Computational analysis of
biological structures and networks

Instructions for the thematic workshop

Manuele Bicego

Computer Science Dept.
University of Verona

From introduction

Assessment methods

Two parts:

- *First part:* ***written exam*** *(during exam sessions)*
- *Second part:* ***talk*** *within a thematic workshop (as in a conference)*

Assessment methods

- *First part:* ***written exam***
  - *few questions on course topics*
    - *Example: “Describe the main properties of Bayesian Networks”*
  - *one question on the lab part (typically understanding a small piece of code)*
    - *Example: “Does this matlab code compute the mean of the vector x? Why?”*

```
% x is a vector of N entries containing numbers

m = 0;
for i = 1:N
   m = m+x(i);
end
m = m/(N-1);
```

Assessment methods

*Second part: **Talk** within a thematic workshop*

- *The topic of the thematic workshop will be decided in advance (before middle of November)*
- *Each student has to choose a scientific paper to be presented in 10 minutes*
- *One thematic workshop will be held at the end of the course (registration needed by early December)*
- *Other sessions in June and September*

Procedure

- All students who want to participate to the first session need to register by sending an email (Deadline: 25/11)
- All registered students have to choose a paper on the assigned topic to be presented at the workshop (Deadline: 16/12)
  - NOTE: One different paper per student (a list of taken papers will be maintained on the web page)

CHECKPOINT: the chosen paper should be approved by the instructor (send an email)

Notes

- Note 1. The first thematic workshop will be held in January (week 20-25 January or week 27-31 January). Others will be held in June and September.

- Note 2. You don’t have to register and to choose the paper if you are **not interested** in participating to the January session

Topic

- The topic for this year is “**Kernel methods in Medical Bioinformatics**”
    - Description of advanced kernel methods
        - Novel kernels, novel kernel procedures
    - Application of “non standard” kernel methods to interesting biomedical problems

Suggestions for the choice of the paper

- The focus should be on kernel methods: try to avoid papers which use “standard SVM” with “standard kernels” (e.g. rbf or polynomial) on vectorial representations
- Good choices:
  - Biomedical applications involving structured objects faced with standard SVM and “kernels for structured objects” (kernels for sequences, kernels for strings, kernels for images,...)

Suggestions for the choice of the paper

- Novel Kernels or novel kernel-based approaches: kernel PCA, kernel ICA, kernel K-means, kernel clustering,…
- Non standard SVM: one-class support vector machines, SVM with two hyperplanes

NOTE: you don’t have to present the math (no time!), just the idea.

The list of already booked paper can be found online, check it before submitting your choice!

Procedure

- **Preferred**: papers published in Briefings in Bioinformatics, Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, BMC Bioinformatics, BMC Genomics, Artificial Intelligence in Medicine or other high impact journals (Nature, Science, ...)
- **Alternatives**:
  - Other papers published in journals of Elsevier, IEEE, ACM, Springer and Oxford Academic can be considered
  - Conference papers published in IEEE-IAPR-ACM conferences

The talk

- 10 minutes (strict!)
- Suggested structure of the talk:
  - Introduction to the problem
  - Main idea (no formulas!) together with the relevance with respect to previous works
  - Some results (if any) and discussion

Important note

- Please send me your slides (in **PDF format**) the **day before** your presentation
  - (to speed up the process, all the slides will be shown using my laptop)