PH296, Section 33
Statistics and Genomics Seminar
Fall 2002

Sandrine Dudoit
sandrine@stat.berkeley.edu
http://www.stat.berkeley.edu/ sandrine
Course structure

The course has two components.

- **Seminar.** A one–hour weekly seminar given by researchers working at the interface between the statistical and biological sciences.

- **Discussion.** A weekly discussion section during which the seminar topics are introduced and related papers are presented and discussed.

Berkely Program in Genomics:
http://computationalbiology.berkeley.edu
Course details

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<th>Course</th>
<th>Details</th>
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<tr>
<td>Discussion</td>
<td>Monday, 4–5pm, 340B Haviland</td>
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<tr>
<td>Seminar</td>
<td>Thursday, 4–5pm, 334 Evans Hall</td>
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Topics (non–exhaustive list)

• Genetic mapping;
• DNA microarray experiments;
• Computational gene finding;
• Sequence alignment;
• Protein structure prediction;
• etc.
Responsibilities

Class presentation of an article(s)/software package(s) which involve the application of statistical methodology to address a biological question.

- One-hour presentation during Monday section.
- Topic of your choice.
- Individual or group presentations.
- Must meet with instructor prior to the presentation to get the topic approved and discuss the presentation content and format.
Class presentations

- Background on the biological question.
- Background on the statistical and computational methods used to address the question.
- How are these methods used to address the biological question?
- Are the methods appropriate?
- Can you suggest possible improvements and extensions?
- Optional: reproduce analysis and perform other analyses of the data.