Introduction to the Special Issue on Bioinformatics and Constraints

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In the last decades, modern Biology has revealed its potential thanks to the fruitful collaboration with Computer Science. This new research field, known as *Bioinformatics*, has attracted scientists with new challenges and everyday we experience significant results, thanks to the joint efforts of researchers.

When experimental sciences started producing high-throughput data, the manual analysis, mining and synthesis of models became infeasible. The organization of information required an automated and efficient set of algorithms to allow the interpretation of the phenomena being studied. Just to cite a few examples, we can think of the task of recovering and analyzing DNA sequences.

Another central interest regards the field of simulation and prediction, for example applied to biological systems (for metabolic or regulatory networks) and to the spatial conformations and interactions of biological polymers (e.g., proteins, RNA).

In general, Computer Science has developed general and robust techniques that, once applied to these problems, were able to achieve remarkable results, such as the annotation of the Human genome. The methods to tackle Bioinformatics problems span across various areas, such as semantics of concurrent processes, string and substring matching, optimization techniques, just to cite a few. There is a vivid interest in producing new solutions and tools to the challenging biological problems, since an improvement and/or solution of one of them can provide significant benefits in medicine, agriculture, and industry.

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Technically, Bioinformatics problems are often computationally expensive tasks that can be encoded exploiting the application of recent and general techniques of constraint programming. As evidence of this trend, various workshops (Constraints and Bioinformatics/Biocomputing at CP97, CP98 and Constraint based methods for Bioinformatics at ICLP2005, CP2006, and ICLP2007) witness the interest and the importance of research in the topic. Moreover the study of these problems has the side effect of pushing the development of constraint technology.

The accepted contributions of this special issue are extended, revised and reviewed versions of contributions to the workshops WCB05, WCB06, and to the conferences CP06, ICLP06, and SAT06. They can be split into four categories that cover the whole range of Bioinformatics:

Structure Prediction   The contribution by Barahona and Kripphal shows the constraint basis and the main features of the tools BiGGER and Chemera, that are currently used by many biologist for protein structure prediction and docking.

Systems Biology   In this area, Grell, Nikiforova, Schaub, Selbig show how Modelling biological networks by action languages, and how to solve them using *answer set programming* which can be seen as a Boolean constraint solver. Bortolussi and Policriti present how Modeling Biological Systems in Stochastic Concurrent Constraint Programming.

Haplotype inference/Pedigree   There are two contributions on this topic. The first, by Lynce, Marques-Silva, and Prestwich deals with the problem oh Haplotype inference. The proposed solution is based on constraint programming and local search. In the second paper, Sanchez, de Givry, Schiex show how to use constraint satisfaction techniques for detecting Mendelian error in complex pedigrees, and they develop the solver `toulbar`.

Motif localization, alignments   This topic also has two accepted contributions. In the first, Gaspin, Schiex, and Zytnicki present their tool *DARN!*, a soft constraint solver for RNA motif localization. The second, by Busch, Backofen, and Will illustrates how to use the technique of cluster tree elimination for efficient sequence alignment with side-constraints.

We thank the external reviewers and the editor in chief of the Constraints Journal for giving us the opportunity of editing this special issue.[1]

With this publication, we wish to report to the Bioinformatics community on the effective use of the constraint-based techniques in building tools for solving their problems. Moreover we would like to show to the constraints community that it is possible to help biologists working at an abstraction level where full knowledge of the underlying biological processes is not needed.