

# **Conceptual Model-based Systems Biology**

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#### Introduction

Biological wet-lab experiments are costly and longlasting

Additionally, there is a need for making system-level sense from the countless pieces of biological information, which can be used to refine biological experiments

OPM-Object-Process Methodology, originated in specifying information systems

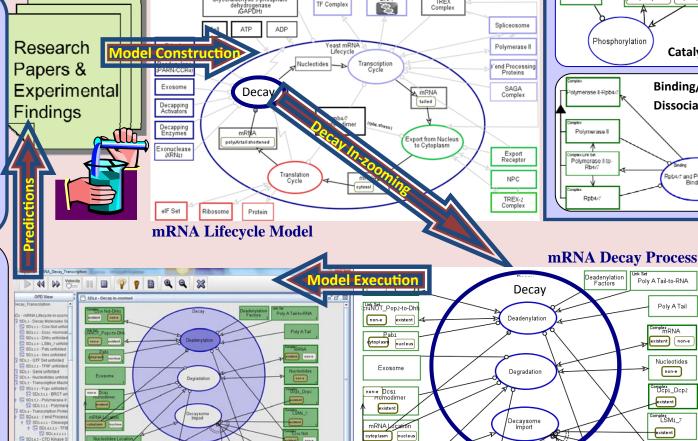
### **Model Execution and Analysis**

Compare the mechanistic model execution to qualitative experimental findings (desired input and output)

Adjust the model when inconsistencies are found and evaluate conjectures

### Results—mRNA Decay Model:

- 1. Find knowledge gaps—26 knowledge gaps were found
- 2. Evaluate Conjectures—the conjecture about Dcp1/2 complex recruiting Xrn1 and stays bound to it during degradation complies with current experimental findings
- 3. Predict New Hypotheses we predict that Pat1 deletion effects on Xrn1, Dhh1 and Rpb4/7 import into the nucle-

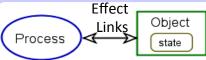


Nucleotides Location

Xrn1-to-Dcs1

existent





Results: **OPM templates for modeling Molecular Biology:** 

Poly A Tail-to-RNA

Poly A Tail

mRNA

Nucleotides

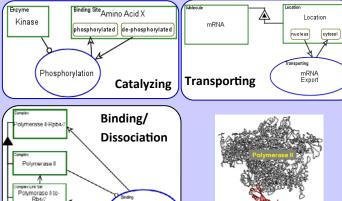
non-e

Complex Dcp1\_Dcp2

mplex LSM1\_7

mplex Ccr4 Not

xistent non-e



## **Model Construction**

Decay model construction based on 70 mechanistic qualitative facts

Conjectures incorporated

Using in-zooming mechanism to handle big models

Decay model includes 130 objects and 60 processes

#### **Conclusions**

SD1721-Pre Initial
SD17211-Pel Initial
SD17211-Pel I

Our conceptual method enables user-friendly graphical, qualitative and executable representation of complex biological processes and structures from the lower level molecular functions to the entire mRNA decay process

Conceptual modeling can help evaluate the correctness of biological hypotheses before conducting a wet-lab costly experiments

Conceptual modeling can predict new testable hypothesis

#### Selected References

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