# Building a Regulatory Network to Explore the Immune Landscape of Mesothelioma

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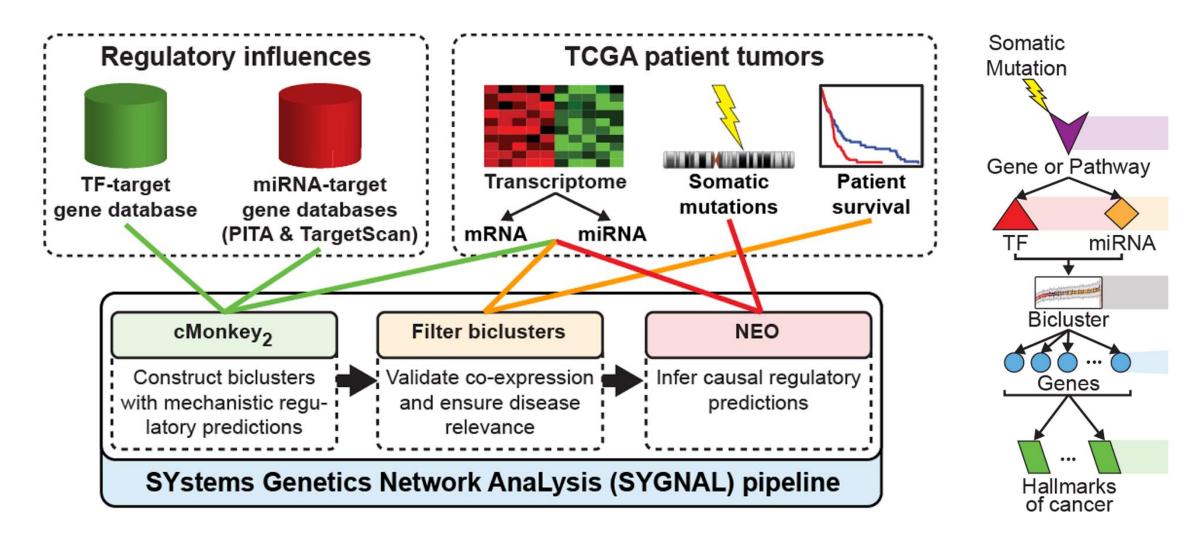
## INTRODUCTION

Mesothelioma is a malignant and incurable cancer that typically takes the form of tumors in the pleural space of the lungs. Currently, the treatments for mesothelioma include surgery, chemotherapy, and immunotherapy. While surgery is the most effective, most treatments are intended only to ease symptoms. The typical prognosis for a patient diagnosed with mesothelioma ranges from 12-21 months.¹ The goal of this project was to build a regulatory network using the previously built SYGNAL network and patient data to identify target regulators that could be used to inspire targeted and effective treatments.²

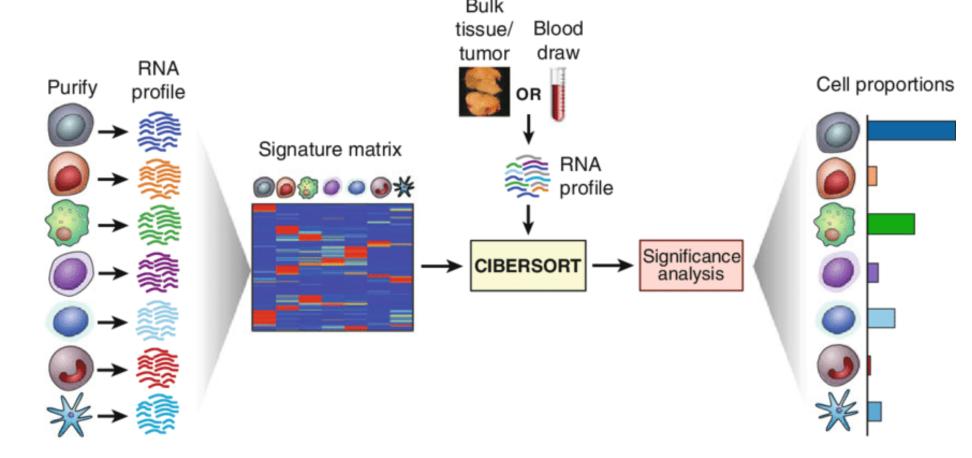
## RESULTS T = -0.89; pv = 3.76E-01 Immunomodulator/ Immune **Bicluster** Mutation Regulator Chemokine Subtype RIOX1 CNA Deletion **Activated NK Cells** C10orf54 R = -0.22; pv = 1.05E-02 R = 0.26; pv = 2.82E-030.0 0.1 12

## **RESEARCH METHODS**

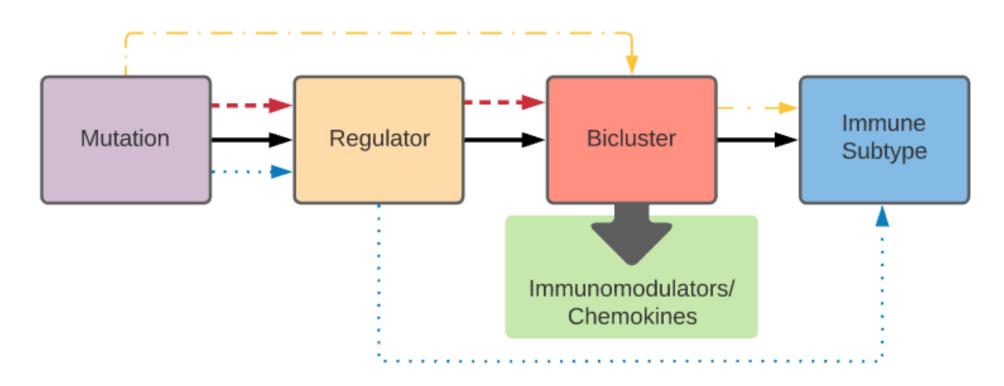
1. Run SYGNAL pipeline to achieve initial causal flow



2. Run CIBERSORT to gather immune data on TCGA tumors

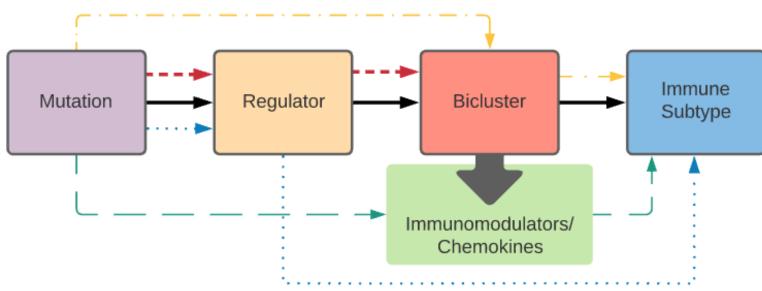


3. Re-run SYGNAL with immune information and combine flows



#### **FUTURE DIRECTIONS**

To get closer to building a mechanistic picture of cause and effect, we will continue to build smaller parts of the causal flows individually and integrate them into the larger overall causal flow.



Using the resulting causal flows, a small number will be reviewed for clinical significance and will be tested *in vitro* to determine accuracy of the predicted causal flow. Long term, the results from this analysis could be used in targeted immune therapies for mesothelioma patients, and the network could be adapted and expanded for other cancers with similar aggregated clinical data.

#### REFERENCES

[1] Robinson B. M. (2012). Malignant pleural mesothelioma: an epidemiological perspective. Annals of cardiothoracic surgery, 1(4), 491–496. https://doi.org/10.3978/j.issn.2225-319X.2012.11.04

[2] Plaisier, C. L., O'Brien, S., Bernard, B., Reynolds, S., Simon, Z., Toledo, C. M., Ding, Y., Reiss, D. J., Paddison, P. J., & Baliga, N. S. (2016). Causal Mechanistic Regulatory Network for Glioblastoma Deciphered Using Systems Genetics Network Analysis. Cell systems, 3(2), 172–186. https://doi.org/10.1016/j.cels.2016.06.006

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