Gene Expression Simulations Gene mRNA Protein Transcription Translation Simulated trajectories (f xed delay (gamma delay) across lineage of cells Deterministic Empirical 0.12 Degradation 17.5 Exact 35 Stochastic (No Delay Stochastic + Delay 15.0 0.10 30 12.5 25 and 20 and 20 and 25 Probability 90.0 mRNA (nM) b Bioscrape Model 10.0 from bioscrape.types import Model 7.5 0.04 M = Model()5.0 10 M.create_reaction(0.02 2.5 reactants = [], products = []. products - Li, propensity_type = "massaction", propensity_param_dict = {"k":"beta"}, delay_reactants = [], delay_products = ["mRNA"], delay_type = "fxed", delay_param_dict = {"delay":"tx_delay"}) 0.0 0.00 20 100 150 200 10 20 Time (min) Time (min) mRNA Count Deterministic 1.0 Simulations 1400 M.create_reaction(Stochastic Exact reactants = ["mRNA"]. 800 Stochastic + Delay products = []. 1200 0.8 propensity_type = "massaction", propensity_param_dict = {"k":"beta"}) Protein (nM) 38 (0001 Autocorrelation .0 .0 .0 Protein (nM) 009 009 M.set_parameter("beta", 2) M.set_parameter("delta", 0.2) M.set_parameter("tx_delay", 10) 400 M.set_species("mRNA", 0) ...Translation and Protein Degradation Not Shown... 400 200 0.2

0.0

Lag time (min)

150

Time (min)

200

200

20 30 40

Time (min)

C Simulation Code

from bioscrape.simulator import by simul

Results = py_simulate(time, Model = M)

from bioscrape.simulator import py_simulate_model time = [0.01*s for s in range(1000)]