[BIOINFO 2025]

GARFold: Massively Parallel GPU-Accelerated RNA Secondary Structure Prediction

Hanju Lee[1,2] and Hyeshik Chang[1,2,3*]

[1] *Center for RNA Research, Institute for Basic Science (IBS), Seoul National University*
[2] *Interdisciplinary Program in Bioinformatics, Seoul National University*
[3] *School of Biological Sciences, Seoul National University*
**Corresponding author: hyeshik@snu.ac.kr*

RNA secondary structure prediction is essential for applications ranging from functional genomics to cis-regulatory element screening and mRNA vaccine design. However, computational bottlenecks limit high-throughput workflows that require evaluating millions of RNA sequences. Traditional dynamic programming algorithms like ViennaRNA exhibit the cubic time complexity, while recent linear-time methods such as LinearFold still struggle to meet the demands of high-throughput computational screening pipelines. We present GARFold, a GPU-accelerated RNA folding algorithm that fundamentally restructures the computational approach to secondary structure prediction. Unlike CPU-based methods that process base pairs sequentially, GARFold exploits the massively parallel architecture of modern GPUs to compute optimal substructures for all possible base pairs simultaneously across tens of thousands of inputs. This parallelization strategy enables linear-time complexity per sequence while maintaining prediction accuracy. GARFold provides the identical prediction accuracy as the conventional CPU implementations while maximizing GPU resource utilization. GARFold transforms RNA secondary structure prediction from a computational bottleneck into a scalable component of high-throughput workflows, enabling substantial efficiency in RNA design pipelines and large-scale genomic analyses.