

# Model inference from protein time-course in Hematopoietic Stem Cells (HSC)

Pandu Raharja <sup>1,2</sup>   Rene Schoeffel <sup>1,2</sup>   Michael Strasser <sup>3</sup>

<sup>1</sup>Technische Universität München

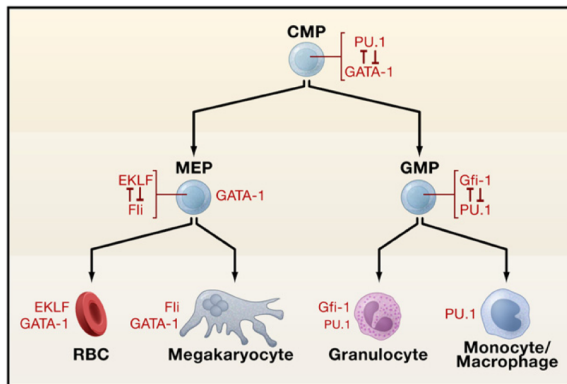
<sup>2</sup>Ludwig-Maximilians-Universität München

<sup>2</sup>Institute of Computational Biology (ICB), Helmholtz Zentrum München

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# Introduction

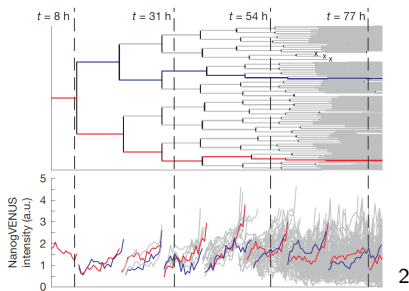
- Dynamics of hematopoietic stem cell maturation cell from Common Myeloid Progenitor (CMP) to Megakaryocyte-Erythroid Progenitor (MEP) and Granulocyte-Macrophage Progenitor (GMP)



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## Introduction (cont'd)

- ▶ MEP and GMP yield not 50% : 50% as previously thought, but 70% : 30%
- ▶ Assumed dynamics between Pu.1 and Gata1 in cell maturation fate
  - ▶ Dynamics assumed to be a bistable toggle-switch system
- ▶ Analysis on single-cell time-lapsed data



# Problems

- ▶ Stochasticity in single cell resolution is more punctuated
- ▶ Tree structure of the data add ore complexity: inheritance of information during inference process is not trivial

# Ideas

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- ▶ Sequential Monte Carlo simulations along the time-apsed data to infer "good" parameters
- ▶ **problem:** Overfitting due to single-cell biased
- ▶ **solution:** Inference across cell lineages
- ▶ Inferred parameters from all simulated lineages are represented as distribution
- ▶ Final inferred parameters are expected value  $E$  of the distribution

# Particle Filtering (6)

# Particle Filtering (7)

# Particle Filtering (8)

# Particle Filtering (9)