Toward a Genome Scale Dynamic Model of Cell Free Protein Synthesis in *Escherichia coli*

Nicholas Horvath, Michael Vilkhovoy, James Swartz[1] and Jeffrey D. Varner*

School of Chemical and Biomolecular Engineering

Cornell University, Ithaca NY 14853

[1]School of Chemical Engineering

Stanford University, Stanford, California 94305

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*Corresponding author:

Jeffrey D. Varner,

Professor, School of Chemical and Biomolecular Engineering,

244 Olin Hall, Cornell University, Ithaca NY, 14853

Email: jdv27@cornell.edu

Phone: (607) 255 - 4258

Fax: (607) 255 - 9166

Abstract

Fill me in.

Keywords: Biochemical engineering, systems biology, cell free protein synthesis

Introduction

The introduction has four paragraphs (introduction no longer than 3 pages). Follow the cell free paper from last year:

1. **First paragraph**: Introduce mathematical modeling, and its role in biochemical engineering.
2. **Second paragraph**: Contrast current static metabolic modeling approaches e.g., FBA with dynamic models.
3. **Third paragraph**: Introduce cell free protein synthesis.
4. **Fourth paragraph**: In this study, [Repeat the abstract with some additional detail]. Taken together, [killer statement].

Results

The results are presented in **past tense**. Each paragraph starts with a statement of the result in that paragraph in active voice. Each results paragraph ends with a Taken together type statement followed by a link statement e.g., Next we considered etc. When referring to figures, state what the figures shows (Fig. ZZ).

1. **First section**:Description of the model biology
2. **Second section**:Estimation of the model parameters, and refinement of the model structure (inclusion of the AA degradation pathways)
3. **Third section**:Analysis of the flux distribution (over the ensemble?), sensitivity results (first parameters, then AA)

Discussion

The discussion has three (sometimes four) paragraphs:

1. **First paragraph**: Present a modified version of the last paragraph of the introduction. In this study, [...]. Taken together, [killer statement]

2. **Second paragraph**: Contrast the key findings of the study with other computational/experimental studies

3. **Third paragraph**: Present future directions. If you had more time, what would like to do? Highlight the key shortcomings of the approach and how will we address them in the future. In this case, we will have a scaling issue if we extend to genome scale. We should extend to dynamic cases, and we need to experimentally validate the findings.

Materials and Methods

Follow the cell free paper from last year:

1. **Model formulation**: Present the spatial flux balance approach, and enzyme balances for the (un)channeled case. Outline any bounds formulation, and state all parameter assumptions.

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References