



## Introduction to the Special Issue on Bioinformatics

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This special issue of the *Journal of Constraints* grew out of a series of workshops on Bioinformatics and Constraints as part of the Constraint Programming conferences held in 1997 and 1998. The papers range over a wide area of applications within Bioinformatics, and the computational approaches are equally diverse.

Roland Yap's paper extends the usual sequence alignment algorithm. Such algorithms rely on some cost function to distinguish between good and bad alignments. His approach employs costs which can be parameters of the query instead of the usual fixed cost functions.

Two papers deal with RNA secondary structure. I. Eidhammer et al. describe a constraint-based description language for structures in biosequences and two constraint-based algorithms for searching for structures in biosequence databases, given a query in this language. Their approach can be applied to any domain where secondary structures are significant. Christine Gaspin describes both the prediction and representation of RNA secondary structures, using constraint satisfaction techniques.

There are three papers on the prediction of three-dimensional structures. Rolf Backofen tackles the problem of structure prediction using simplified lattice models of proteins using constraint optimisation techniques. Robert Rodošek presents a hybrid algorithm for deriving 3-D structures of cyclic polypeptides. The algorithm combines constraint-based techniques with the most widely used methods for non-cyclic polypeptides. Yadgari et al address another problem, namely protein threading, which as we have already mentioned uses a mixture of sequence alignment and structure alignment. The novelty of their approach is the use of genetic algorithms where known structures are used as constraints to restrict the search for the native conformation.

It has been fun and challenging to both gather papers in Bioinformatics from computer scientists working in constraints, and also finding people to review the papers. We certainly learnt a lot in the process!

We would like to thank all the authors as well as the anonymous reviewers for their time and patience.