08/28/2018

Tools

1. GitHub (create 1 & share)
   python — Jupiter Notebook

   ShareLaTeX

Ideas

2. when work ? when not?
   • simple single gene cases (w/o regulation, w/ self-regulation
   • common motifs w/ >1 gene

goal: how accurate ~~this~~ model?

try to
understand
protein
dynamic

4 models:
① CME only   ② SDE-protein w/ Gillespie (QSS + QSS)
③ w/ additive noise   ④ w/ multiplicative noise

Compare via Kullback-Leibler divergence:

Interested: 1. CME dist. w/ Gillespie noise dist.
skewness   2. Gillespie w/ additive
(find a way   [calletbrating noise value to minimize mean difference
to constraint)   pick one from a range, then fix it]
                3. Gillespie w/ mutiplicative
                              tend to produce heavier tail
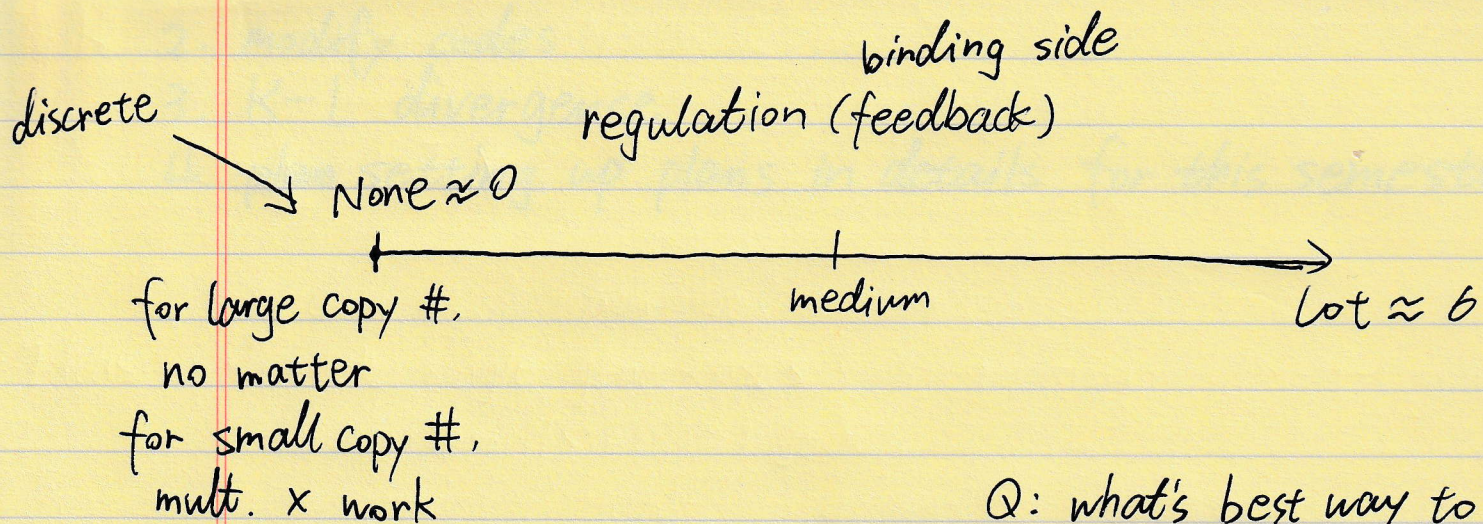
Fokker - Planck

Q: how good are they when no ~~feedback~~ ?
                                w/
which model is ~~approp~~ proper ?
with lots of regulations

with ~~simg~~ simple gene model, additive noise is better.

binding side
regulation (feedback)

discrete

None ≈ 0

medium   Lot ≈ 6

for large copy #,
no matter
for small copy #,
mult. x work

Q: what's best way to do?
— compare
— obtain

pick proper noise value

x write codes in generalized way
each change x need large new codes

keeping log of results

With John
Meeting: Tuesday 3 ~~pm~~ — 3:30 pm
　　　　　 Friday   2 — 2:30pm