Integrating time-series data on large-scale cell-based models
application to skin differentiation
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Objectives
→ Formal modeling of large scale biological network
→ Inference parameters for stochastic simulation

Table of patterns

<table>
<thead>
<tr>
<th>Biological Patterns</th>
<th>Process Hitting (PH)</th>
<th>Translation</th>
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</thead>
<tbody>
<tr>
<td>Simple activation</td>
<td><img src="image" alt="Simple activation" /></td>
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<tr>
<td>Simple inhibition</td>
<td><img src="image" alt="Simple inhibition" /></td>
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<tr>
<td>Activation or inhibition</td>
<td><img src="image" alt="Activation or inhibition" /></td>
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</tbody>
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Biological network (RSTC) [1]

→ RSTC: multi-layer receptor-signaling-transcription-cell state
→ 293 nodes: signaling proteins, transcription factors, genes
→ 375 interactions: activations, inhibitions, complex decompositions

Times series data
(gene expression)

Parameter estimation
(for stochastic simulation)

→ Introduces time features
→ Parameters: either \((r, w_0)\), or the firing interval \([d, D]\)

Results and simulations

Conclusions
→ Hybrid approach for modeling an RSTC network
→ Formalizing biological knowledge: Translation of motifs
→ Inference and integration of temporal parameters
→ Validation with discrete times series data

Perspectives
→ Refining the dynamics of PH Model
→ sub-networks
→ aggregate different sub-network to build the original network

References
Lecture Notes in Computer Science, 171-191