

Inferring Networks from Distances: the “Landscape” of Glycosidase Protein Structures

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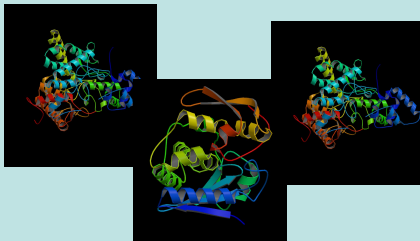
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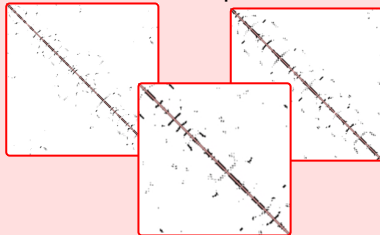
Nov 21, 2011

Graphical Abstract

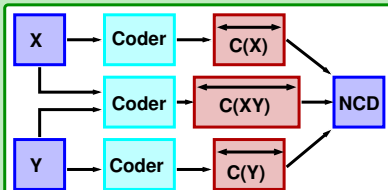
Objects: protein structures



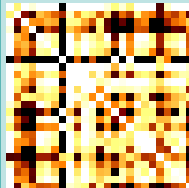
Contact maps



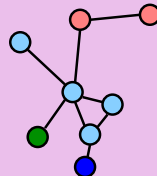
Compression-based distances



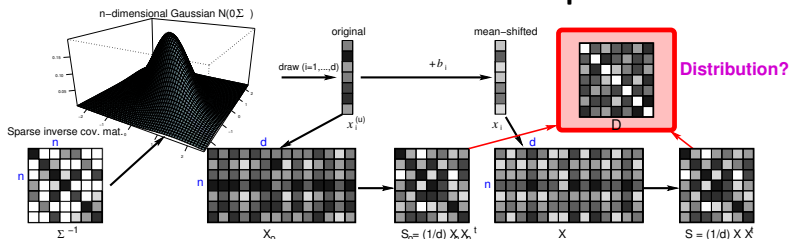
Distance matrix



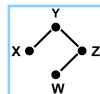
Network inference



- Idea: construct **probabilistic generative model**, condition on **observed data** and **infer distribution of parameters**.



- We observe pairwise distances D .
- $D \sim$ **singular Wishart**, parametrized by inverse covariance Ψ .
- Link to Gaussian graphical models:
 $\Psi_{ij} = 0 \rightsquigarrow (i, j)$ conditionally independent
 \rightsquigarrow no edge.
- Infer Ψ by **Markov Chain Monte Carlo sampling**.



Compression Distance between Protein Structures

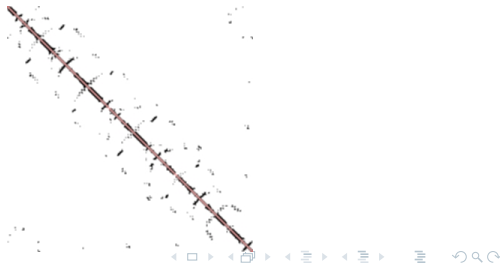
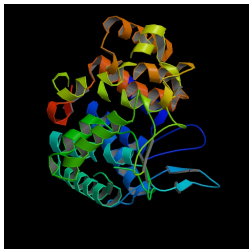
- **Normalized Information Distance:** length of the shortest program that computes $x|y$ and $y|x$.

$$NID(x, y) \propto \max\{K(x|y), K(y|x)\} = K(xy) - \min\{K(x), K(y)\}$$

- Approximation: **Normalized Compression Distance:**

$$NCD(x, y) \propto C(xy) - \min\{C(x), C(y)\}.$$

- **In our application:** x, y are vectorized **contact maps** for **Glycosidase enzymes** in **Escherichia coli**.



The “Landscape” of Glycosidase Protein Structures

