Methods of Genomic Data Fusion

An Overview

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Motivation: Why combine data?

- “High-throughput” methods are increasingly popular.
- They produce lots of indirect, generic and partial data.
- The data produced is often very noisy.
- Combination of different kinds of evidence might improve statistical significance and reduce the noise.
What is Data Fusion

- Many kinds of analyses obtain results by combining *certain* different datasets in one way or another.
- We are, however, interested in approaches that can *scale* to integrating different and *nearly arbitrary* kinds of data.
Outline

- Data fusion “in general”
- Case study: Bayes nets
- Case study: kernel methods
A General Data Analysis Strategy

- Any data analysis looks like that:
  1. Represent the data in an appropriate form
  2. Perform a certain statistical procedure
  3. Convert the results to a useful form
- Data fusion is easiest at step 1 (*early integration*) or 3 (*late integration*).
Common Representation

- In most cases the choice of common data representation pretty much defines the algorithm to be used:
  - Data vectors/matrices
  - Distance metrics/Kernel matrices
  - Graphs/binary predicates
Example: Bayes Nets

Example: Bayes Nets
Example: Kernel Methods

- Often *pairwise inner products* suffice for analysis.
- \( \Rightarrow \) the *kernel matrix* as a common representation.
- A variety of kernels exist for all kinds of data.
- Different kernels can be combined by summing.
Kernels

- Protein sequence kernels
- Protein interaction kernels
- Gene expression kernels
Kernel combination

- Different kernels can be weighed and summed:

  \[ K = \lambda_1 K_1 + \lambda_2 K_2 + \cdots + \lambda_n K_n \]

- Lancriet et al. present an SVM classification algorithm that can figure out the weights automatically.
Example: Membrane proteins

- Input: the collection of different kernel matrices + CYGD annotations.
- Procedure: split the data into training/test sets, predict values for test set.
- Evaluation: compare the performance to alternative methods.
Example: Membrane proteins
More applications

- Yeast protein function prediction
- Biological pathway prediction
- Protein-protein interaction prediction
- Clustering & search for motifs
Summary

- Although a recent development, there are already several frameworks for data fusion
- The major approaches are clustering, Bayesian inference and kernel methods.
Hope you don’t have any questions...