

Syllabus

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Chapter 5: How Do We Compare Biological Sequences? (Dynamic Programming Algorithms)

Week 1

Cracking the Non-Ribosomal Code

What is Sequence Alignment?

The Manhattan Tourist Problem

Sequence Alignment is the Manhattan Tourist Problem in Disguise

The Change Problem

The Manhattan Tourist Problem Revisited

From Manhattan to an Arbitrary DAG

Backtracking in the Alignment Graph

Detour: Non-Ribosomal Code

Detour: Topological Orderings in Graphs

Week 2

Scoring Alignments

Local Versus Global Sequence Alignment

The Myriad Faces of Sequence Alignment

Detour: PAM Scoring Matrices

Week 3

Penalizing Insertions and Deletions in Sequence Alignment

Space-Efficient Sequence Alignment

Epilogue: Multiple Sequence Alignment

Challenge Problem: Reconstructing the Non-Ribosomal Code

Detour: Divide-and-Conquer Algorithms

Detour: Scoring Multiple Alignments

Chapter 6: Are There Fragile Regions in the Human

Genome? (Combinatorial Algorithms)

Week 4

Of Mice and Men

The Random Breakage Model of Chromosome Evolution

Modeling Chromosomes by Signed Permutations

Reversal Distance

Sorting by Reversals: Greed is Good But Not Great

Breakpoints

Rearrangements in Tumor Genomes

From Unichromosomal to Multichromosomal Genomes

Two-Breaks

Breakpoint Graphs

Rearrangement Hotspots in the Human Genome

Epilogue: Constructing Synteny Blocks

Challenge Problem: Construct Synteny Blocks for Human and Mouse

Charging Station: From Genomes to the Breakpoint Graph

Charging Station: Solving the 2-Break Sorting Problem

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