# FAIRification of Augusta, a Python package for RNA-Seq-Based Inference of Gene Regulatory and Boolean Networks

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Gene regulation plays a central role in controlling biological processes. RNA Sequencing (RNA-Seq) has become a widely adopted technique to measure gene expression across the genome under various conditions, providing comprehensive data for studying these regulatory mechanisms. Computational models such as Gene Regulatory Networks (GRNs) and Boolean Networks (BNs) offer valuable approaches for capturing gene interactions in silico and uncovering the regulatory logic underlying gene expression. Despite their importance, accurate inference of these networks on a genome-wide scale remains a major challenge in bioinformatics.

Augusta is an open-source Python package developed to reconstruct computational models from time-series RNA-Seq datasets, supporting the inference of both GRNs and BNs at the genome scale. The workflow in Augusta encompasses several key stages: it begins with normalization of gene expression count tables, proceeds to GRN inference via mutual information computation, and incorporates a two-step validation process. This validation involves the *de novo* identification of transcription factor binding motifs (TFBM), followed by integration of curated database evidence to refine the resulting network. For BN inference, Augusta combines curated knowledge with logical rule assignments, enabling a more holistic analysis of regulatory interactions.

The ongoing development of Augusta is focused on adhering to the FAIR-RS (Findability, Accessibility, Interoperability, and Reusability for Research Software) principles. Backed by the FAIR-IMPACT initiative under the "Assessment and improvement of Research Software" support action, Augusta is committed to promoting transparent, reproducible methods in the analysis of gene regulatory systems.

Augusta is available from github.com/JanaMus/Augusta along with documentation, examples, and tutorials.

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