**Getting started with the E. Coli whole cell model: A brief tutorial**

**Basics**

The knowledge base and the code that fits the knowledge base is located in the wcEcoli/reconstruction/ecoli/ directory. The input information files are in wcEcoli/reconstruction/ecoli/flat, and the code that loads it into an object is in knowledge\_base\_raw.py.

Processes are located in wcEcoli/models/ecoli/processes/

Each process has three components: initialize (called only once at the beginning of a simulation), calculateRequest (called at the beginning of each timestep), and evolveState (called after resources are allocated at each timestep).

*In initialize:* get needed parameters from the knowledge base, get views of bulk and unique molecules (bulk molecules are “indistinguishable” from each other, e.g. inactive RNAP molecules, unique molecules can be distinguished from each other, e.g. active RNAP molecules are each assigned to a specific transcript), create a view so that you can get counts, change counts, and change properties.

*In calculateRequest:* request the resources that you want for that timestep (don’t request all unless you are certain that another process doesn’t need this resource as well, don’t forget about metabolism).

*In evolveState:* resources have been allocated, perform the process, update counts, and update masses (mass must be conserved between steps).

If you need new output, you must write this out as a listener. To add a listener, add the file to wcEcoli/models/ecoli/listeners/, and both add an import statement and add the listener to \_listenerClasses in wcEcoli/models/ecoli/sim/simulation.py.

To change the cell’s initial conditions:

Change wcEcoli/models/ecoli/sim/initial\_conditions.py

To load the knowledge base into ipython:

ipython

import reconstruction.ecoli.knowledge\_base\_raw as kbr

kb=kbr.KnowledgeBaseEcoli()

The kb object now contains all the values in the knowledge base. The code reading and constructing the KnowledgeBaseEcoli object is in knowledge\_base\_raw.py.

**Setup**

This tutorial assumes you have setup access to the Sherlock cluster. If necessary before following the proceeding steps, do the following setup:

1. Email the research computing staff at research-computing-support@stanford.edu, and cc Professor Covert. Request access to the Sherlock cluster, and ask Professor Covert to confirm your request in the email.
2. Follow the setup instructions for logging in to Sherlock on<http://covert.stanford.edu/computational>\\_resources/sherlock/home/.
3. Follow all setup instructions in the wcEcoli/README.md file (also on the web at https://github.com/CovertLab/wcEcoli/blob/master/README.md).

Once done with setup and these basic tutorials on Sherlock and the cluster, return to here to complete the example.

**Example: varying transcription rate**

***Background***

Genes encoding for stable RNA are transcribed at a faster rate in E. Coli. In the model (prior to this tutorial), all genes were transcribed at the same rate of 42nt/s. In this tutorial, we will change the model so that genes for rRNA and tRNA are transcribed at 80nt/s while everything else is still transcribed at 80nt/s.

The code has inevitably evolved since I wrote this tutorial, so let’s get on the same page by going back to an older version of the code. Let’s do this tutorial on a new branch. cd into your wcEcoli directory and type:

git checkout –b tutorial b16293cb008135425

***Add a new parameter to the model***

First, let’s add a new elongation rate to the knowledge base. In reconstruction/ecoli/flat is a tsv called growthRateDependentParameters.tsv. Add a new column for the fast rna polymerase rate (estimate that it is double the normal rate). The normal rate at each growth rate is stored in the column 'rnaPolymeraseElongationRate'. This command will generate the file with the new column appended, or edit the file in a different way if desired.

awk '{if(NR==1){print $0 "\t" "rnaPolymeraseElongationRateFast (units.nt/units.min)"}else{print $0 "\t" ($9\*2)}}' growthRateDependentParameters.tsv > temp && mv temp growthRateDependentParameters.tsv

To check that the parameter was added, examine the knowledge base object in ipython.

ipython

import reconstruction.ecoli.knowledge\_base\_raw as kbr

kb=kbr.KnowledgeBaseEcoli()

kb.growthRateDependentParameters[0]

You should see the 'rnaPolymeraseElongationRateFast': 78 [nucleotide/min]' entry in the resulting dictionary.

***Create a new process***

Let’s split the transcript elongation process into a slow process and a fast process. Go to models/ecoli/processes/ :

cd models/ecoli/processes/

cp transcript\_elongation.py transcript\_elongation\_fast.py

mv transcript\_elongation.py transcript\_elongation\_slow.py

Now we need to add these processes to the simulation, so that they actually get called. Let’s go back to the wcEcoli directory. Open models/ecoli/sim/simulation.py and change line 19 to read:

from models.ecoli.processes.transcript\_elongation\_slow import TranscriptElongationSlow

Then add a line just under this:

from models.ecoli.processes.transcript\_elongation\_fast import TranscriptElongationFast

Under process classes, add TranscriptElongationFast and change TranscriptElongation to TranscriptElongationSlow. \_processClasses should now look like this:

\_processClasses = (

Metabolism,

RnaDegradation,

TranscriptInitiation,

TranscriptElongationSlow,

TranscriptElongationFast,

PolypeptideInitiation,

PolypeptideElongation,

Replication,

ProteinDegradation,

Complexation,

AtpUsage

)

***Change the model output***

Now let’s change the listeners to record output from these new processes. The only listener that takes output from TranscriptElongation is ntp\_usage, so let’s modify this. Open models/ecoli/listeners/ntp\_usage.py and go to line 49. Change this line from:

self.transcriptionProcessIdx = sim.processes.keys().index("TranscriptElongation")

to now read:

self.transcriptionProcessSlowIdx = sim.processes.keys().index("TranscriptElongationSlow")

Under this, let’s add a process index for the fast transcription:

self.transcriptionProcessFastIdx = sim.processes.keys().index("TranscriptElongationFast")

In the update function in this file, let’s change the calculation of NTPUsageCurrent. Change it to read:

self.transcriptionNtpUsageCurrent = (self.bulkMolecules.\_countsAllocatedInitial[self.metaboliteIdxs, self.transcriptionProcessSlowIdx] + self.bulkMolecules.\_countsAllocatedInitial[self.metaboliteIdxs, self.transcriptionProcessFastIdx] - self.bulkMolecules.\_countsAllocatedFinal[

self.metaboliteIdxs, self.transcriptionProcessSlowIdx] - self.bulkMolecules.\_countsAllocatedFinal[self.metaboliteIdxs, self.transcriptionProcessFastIdx])

***Modify a process***

Now let’s modify the new processes. Open models/ecoli/processes/transcript\_elongation\_slow.py and change all references of TranscriptElongation to TranscriptElongationSlow. If you’re using vi you can do this with the following command:

:%s/TranscriptElongation/TranscriptElongationSlow/g

Now, let’s create a Boolean vector that is True at the indices of transcripts that should be elongated at the slow rate and False at the indices of transcripts that should be elongated at the fast rate. In the initialize function add the following line (after line 70):

self.slowRnaBool = ~(kb.process.transcription.rnaData["isRRna5S"] | kb.process.transcription.rnaData["isRRna16S"] | kb.process.transcription.rnaData["isRRna23S"] | kb.process.transcription.rnaData["isTRna"])

“isRRna5S”, “isRRna16S”, “isRRna23S”, and “isTRna” are properties of rnaData, which is found in the knowledge base (kb). These are vectors of Boolean values. The tilde inverts the boolean value, so this creates a vector that is False for all 5S rRNA, 16S rRNA, 23S rRNA, and tRNA, and True for everything else.

Now let’s change the view onto the active rna polymerases to a view onto only the active rna polymerases that are on transcripts that should be elongated at the slow rate. Change the definition of self.activeRnaPolys (line 75) to read:

self.activeRnaPolys = self.uniqueMoleculesView(

'activeRnaPoly',

rnaIndex = ("in", np.where(self.slowRnaBool)[0])

)

This is all we need to change in this file. Now let’s open the fast transcript elongation file models/ecoli/processes/transcript\_elongation\_fast.py. Similarly to what we did in the slow elongation file, let’s change all references of TranscriptElongation to TranscriptElongationFast. If you’re using vi you can do this with the following command:

:%s/TranscriptElongation/TranscriptElongationFast/g

Now, let’s create the opposite of the Boolean vector that we created in the transcript\_elongation\_slow. In the initialize function add the following line (after line 70):

self.fastRnaBool = kb.process.transcription.rnaData["isRRna5S"] | kb.process.transcription.rnaData["isRRna16S"] | kb.process.transcription.rnaData["isRRna23S"] | kb.process.transcription.rnaData["isTRna"]

Now let’s change the view onto the active rna polymerases to a view onto only the active rna polymerases that are on transcripts that should be elongated at the fast rate (line 75):

self.activeRnaPolys = self.uniqueMoleculesView(

'activeRnaPoly',

rnaIndex = ("in", np.where(self.fastRnaBool)[0])

)

Finally, let’s change the elongation rate. Change line 59 to read:

self.elngRate = kb.rnaPolymeraseElongationRateFast.asNumber(units.nt / units.s) \* self.timeStepSec

Now we’re done changing this file as well.

Now we can run a simulation and rRNA and tRNA would be transcribed at the new fast rate, while everything else was transcribed at the same slow rate before. Follow these steps to run the new simulation code:

Queue up the tasks in fireworks:

DESC="Tutorial run, adding different RNA polymerization rate for r- and t- RNAs." python runscripts/fw\_queue.py

Run the tasks in the queue until finished:

qlaunch -r rapidfire --nlaunches infinite --sleep 5

To check if the success of your simulation, open the /out/ folder, and the folder timestamped to the simulation just run, then click through to the output plots. Specifically look at the rnapActiveFraction plot. This should be around 20%. Is it?

***Changing the fitting***

However, the simulation would be initialized the same way as before. This is a problem because before running a simulation, we need to fit several initial parameters including the initial counts of RNA polymerases and the activation rate of the RNA polymerases. Because some things are now being transcribed at a faster rate, we should need fewer RNA polymerases to make the same number of transcripts. Additionally, if some things are being transcribed more quickly, then RNA polymerases will be inactivating more quickly. In order to maintain a constant ratio of active to inactive RNA polymerases (experimentally shown to be around 20%), the activation rate must also increase now.

We calculate the number of RNA polymerases that we need initially by writing an equation for the rate of change of some RNA Ri (rate of synthesis – rate of degradation = rate of dilution due to growth):

Li is the length of transcript i; Pi is the number of RNA polymerases actively transcribing Ri at time t; hi is the half life of Ri; τd is the length of the cell cycle; kelong is the transcript elongation rate. Right now this is a constant value for all transcripts. We want to change this to be different for rRNA and tRNA. Let’s change this in the code. Open the file reconstruction/ecoli/fitkb1.py and go to the setRNAPCountsConstrainedByPhysiology function. This is what we need to change. Let’s add the Boolean vectors for fast and slow transcripts. After line 383 add these two lines:

slowRnaBool = ~(kb.process.transcription.rnaData["isRRna5S"] | kb.process.transcription.rnaData["isRRna16S"] | kb.process.transcription.rnaData["isRRna23S"] | kb.process.transcription.rnaData["isTRna"])

fastRnaBool = kb.process.transcription.rnaData["isRRna5S"] | kb.process.transcription.rnaData["isRRna16S"] | kb.process.transcription.rnaData["isRRna23S"] | kb.process.transcription.rnaData["isTRna"]

Let’s break up the calculation of nActiveRnapNeeded into nActiveRnapNeededforFast and nActiveRnapNeededforSlow. Change the nActiveRnapNeeded calculation to read:

nActiveRnapNeededforSlow = calculateMinPolymerizingEnzymeByProductDistribution(rnaLengths[slowRnaBool], kb.rnaPolymeraseElongationRateSlow, rnaLossRate[slowRnaBool], rnaCounts[slowRnaBool])

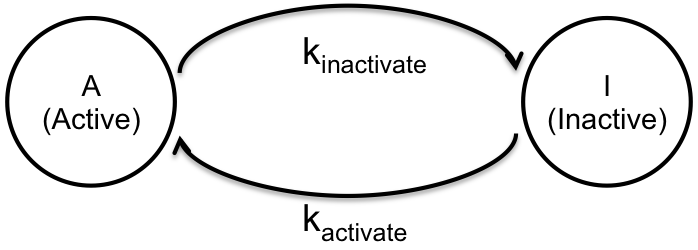
Add a line under this for the calculation for the fast transcripts:

nActiveRnapNeededforFast = calculateMinPolymerizingEnzymeByProductDistribution(rnaLengths[fastRnaBool], kb.rnaPolymeraseElongationRateFast, rnaLossRate[fastRnaBool], rnaCounts[fastRnaBool])

Below this, add a line to calculate the total number of RNA polymerases needed:

nActiveRnapNeeded = nActiveRnapNeededforFast + nActiveRnapNeededforSlow

Now let’s change the calculation of the RNA polymerase activation rate. In the model, an RNA polymerase can either be active or inactive:



To calculate the rate of activation, kactivate, we write an equation for the rate of change of the number of RNAP active at steady state:

We know the experimentally determined fraction of RNA polymerases that are active, factive:

Rearranging and solving for the rate of activation:

We can calculate the rate of inactivation from the elongation rate, the transcript lengths, and the synthesis probabilities:

We want to change the elongation rate to be a vector, rather than a constant:

Now let’s do this in the code. In reconstruction/ecoli/fitkb1.py, in the fitRNAPolyTransitionRates function (on line 483), at the top add these lines:

slowRnaBool = ~(kb.process.transcription.rnaData["isRRna5S"] | kb.process.transcription.rnaData["isRRna16S"] | kb.process.transcription.rnaData["isRRna23S"] | kb.process.transcription.rnaData["isTRna"])

fastRnaBool = kb.process.transcription.rnaData["isRRna5S"] | kb.process.transcription.rnaData["isRRna16S"] | kb.process.transcription.rnaData["isRRna23S"] | kb.process.transcription.rnaData["isTRna"]

Now, delete the elngRate definition (elngRate = kb.rnaPolymeraseElongationRate) and add an elongation rate vector:

elngRateVector = slowRnaBool\*kb.rnaPolymeraseElongationRate + fastRnaBool\*kb.rnaPolymeraseElongationRateFast

Delete the calculation of averageTranscriptLength and expectedTerminationRate and add the following three lines:

expectedTranscriptionTime = rnaLengths/elngRateVector

weightedExpectedTranscriptionTime = units.dot(expectedTranscriptionTime, synthProb)

expectedTerminationRate = 1/weightedExpectedTranscriptionTime

We’re done editing this file now. Now the fitting of the initial number of RNA polymerases and the activation rate is fixed.

***Running simulations***

Now we can run some simulations. First, if you haven't alreadt, log in to a sherlock node. Replace 'username' with your username in the command below:

ssh username@sherlock

Now log in to a non-login node, so that the simulation can be run in interactive mode (running in interactive mode on a login node can result in getting booted from the cluster).

srun -p mcovert –ntasks-per-node=1 –time=12:00:00 –pty bash

Now prepare the fireworks queue with your simulation task.

Once setup is complete, change the DESC description text as desired, and run:

DESC="Tutorial run, adding different RNA polymerization rate for r- and t- RNAs." python runscripts/fw\_queue.py

Now the simulation task is queued up in fireworks and can be launched via:

rlaunch rapidfire

After about a minute, this should start producing output looking something like this:

[mpaull@sh-8-31 ~/wcEcoli]$ rlaunch rapidfire

2015-06-23 19:09:29,106 INFO Hostname/IP lookup (this will take a few seconds)

2015-06-23 19:09:29,814 INFO Created new dir /home/mpaull/wcEcoli/launcher\_2015-06-24-02-09-29-810292

2015-06-23 19:09:29,817 INFO Launching Rocket

2015-06-23 19:09:32,285 INFO RUNNING fw\_id: 12 in directory: /home/mpaull/wcEcoli/launcher\_2015-06-24-02-09-29-810292

2015-06-23 19:09:32,289 INFO Task started: {{wholecell.fireworks.firetasks.initKb.InitKbTask}}.

Tue Jun 23 19:09:32 2015: Instantiating unfit knowledgebase

Tue Jun 23 19:09:32 2015: Saving unfit knowledgebase

2015-06-23 19:09:32,292 INFO Task completed: {{wholecell.fireworks.firetasks.initKb.InitKbTask}}

2015-06-23 19:09:34,950 INFO Rocket finished

2015-06-23 19:09:35,328 INFO Created new dir /home/mpaull/wcEcoli/launcher\_2015-06-24-02-09-35-326470

2015-06-23 19:09:35,330 INFO Launching Rocket

2015-06-23 19:09:37,772 INFO RUNNING fw\_id: 10 in directory: /home/mpaull/wcEcoli/launcher\_2015-06-24-02-09-35-326470

2015-06-23 19:09:37,775 INFO Task started: {{wholecell.fireworks.firetasks.symlink.SymlinkTask}}.

Tue Jun 23 19:09:37 2015: Creating symlink

2015-06-23 19:09:37,777 INFO Task completed: {{wholecell.fireworks.firetasks.symlink.SymlinkTask}}

2015-06-23 19:09:40,154 INFO Rocket finished

2015-06-23 19:09:40,531 INFO Created new dir /home/mpaull/wcEcoli/launcher\_2015-06-24-02-09-40-530368

2015-06-23 19:09:40,533 INFO Launching Rocket

2015-06-23 19:09:42,981 INFO RUNNING fw\_id: 9 in directory: /home/mpaull/wcEcoli/launcher\_2015-06-24-02-09-40-530368

2015-06-23 19:09:42,984 INFO Task started: {{wholecell.fireworks.firetasks.fitKb.FitKbTask}}.

Tue Jun 23 19:09:42 2015: Fitting knowledgebase (Level 1)

Then once the actual simulation starts, you will see:

Tue Jun 23 19:10:13 2015: Running simulation

Time (s) Dry mass Dry mass Protein RNA Expected

(fg) fold change fold change fold change fold change

======== ======== =========== =========== =========== ===========

0 245.19 1.000 1.000 1.000 1.000

Warning - converting 'reactionIDs' attribute from ndarray to list for JSON serialization.

1 245.27 1.000 1.000 1.000 1.000

2 245.20 1.000 1.000 1.000 1.000

3 244.50 0.997 1.000 1.000 1.001

4 244.52 0.997 1.000 1.000 1.001

5 244.58 0.998 1.001 1.001 1.001

6 244.63 0.998 1.001 1.002 1.001

7 244.64 0.998 1.001 1.003 1.001

8 244.63 0.998 1.001 1.004 1.002

9 244.73 0.998 1.001 1.005 1.002

10 244.79 0.998 1.002 1.007 1.002

11 244.87 0.999 1.002 1.008 1.002

12 244.96 0.999 1.002 1.010 1.002

13 245.08 1.000 1.002 1.012 1.003

14 245.10 1.000 1.002 1.014 1.003

15 245.21 1.000 1.003 1.016 1.003

16 245.32 1.001 1.003 1.018 1.003

17 245.41 1.001 1.003 1.021 1.003

18 245.49 1.001 1.003 1.023 1.003

19 245.59 1.002 1.003 1.026 1.004

20 245.69 1.002 1.004 1.028 1.004

21 245.79 1.002 1.004 1.031 1.004

22 245.89 1.003 1.004 1.034 1.004

23 245.95 1.003 1.004 1.037 1.004

24 246.04 1.003 1.005 1.040 1.005

25 246.14 1.004 1.005 1.043 1.005

26 246.23 1.004 1.005 1.046 1.005

27 246.33 1.005 1.005 1.049 1.005

28 246.41 1.005 1.005 1.052 1.005

29 246.51 1.005 1.006 1.056 1.006

30 246.60 1.006 1.006 1.059 1.006

31 246.70 1.006 1.006 1.062 1.006

32 246.79 1.007 1.006 1.066 1.006

33 246.88 1.007 1.006 1.069 1.006

34 246.98 1.007 1.007 1.073 1.007

35 247.07 1.008 1.007 1.076 1.007

36 247.16 1.008 1.007 1.079 1.007

37 247.26 1.008 1.007 1.083 1.007

38 247.35 1.009 1.007 1.087 1.007

39 247.43 1.009 1.008 1.090 1.008

40 247.52 1.010 1.008 1.094 1.008

41 247.61 1.010 1.008 1.098 1.008

42 247.70 1.010 1.008 1.101 1.008

43 247.79 1.011 1.008 1.105 1.008

44 247.88 1.011 1.009 1.109 1.009

45 247.97 1.011 1.009 1.113 1.009

46 248.05 1.012 1.009 1.116 1.009

47 248.14 1.012 1.009 1.120 1.009

48 248.23 1.012 1.009 1.124 1.009

49 248.31 1.013 1.010 1.128 1.009

This will take a few minutes to run. At the end you can find the output in the out/timestamp directory (timestamp obviously replaced with the actual timestamp of when you started the simulation). Look at the plots in the /wcEcoli/out/20150623.190922.827654/wildtype\_000000/000000/generation\_00

0000/000000/plotOut directory (replacing the timestamp directory with your own timestamped directory name).