

# Computer simulation of a translational roadblock model - Outline

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## 1 Abstract (100-200)

## 2 Introduction (1000-1500)

- Translation initiation and scanning
- Ssd1 and translational control in the 5'UTR
- TASEP and its usage in modeling translation
- Aims and Objectives (100-200)

## **3 Materials and Methods(1000-1500)**

### **3.1 Materials**

- Prior data: Edward's flow cytometry results
- Programming resources (language, environment etc.)

### **3.2 Methods**

- Writing rini: a TASEP model with targeted and dynamic defects (general principle)
- Two models for two hypotheses (independent model vs cooperative explanation)
- Collecting appropriate data (from raw exit rates to median standardised rates)
- Parameter optimisation (dealing with model data vs experimental data, the scoring system to test parameter set similarity with the experiment)

## **4 Results (1000-1500)**

- Assessing the functionality of the model (phase diagram: the model matches the behaviour of good TASEP simulations)
- Simulation output (model vs experiment boxplots)
- Parameter optimisation

## **5 Discussion (based on the results we have so far) (500-1000)**

- Cooperative roadblocking should explain the results much better than independent roadblocking, and why that is.
- Can we identify certain parameters that are especially important in finding near-identical results? (after testing a range of parameter sets that fit reasonable boundaries.)
- Can we make predictions about results we could experimentally obtain with more roadblock sites than just 2? How should we characterise cooperativity in these more complex scenarios? (since cooperativity doesn't really scale with the addition of more than 2 sites for now).
- Knowing this, what would be the next step to elucidate Ssd1's role in translational control?

## **6 Acknowledgements**

## **7 References (Alphabetical & Chronological)**