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主要研究領域：計算生物學及生物資訊學、演算法、套裝軟體

Research Interests (ABC'S): Algorithms, Bioinformatics, Computational Molecular Biology, and Software Tools

## 演算法與計算生物學實驗室

### **Algorithms and Computational Biology Lab.**

演算法與計算生物學實驗室創立於 2002 年 8 月。我們的研究主軸為「序列」與「樹狀結構」主題相關的演算法設計，以及利用這些演算法為基礎的生物資訊軟體工具開發，可說是「計算理論為體，生物資訊為用」。在過去幾年裡，我們的研究主軸是關於序列及樹狀結構上的有效演算法設計與分析。在序列方面，包括生物序列分析，如：單套體預測問題、標記 SNP、複製數目變異問題、各種不同評分準則等，以及數列分析，如：最大總和區段問題、最大平均區段問題、不同條件的最佳化問題等。在樹狀結構方面，包括樹的建構問題，如：演化樹建構、最小繞線代價伸張樹問題等，以及樹的探索問題，如：樹邊分割問題、樹的查詢問題、樹邊置換問題等。這是非常有樂趣及成果的研究歷程，我們最終的目標是開發更多關於序列及樹狀結構的基本性質，並充分運用它們來設計解決這方面計算難題的實用演算法。

The Algorithms and Computational Biology Laboratory was established in August, 2002. We are interested in all aspects of the design and analysis of combinatorial algorithms. In particular, we solve algorithmic problems arising in computational molecular biology and networking. For the past few years, we have been mostly focused on the design and analysis of efficient algorithms for analyzing sequences and trees. For sequences, we mainly work on problems related to biological

sequence analysis (haplotype vs. genotype; tag SNPs; copy number variations; variant scoring schemes), and numerical sequence analysis (maximum-sum segments; maximum-average segments; other maximization criteria). For trees, we mainly work on some tree construction problems (evolutionary trees; minimum routing cost spanning trees), and tree exploring problems (tree edge partition; tree querying; swap edges). This has been a joyful and fruitful journey to us. Our ultimate goal is to reveal more properties related to sequences and trees, and fully utilize them to design practical algorithms for solving hard problems in that line of investigation.

