

**Riconoscimento e Recupero dell'informazione per Bioinformatica**  
**Risultati seminari**

<u>Voto</u>	<u>Argomento</u>
14/15	A pattern matching approach to the automatic selection of particles from low-contrast electron micrographs
14/15	A quantitative model for transcriptional differentiation driving host-pathogen interactions
15/15	Accounting for noise when clustering biological data
12.5/15	Predicting Protein-Ligand Binding site using SVM with protein properties
13/15	Machine Learning approaches for the discovery of gene-gene interactions in disease data
12.5/15	A comparative analysis of biclustering algorithms for gene-expression data