Department of Information and Computer Science

Bayesian Multi-Way Models for Data Translation in Computational Biology



Introduction

- Molecular measurements of biological organisms to study response to:
 - disease
 - medical treatment
 - environment

- Measurements can be made:
 - in vivo: cell extracts from humans or model organisms
 - in vitro: cell lines grown in laboratory



Molecular activity in biological cell



Joyce & Palsson, Nat. Rev. Mol. Cell Biol. 2006

Machine learning for computational biology

- Molecular measurements:
 - Large data sets
 - Uncertainty/noise
 - ⇒ Automated and robust *data-driven* analysis tools needed
- Bayesian approach to probability:
 - Take uncertainty into account
 - Describe the generative process of the data
 - ⇒ Integration of multiple measurement sources
 - Incorporate existing knowledge by specifying:
 - the model structure
 - priors



Computational medicine & contributions

- Model organisms for studying effects of:
 - genomic mutations
 - new medical treatments, potentially dangerous

Computational medicine & contributions

- Model organisms for studying effects of:
 - genomic mutations
 - new medical treatments, potentially dangerous
- Dissertation: statistical modeling of effects in molecular measurement data with
 - high-dimensional, noisy measurements
 - multiple measurement types
 - multiple organisms



Computational medicine & contributions

- Model organisms for studying effects of:
 - genomic mutations
 - new medical treatments, potentially dangerous
- Dissertation: statistical modeling of effects in molecular measurement data with
 - high-dimensional, noisy measurements
 - multiple measurement types
 - multiple organisms



P I: Multi-Way Model for "n < p"



(2) Model: (3) Result:





P II-III: Multi-Way Models for Multi-Peak Metabolomics

a) Peak clustering based on shapes



b) Inference of covariate effects based on intensity





LIPID MAPS 2014

··//=

ни т

P IV: Multi-Way Model for Multiple Sources

(vy

vx

F



a^g)

n samples

a

ъ

0

20 22 20 50 20 50

n samples

8

8

20 20 20 20

n samples

P V: Cross-Organism Toxicogenomics



P VI–VII: Cross-Organism Multi-Way Model



Summary

New machine learning models for:

- P I Small sample size, high dimensionality (n < p)
- P II–III Incorporating prior information about the measurement process
- P IV–V Multiple data sources with co-occurring samples
- P VI–VII Multiple data sources without co-occurring samples

Department of Information and Computer Science

Bayesian Multi-Way Models for Data Translation in Computational Biology

