Introduction to Independent Component Analysis (ICA) applied to transcriptomics data

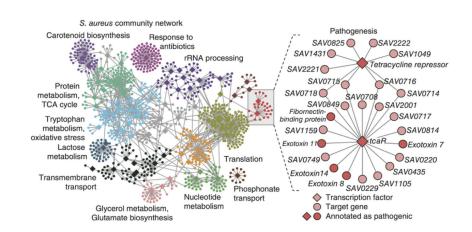
Anand Sastry Saugat Poudel

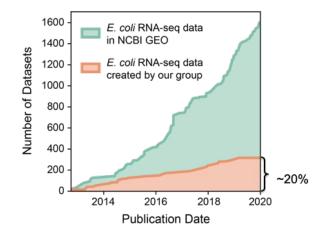
Outline

- Introduction to ICA and i-modulons
- Jupyter notebook live tutorials
 - a. Pre-processing data
 - b. Interpreting i-modulons
 - c. Applying i-modulons to new data
- Discussion

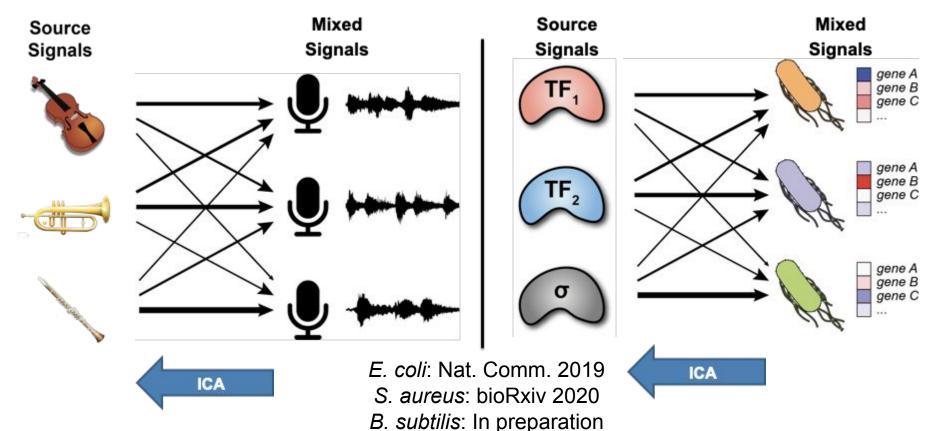
Goals of the method

- Build a model of the Transcriptional Regulatory Network (TRN)
 - Allows us to better understand how an organism responds to changes in the environment
 - Makes it easier understand complex differential expression patterns
- Use RNA-seq data to build the model
 - Most non-model organisms lack antibodies against TF
 - But growing number of organisms have large RNA-seq data publically available

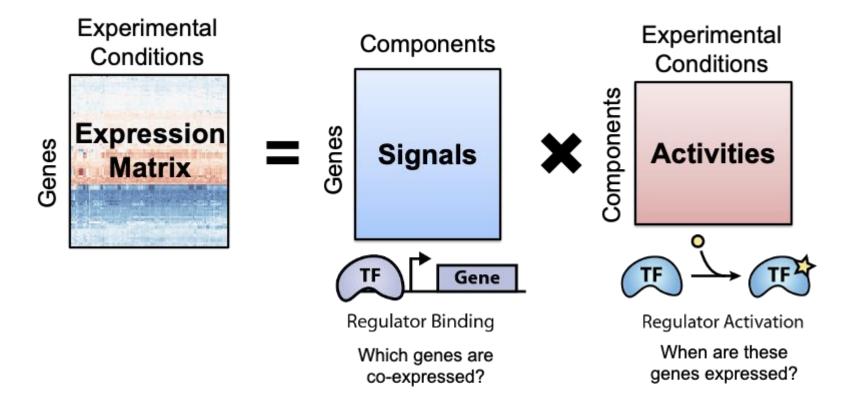




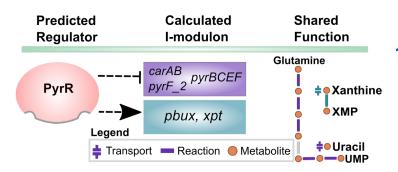
Independent Component Analysis



ICA of Gene Expression Data



Anatomy of an I-modulon

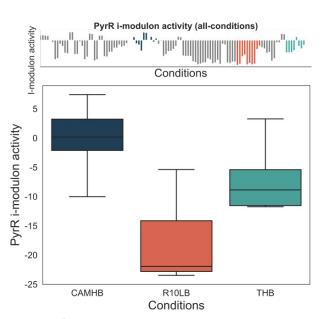


Independently modulated sets of genes (S-matrix)

Expression of genes in an i-modulon vary with each other and independent of all other genes not in the respective i-modulon.

Activity and gene expression (A-matrix)

The activity represents the strength of signal from the regulator governing the expression of genes in an i-modulon.

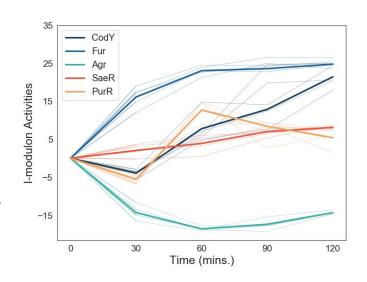


Putting it together

ICA provides both condition-invariant structure of TRN and its condition-specific activity

Applications of ICA

- Discover new interactions between different regulators
- Predict unknown regulons for regulators
- Simplify analysis of complex RNA-seq data
- Integrate it with M-model to understand interactions between metabolic and regulatory networks
- Detailed examples:
 - E.coli: https://doi.org/10.1038/s41467-019-13483-w
 - o S. aureus: https://doi.org/10.1101/2020.03.18.997296



S. aureus i-modulon activities during growth in human blood

Additional resources

Tutorial Github: https://github.com/avsastry/U01 ICA tutorial

PRECISE-DB Github page: https://github.com/SBRG/precise-db

E. coli i-modulon paper: https://www.nature.com/articles/s41467-019-13483-w

S. aureus i-modulon paper:

https://www.biorxiv.org/content/10.1101/2020.03.18.997296v1

Email us at <u>avsastry@ucsd.edu</u> and <u>sapoudel@ucsd.edu</u> for additional code.

Jupyter tutorial

Table of Contents

- 1 The E. coli Expression Dataset
- 2 Experimental Metadata
- 3 Quality Control
- 4 Centering to reference condition
- 5 Save centered dataset
- 6 Run ICA

Table of Contents

- ▼ 1 Load data
 - 1.1 Load expression data and metadata
 - 1.2 Load S and A matrices
- ▼ 2 Exploring the S matrix
 - 2.1 Example: Component #36
 - 2.2 I-modulon thresholds
 - 2.3 Load gene annotation
 - 2.4 Load TRN
 - 2.5 Regulator enrichments
 - 3 Naming I-modulons
- ▼ 4 Exploring the A matrix
 - 4.1 Fear-greed trade-off
 - 4.2 The Fur i-modulons
 - 4.3 Expanding to additional strains