# Predicting Gene Regulatory Networks with Augusta

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Gene Regulatory Network (GRN) inference using transcriptomic data became a relatively common procedure in model organisms, where high-quality single-cell sequencing data, required by bioinformatics tools, are available. Unfortunately, similar data cannot be produced for non-conventional bacteria due to the lack of single-cell culturing techniques. We addressed this limitation by developing the Augusta tool specifically designed for bulk RNA-Seq and non-model organisms. Augusta performs several polishing steps that help remove inherent bias in bulk sequencing data including database searches and sequence motifs predictions. Optionally, Augusta transforms the static GRN into dynamic Boolean Networks (BN) suitable for following dynamic analyses.

GRN inference requires time series data and the precision is highly dependent on sampling that needs to be dense enough to cover all regulatory changes. Nevertheless, there are potentially many applications where the most important regulations happen in relatively long periods and can be inferred from bulk data as the majority of cells in culture are metabolically synchronized. Here, we demonstrate that using an example of *Caldimonas thermodepolymerans*, a non-conventional bacterium and a potent producer of PolyHydroxyAlkanoates, biologically produced polymers that could be used as plastics. Even non-uniformly sampled time series are sufficient to capture important changes coupled with PHA synthesis.

Augusta was developed as an open-source Python package and is available from github.com/JanaMus/Augusta along with documentation, examples, and tutorials.

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