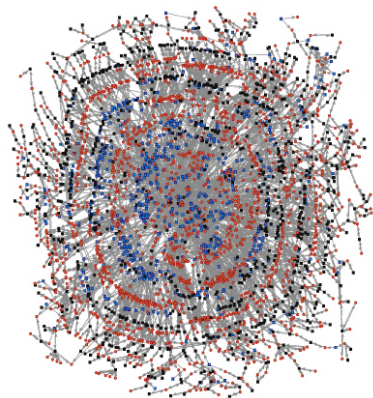


# Model Reduction for Biochemical Systems: Analytical Methods

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- As the field of systems biology continues to grow, increasingly complex models of intracellular reaction networks are becoming common.

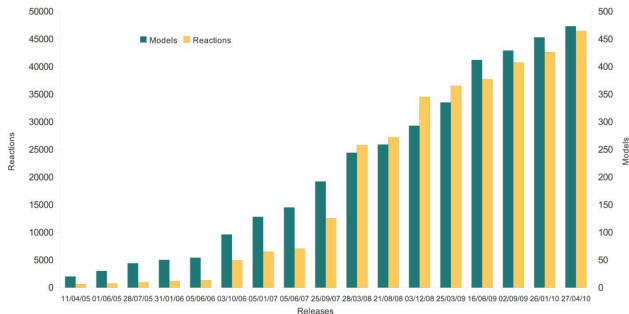
A protein reaction network of *E. Coli* featuring 2846 species and 2774 reactions<sup>1</sup>.

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<sup>1</sup>Axelsen et al., JSTAT, 2008.

# Complexity of Systems Biology models II

Both the number of published models and their average complexity have greatly increased across the last decade.



The BioModels Database, for example, increased the number of models it holds 10-fold between 2005-2010 and the average number of reactions per model increased 3-fold in this same period<sup>2</sup>.

<sup>2</sup>C Li et al, BMC Syst Biol, 2010

Complexity can lead to a number of issues with the practical use of models:

- They can be overparameterised or unidentifiable relative to the volume of experimental data that can be readily collected.
- They can incur an excessive computational burden for simulation in intensive applications such as agent based modelling.
- They can, simply, be too difficult to intuit or understand what drives the dynamics of interest.

Methods of model reduction can offer the means to alleviate some or all of these issues.