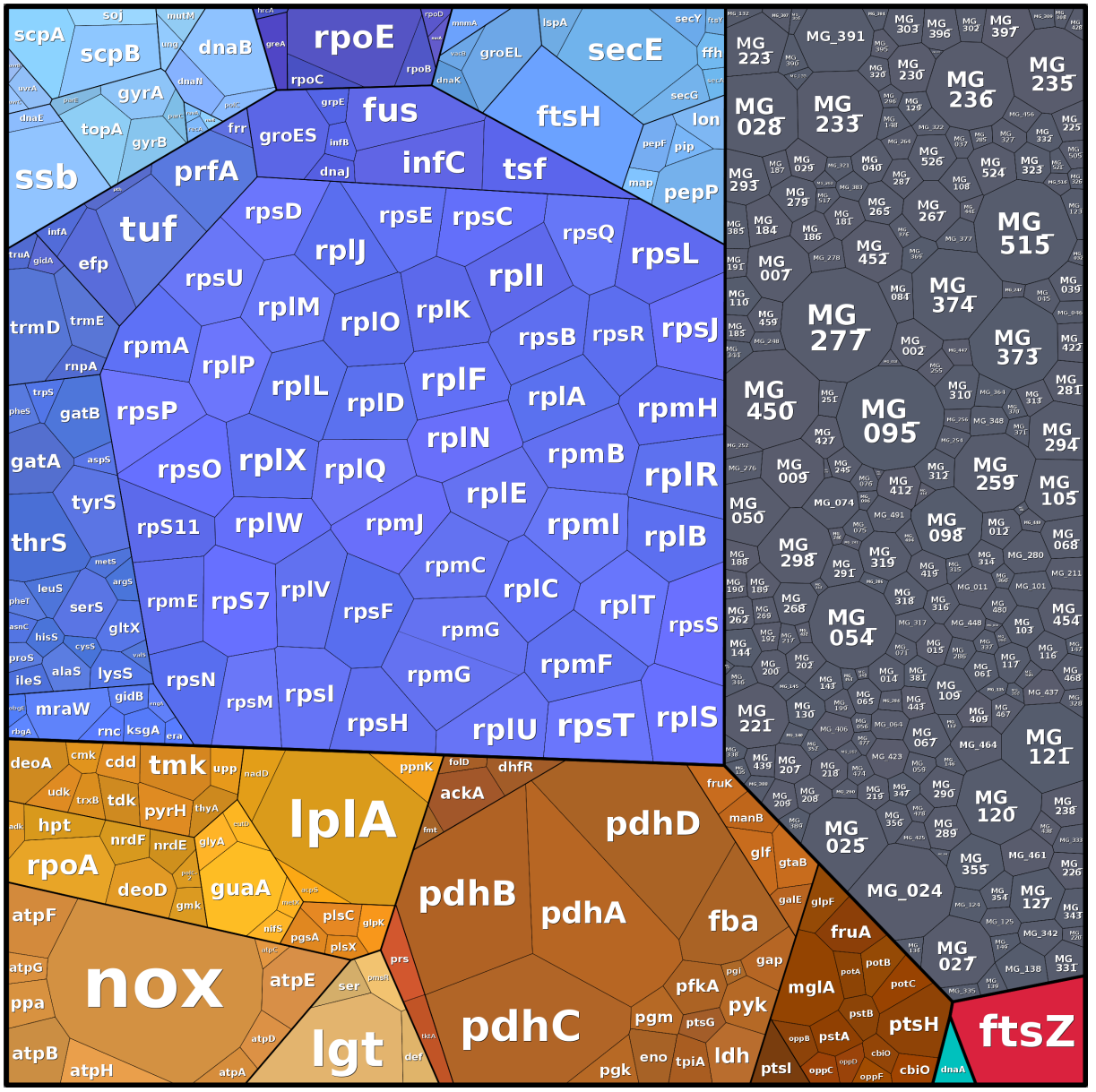
Tool used: BioUML

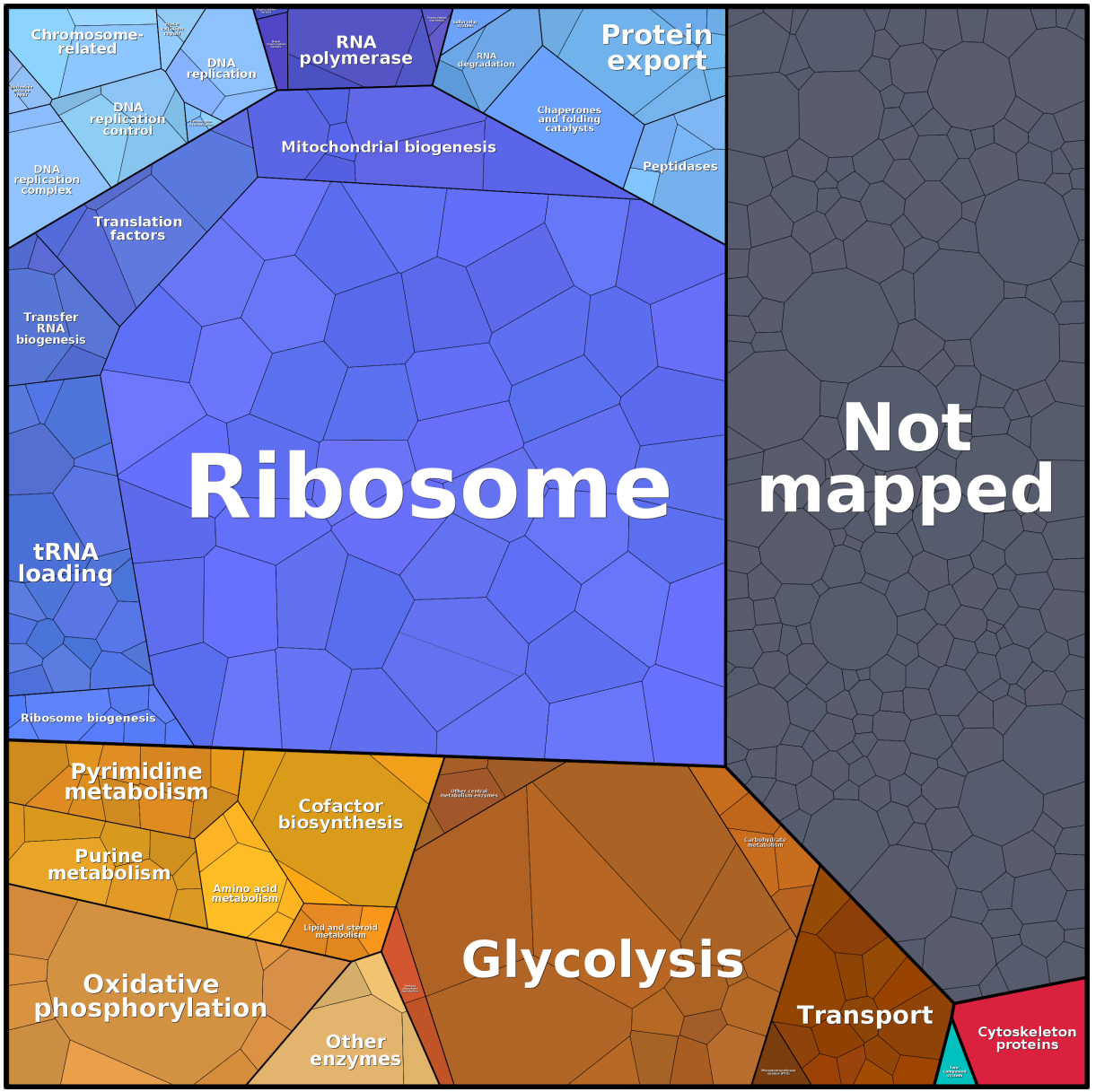
Simulated Mycoplasma genitalium proteome



Simulated proteome using Jonathan's model visualized as “proteomap” (Voronoi treemap)

(Create your own maps at www.proteomaps.net)

Simulated Mycoplasma genitalium proteome



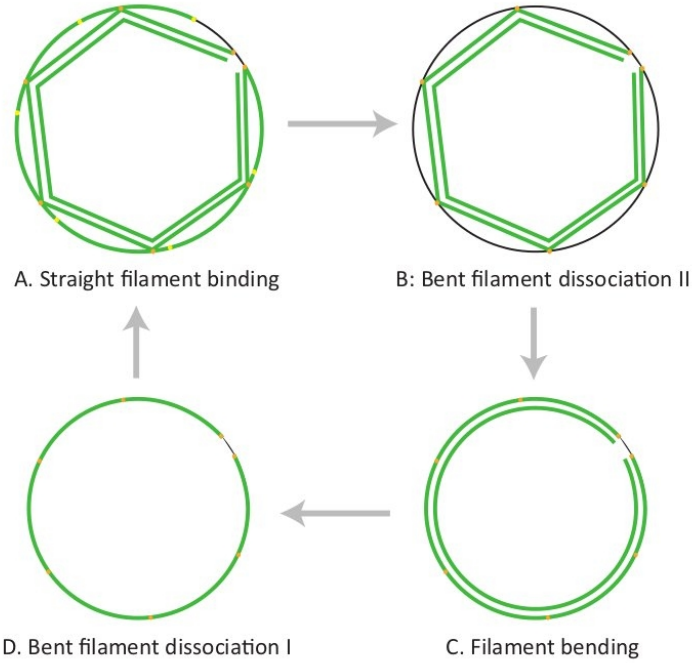
Simulated proteome using Jonathan's model visualized as “proteomap” (Voronoi treemap)

(create your own maps at www.proteomaps.net)

A ring of FtsZ filaments assembling at the membrane enables cell division

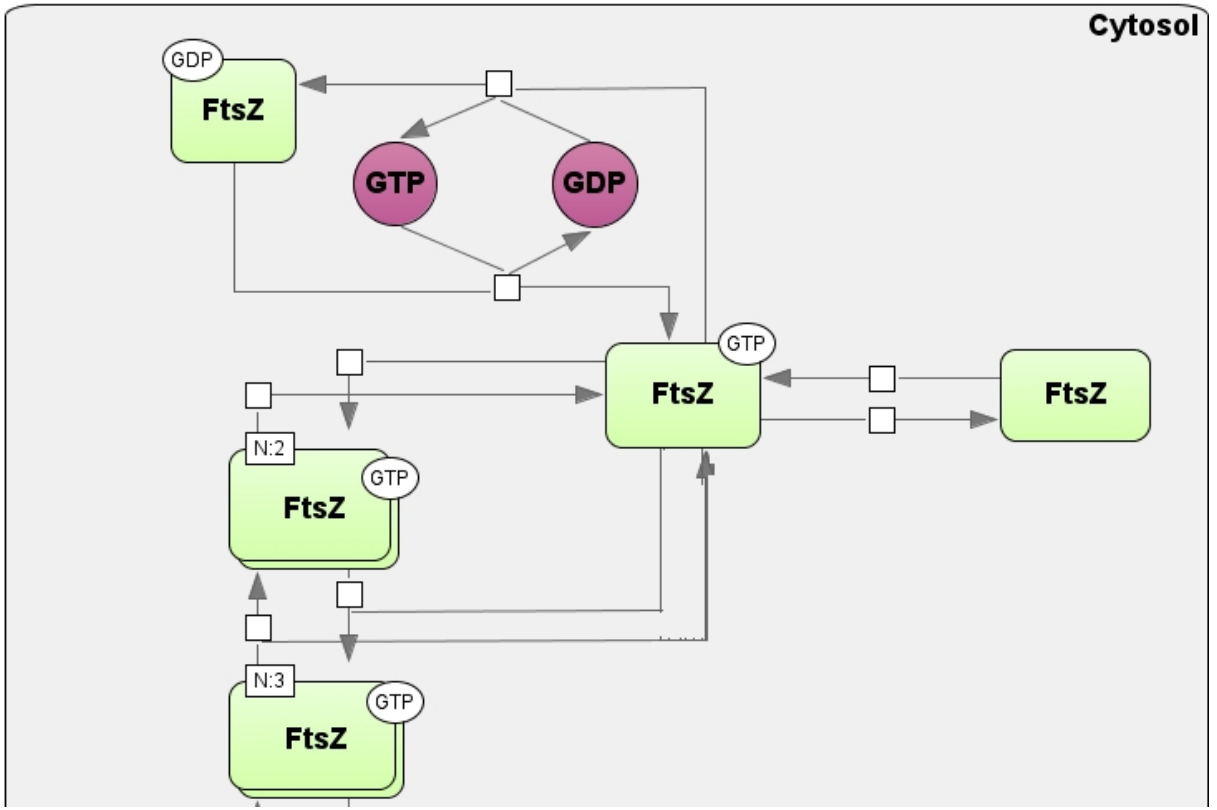
Cell pinching in the septum region

Cycle of ring contractions

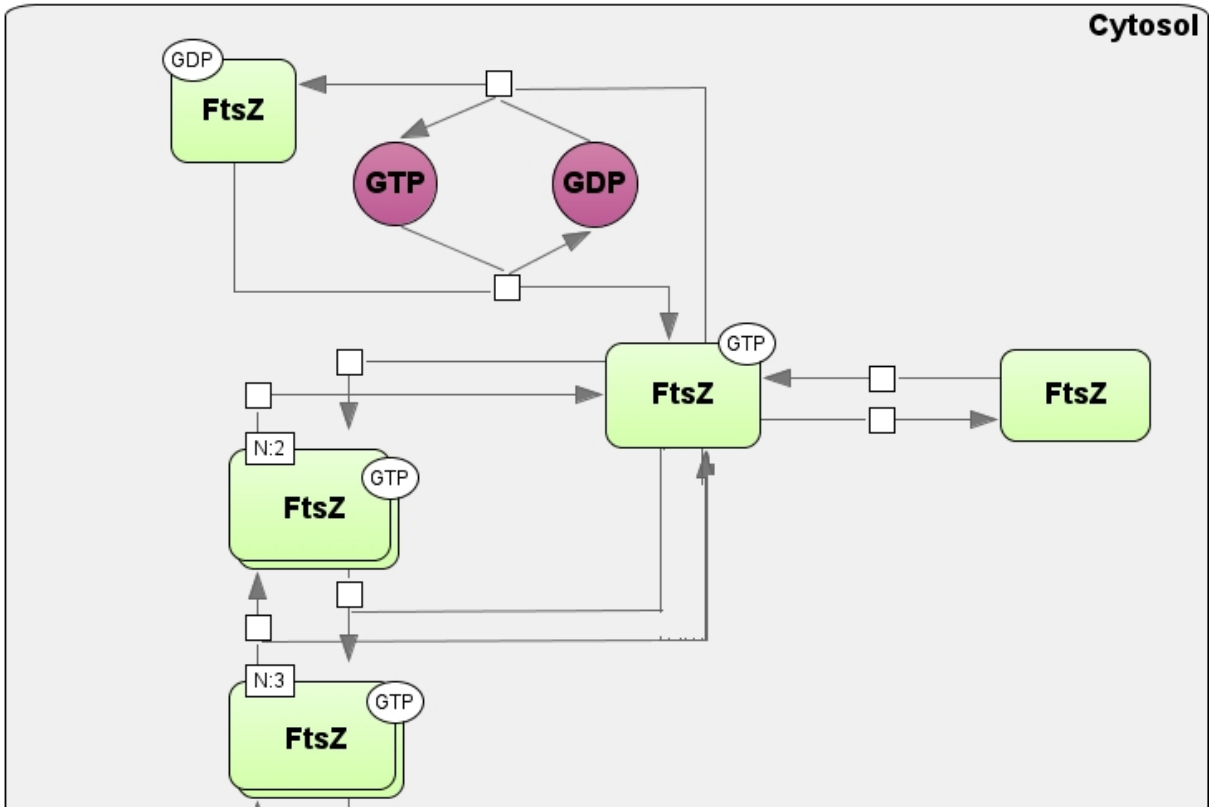


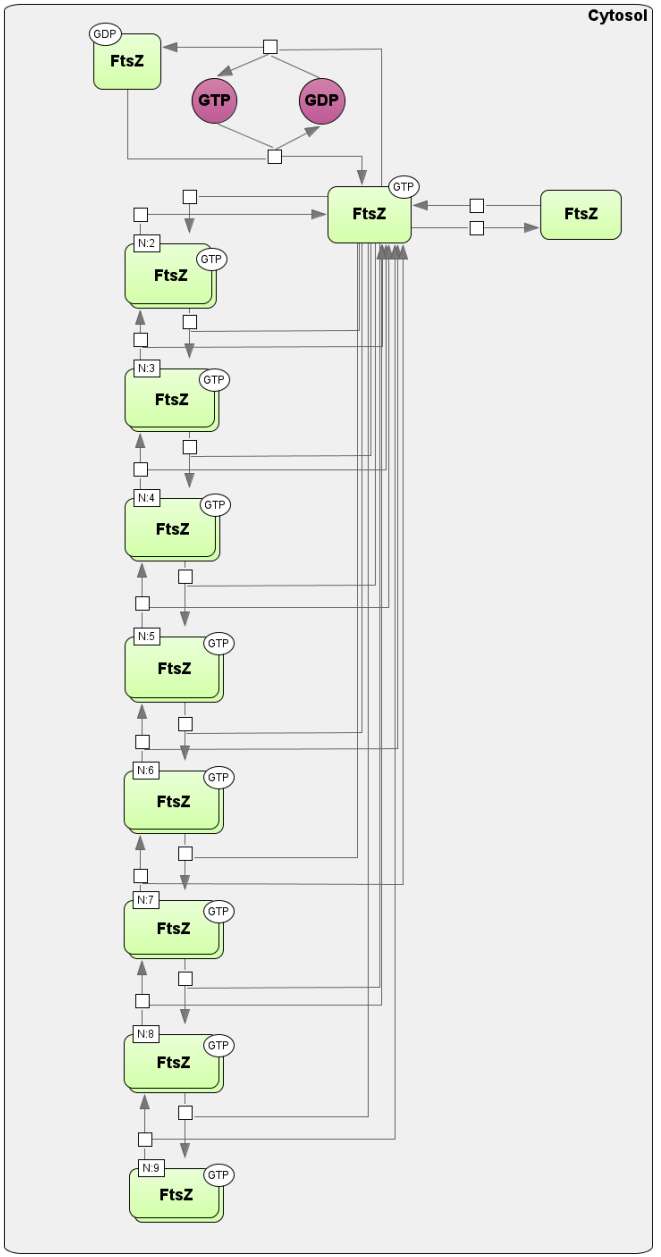
- FtsZ molecules assemble to form 9-mers (“filaments”)
- Filaments assemble at the membrane to form a ring
- Iterative ring formation and contraction leads to pinching of the cell
- Cycle of binding, residual dissociation, bending, dissociation

Submodel `FtsZPolymerization`:
FtsZ monomers assemble into filaments (9-mers)



Submodel `FtsZPolymerization`:
Preliminary SBML model

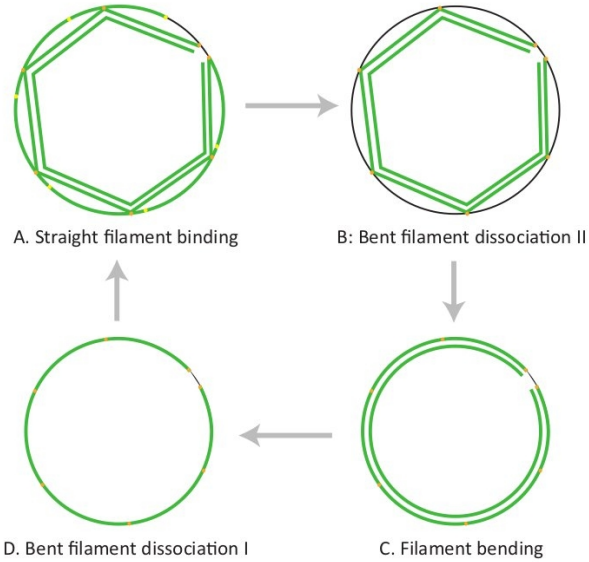




ODE model for concentrations of
FtsZ monomers and n-mers of different length

GDP and GTP appear as cofactors

Submodel `Cytokinesis`:
Model structure



Stochastic model describes:

- FtsZ filament binding / unbinding at the membrane
- FtsZ filaments changing conformation (straight ↔ bent)
- Ring contracts, cell diameter decreases

Difficulties

- In each moment, there is a fixed number of places for filaments to bind (“edges”);
  This number changes during the simulation
- Processes occur under certain conditions (per edge, and determined by the whole ring)
- Processes have a certain probability (in 1-second interval) instead of a stochastic rate

Submodel Cytokinesis:
Preliminary SBML model