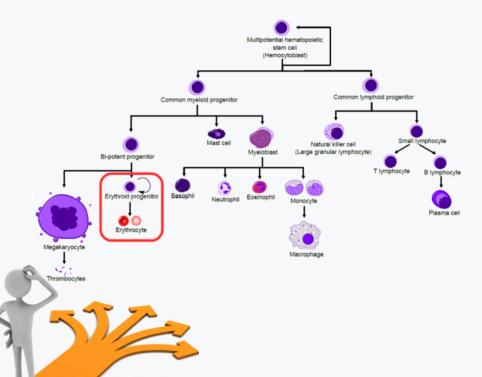
WASABI

Dynamic iterative framework for Gene Regulatory Network (GRN) inference

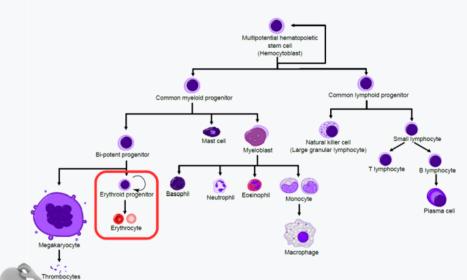
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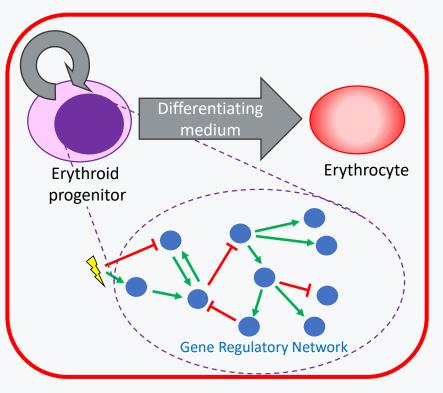
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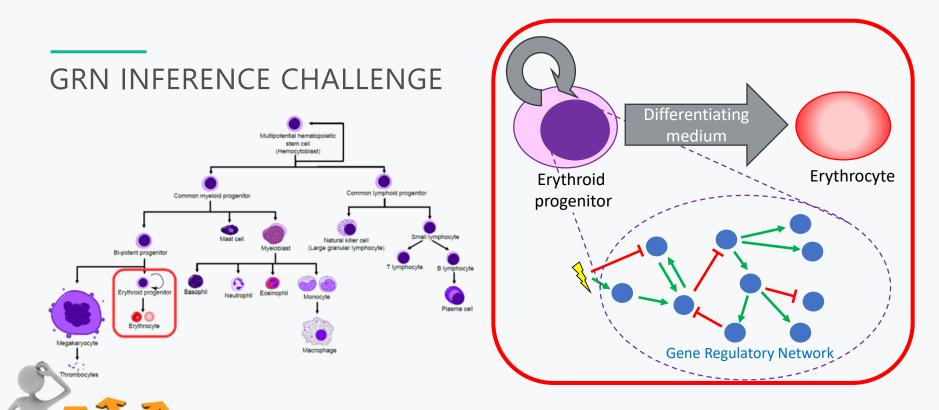
GRN INFERENCE CHALLENGE







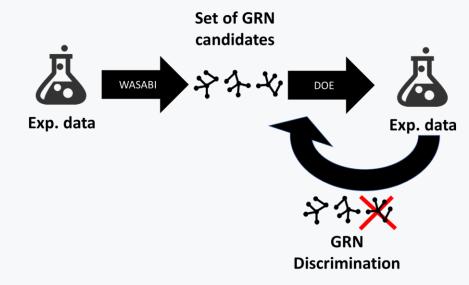


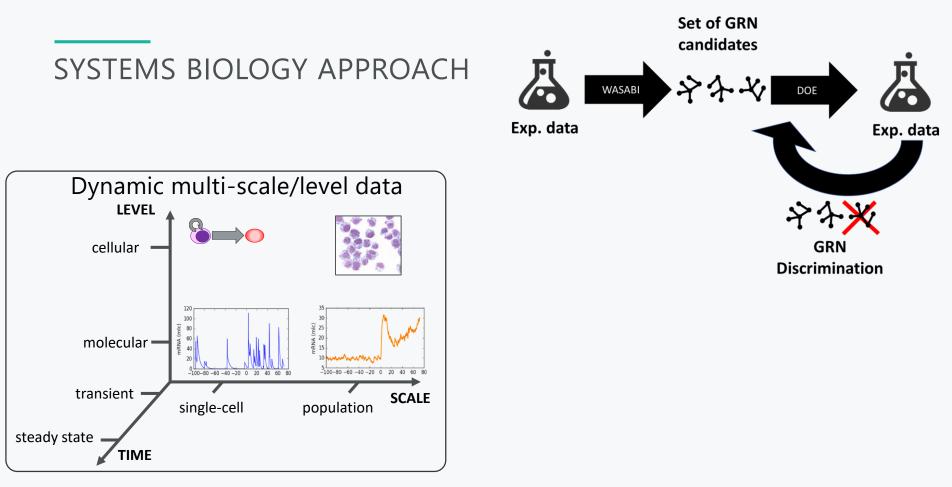


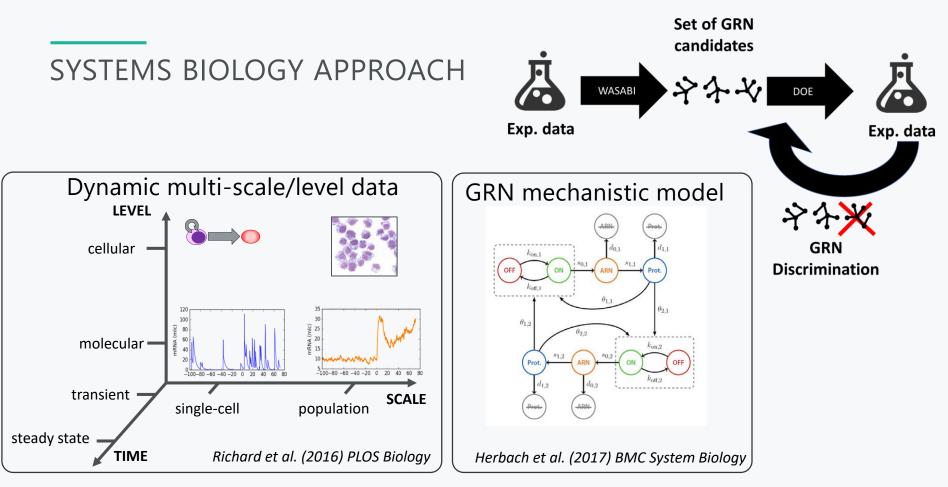
Existing GRN inference solutions face **common limitations** :

- Restriction to correlation
- Interaction centered (≠ network)
- Restriction to Transcription Factor
- Biological **over-simplifying** assumptions
 - Mono-data type

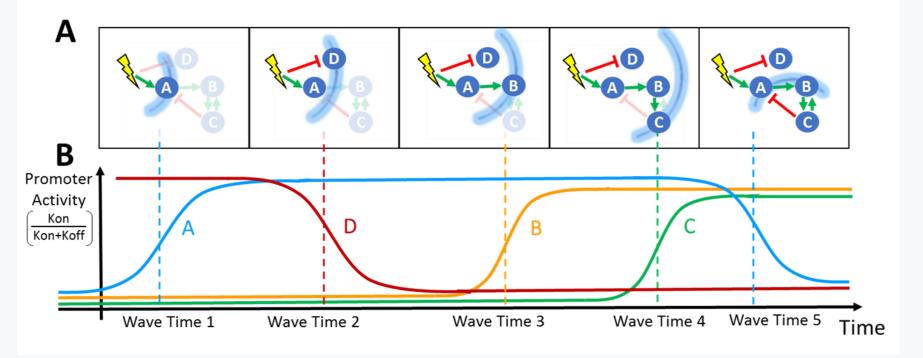
SYSTEMS BIOLOGY APPROACH







WASABI = **WA**VE**S A**NALYSIS **B**ASED **I**NFERENCE



RESULTS

- *In silico* benchmarking → Validation of performances
- *In vitro* application → new insights on GRN topology
- Advantages
 - **Splitting** and **parallelization** (scalable)
 - Inference of **causalities** (circular)
 - Network centered
 - No restriction to Transcription Factors
 - Integration of proteomic data

THANKS FOR WATCHING!

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DRACULA team







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