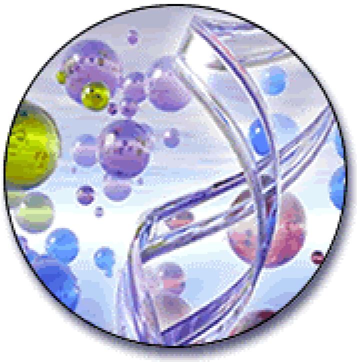

# Machine Learning
## Methods in Functional Genomics

A Special Issue of
**Machine Learning Journal**
**Kluwer Academic Publisher**

**Guest Editors**

**Paola Sebastiani**, University of Massachusetts
**Marco Ramoni**, Harvard Medical School
**Isaac Kohane**, Harvard Medical School

In June 2000, leaders of the Human Genome Project, Craig Venter of Celera Genomics, and U.S. President Clinton announced the completion of a ``working draft" DNA sequence of the human genome: the genetic blueprint for a human being. The legacy of that a announcement is the challenge to annotate this map, by understanding the functions of genes and their interplay with proteins and the environment to create complex, dynamic living systems. This understanding is the goal of functional genomics. Recent technological advances enable biomedical investigators to observe the genome of entire organisms in action by simultaneously measuring the level of activation of thousands of genes under the same experimental conditions. This technology, known as microarrays, provides today unprecedented discovery opportunities and it is reshaping biomedical sciences,

Parallel to these technological advances has been the development of machine learning methods able to integrate and understand the data generated by this new kind of experiments. However, most of this research has been conducted outside the traditional machine learning research community. The aim of this special issue is to bridge this divide by reporting methodological advances in automated learning from functional genomic data to the core machine learning community. The special issue seeks significant methodological contributions of proven or potential impact on functional genomics.

Topics of interest include, but are not limited to:

- Hybridization detection, signal amplification and noise control in microarray experiments.
- Differential analysis and classification of gene expression data.
- Clustering and other unsupervised approaches to class discovery in functional genomics.
- Temporal profiling and analysis of dynamic genomic systems.
- Dependency discovery and reverse engineering of genetic networks.
- Validation methods to assess reliability and reproducibility of experiments.

Articles accepted for the special issue will be permanently posted on the WWW and will constitute the core of a free portal to machine learning resources in bioinformatics (**www.genomethods.org**).

The production of the special issue is expected to proceed according to the following schedule:

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| May 15, 2002 | Abstracts submission. |
| June 15, 2002 | Full articles submission. |
| Sept 1, 2002 | Notification of acceptance |
| December 1, 2002 | Final revisions due. |
| Spring 2003 | Special issue publication. |

Authors who intend to contribute to the special issue should send a tentative title and abstract to the contact address below before May 15, 2002. Manuscripts should conform to the standard formatting instructions of Machine Learning Journal, available from

**http://www.genomethods.org/mlj/initial.pdf**.

Manuscript must be submitted in electronic form, as email file attachments in PDF format, and addressed to **jml@wkap.com**. Authors should also send a copy of the manuscript to Paola Sebastiani, at the address below. The body of the message accompanying the electronic submission should also clearly state that the submission is intended for the special issue "Methods in Functional Genomics".

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