Data search: Komorowski et al. - Analog nitrogen sensing in E. coli

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1 Introduction: Glutamine synthease (GS) regulates responses to environmental nitrogen concentrations in E. coli

- Important role in cell signaling: Post-translational modifications (PTMs)
- Advantage of them is fast responses as modifications of proteins are reversible
- bicyclic nucleotidylation cascade of PII and glutamine synthetase is a bacterial PTM systems that is well studied
- Role: cell needs nitrogen from environment - this regulates the response to how much nitrogen there is around the cell in E. coli
- Measured PII, PII-UMP, GS, GS-AMP, GLN, and α KG in responses to perturbations in nitrogen availability in vivo
- Glutamine (GLN) signals nitrogen
- stimulates the de-uridylylation of PII-UMP
- αKetoglutarate (αKG) binds to PII
- PII also regulates the two-component nitrogen regulators NtrB/NtrC
- thereby directly controlling transcription of 45 genes in response to nitrogen starvation, including the gene coding for GS, glnA
- GS adenylylation state depends on both GLN and αKG
- GLN and αKG define the nitrogen status together

2 Take away

It makes sense to look at all six species together. Try 6d differential equation.

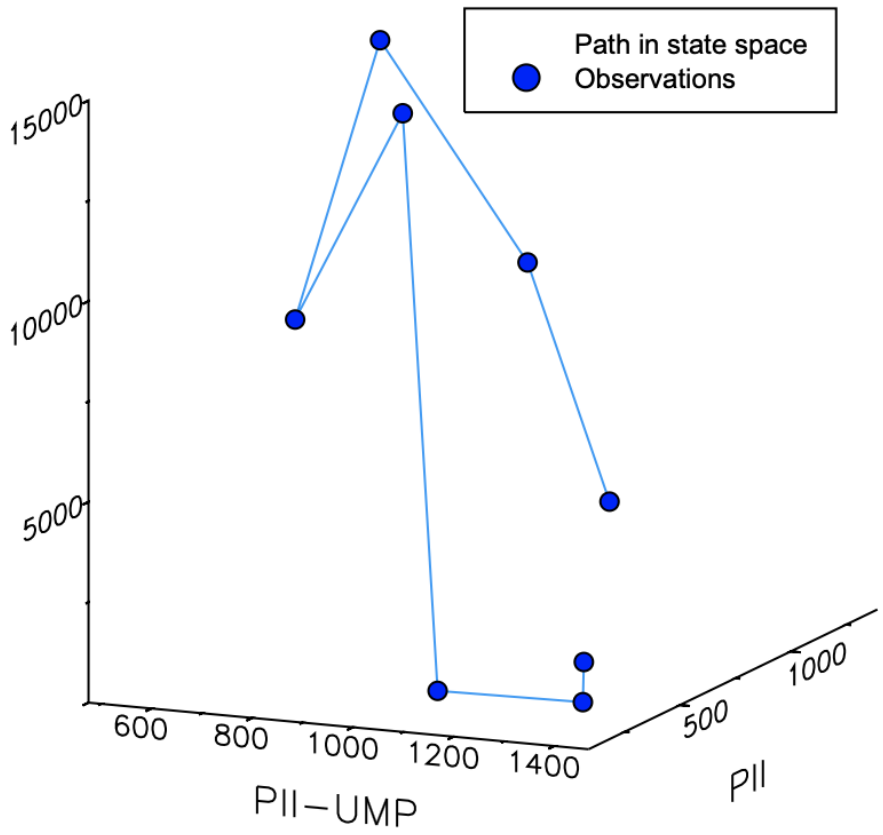

Figure 1: In this figure I show the state space reduced to three dimensions (PII, PII-UMP and GS-AMP). We see that there are no cycles in the path. This is important as cycles cause irritations in the fitting procedure of the gradient.

3 Problems

3.1 Problem: missing values

Measurements are not always available for every species (Figure 2). My temporary solution is to prioritize 100 percent data coverage and therefore take only time points where we have observations for all species (Figure 3.

3.2 problem now: SingularException(3)

Meaning no inverse.

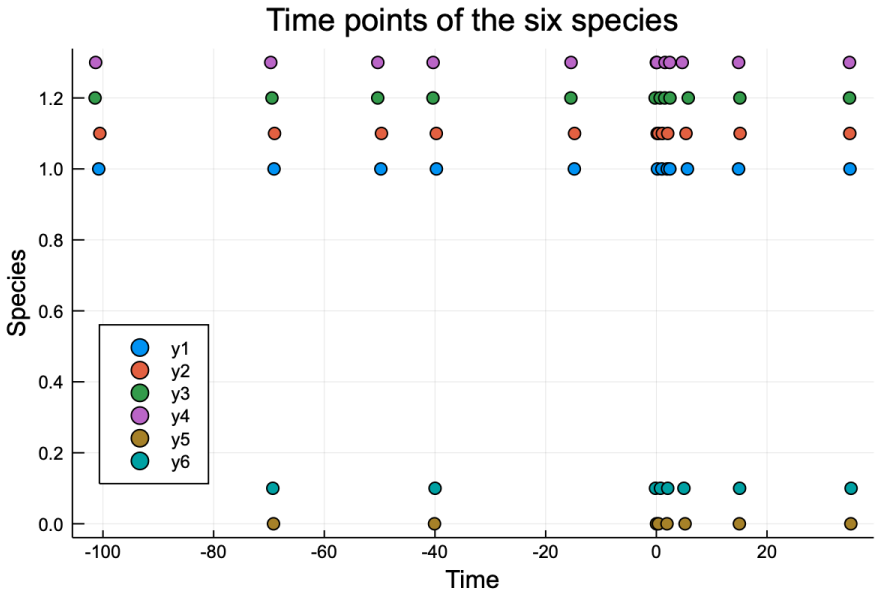

Figure 2: I show the time points of measurements of the six species. They are not the same. y5/6 have 4 missing values at -100, -50, -15 and 5.

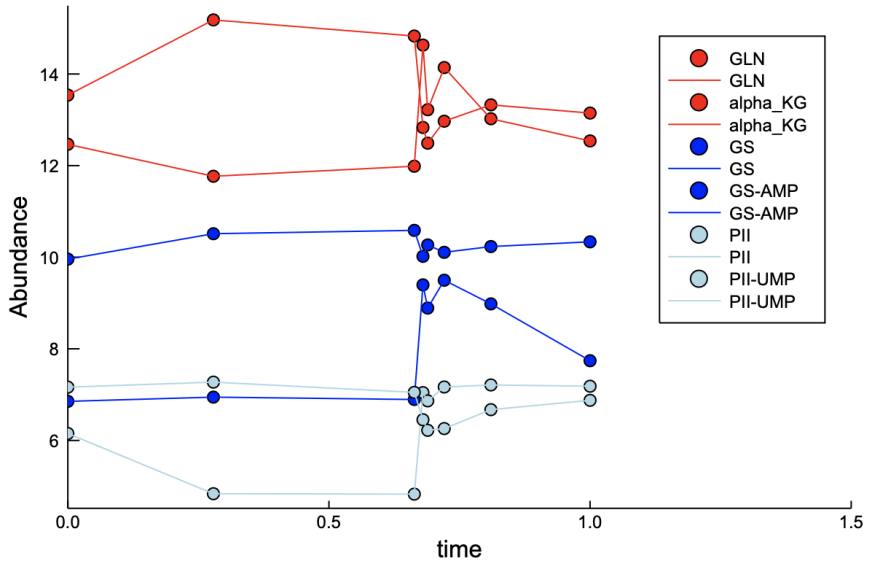

Figure 3: I show the observation used to fit the data. 4 data points are left out to provide 100 data coverage at each point. Also the time scale is normalize to the range between zero and one. The abundance is log scaled.