



SAPIENZA
UNIVERSITÀ DI ROMA

New openings for pre and post-doctoral fellows in the Biocomputing Unit of the Sapienza University in Rome.

We seek:

- **scientists** with a Ph.D. degree and solid research experience in Computational Biology / Bioinformatics, with at least three years of experience and a competitive productivity record.

and:

- **Candidate Ph.D. students** with a solid background in computational or engineering sciences willing to work on biological projects. Basic knowledge of biology will be considered an advantage
- **Candidate Ph.D. students** with a solid background in genomics and/or biotechnology willing to learn computational biology techniques. Basic knowledge of computer science and bioinformatics will be considered an advantage

We offer:

- The opportunity to be part of a productive internationally recognized group that effectively combines basic and applied research.
- An energetic, dynamic working environment with a multidisciplinary approach to computational genomics and proteomics research, equipped with state-of-the-art technology and facilities.
- An excellent scientific and technical platform to work in Computational Biology/Bioinformatics.



- Candidate PhD students will have to apply to one of the Ph.D. schools of the University of Rome
- Bursaries will depend upon experience of the candidate.

The laboratory

The computational biology laboratory of the Sapienza University in Rome is a multidisciplinary Unit established in 2001 composed by physicists, computer scientists, engineers, chemists, pharmaceutical chemists, biotechnologists and biologists. The head of the group, Anna Tramontano, has been working in the area of computational biology and bioinformatics (*ante litteram*) since 1980 in the USA and Europe, in both academic and industrial setups.

Our group research activities are devoted to the computational analysis of biological data, to the development and improvement of methods for the analysis of genomes and proteomes and to the applications of methods to problems of biomedical interest. The synergy among the members of the groups with different backgrounds has allowed the group to select interesting biological problems and tackle them with many different approaches often combining techniques from diverse disciplines. The group is internationally recognized and is involved in many world-wide initiatives aimed at analysing post-genomic biological data in order to improve our understanding of life at a molecular level.

Available computer equipment

- 1 Cluster HP 10 Blade (BL 465c) , 20 CPU (AMD O2220 2.8 GHz Dual Core), 80 GB RAM, 20 Disks SAS 72 GB 15Krpm, 4 Gbit Ethernet. - 4 Switch Gigabit Virtual Connect
- 1 Olidata AMD dual processor server (4GB RAM)
- 1 IBM Z Pro, dual Intel Xeon 3.0 GHz server, 1 GB RAM, 4x Disks 80 GB
- 3 Silicon Graphics Octane machines
- Several Desktops (PC and MACs)

We have local installation of the most widely used modelling, statistical and simulation software packages and biological databases.

In the following two/three years we plan to triplicate the computer power available to us.

The project: systems view of biological organisms.

The main strengths of the group are its long standing experience in three-dimensional modelling of macromolecules and its multidisciplinary nature. We can build on our understanding of the biological system and exploit our expertise in quantitative methodologies to infer properties that can be directly correlated to important biomedical problems and we can address genomic and post-genomic problems by “projecting” them in three-dimensions where biochemical and biophysical knowledge can be applied.

We plan to address the forthcoming new challenges of computational biology using large scale structural analysis of gene products and interactions exploiting, as quickly and effectively as possible, the new wave of data deluge that is impending upon us. It is important to highlight that in computational biology the availability of more data does not only affect quantity, but also quality. Any new information can be linked and correlated to the existing one adding value and biological relevance to it. Similarly, the access to more computational resources does not simply imply that the same things can be done faster, but that intractable problems can suddenly come within our reach.

Our future plan and its components can be mapped to an engineering project where we need to have the parts list of the biological systems, understand their tolerance thresholds, find the assembly instruction and, finally, simulate its behaviour.



Interested candidates should send a CV and the names of two referees to:

anna.tramontano@uniroma1.it

specifying in the subject line:

Application for (post-doc/pre-doc) position: Last name

Short listed candidates will be invited for an interview.

Deadline: May 30th, 2008

Relevant web links:

<http://cassandra.bio.uniroma1.it>

<http://www.kaust.edu.sa/research/investigators.aspx>