

Accelerating Biomolecular Nuclear Magnetic Resonance Assignment with A*

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Overview

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Motivation

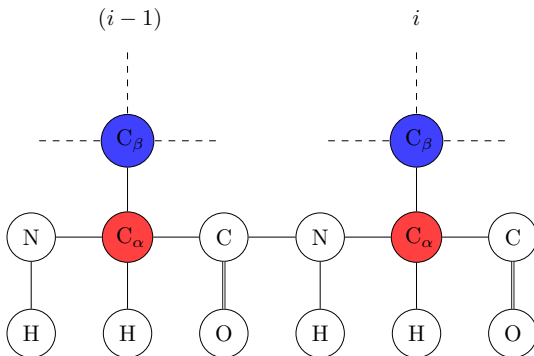
- Nuclear Magnetic Resonance Spectroscopy
 - Gain knowledge about protein structure
 - Study how mutations lead to diseases
- Problems
 - Generates large amounts of data
 - Data analysis is slow and error prone
- Goal
 - Automate the assignment process
 - Decrease human error
 - Increase productivity

Nuclear Magnetic Resonance (NMR)

- Used to obtain structural information
 - Chemical shift values
- HNCACB experiment
 - Generates C_α and C_β residue i and $i - 1$
- CBCA(CO) NH experiment
 - Generates C_α and C_β for residue i
 - Confirms residue data

Chemical Shift Values

HNCACB



Manual Methods

- Most time consuming part
- Missing and ambiguous data forces chunks to be skipped
- Prone to human error

Timeline

Protein
Production
at least 5 days

Data Assignment
20 days to 9 months

NMR
Experiments
1-2 days

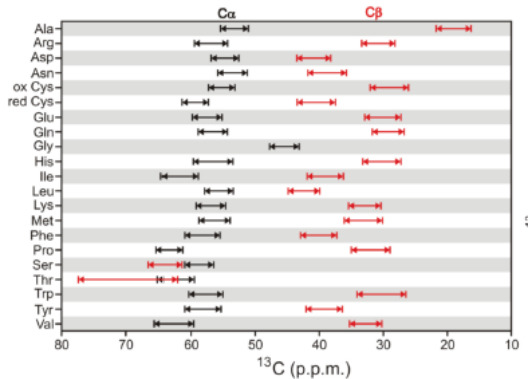
Automating Assingment

- Initialization
- Generating child nodes
- Goal State
- Solution State

Initialization

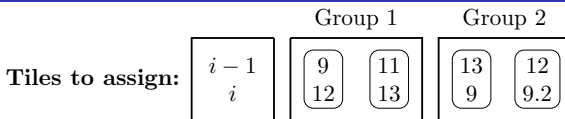
- Expected amino acid sequence
 - Converted to expected chemical shift values
 - Stored as the reference protein chain
- NMR experiment's chemical shift data
 - C_α and C_β for residue i and $i - 1$
 - Stored in a tile
- Missing data
 - Place holder tile generation
- Grouping

Grouping



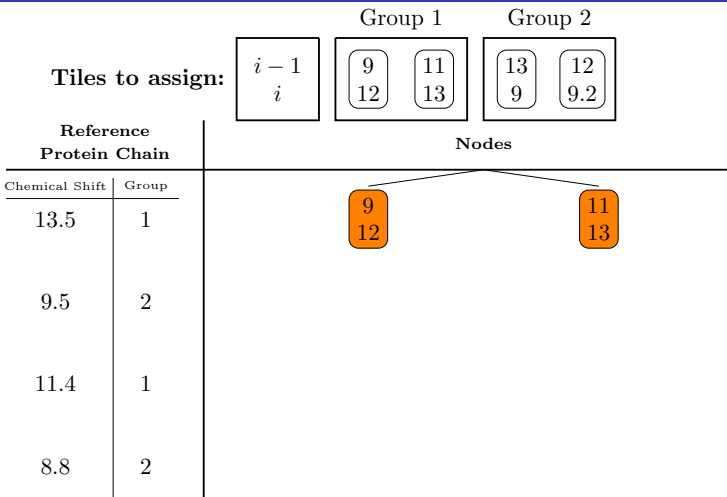
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Starting the assignment



Reference Protein Chain		Nodes
Chemical Shift	Group	
13.5	1	
9.5	2	
11.4	1	
8.8	2	

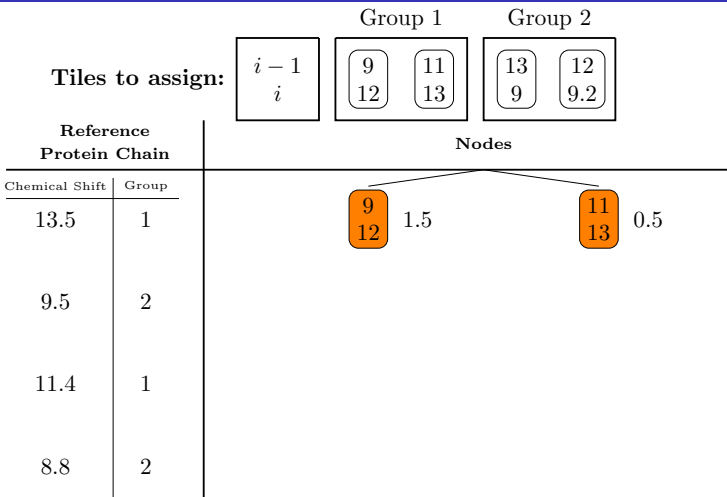
Starting the assignment



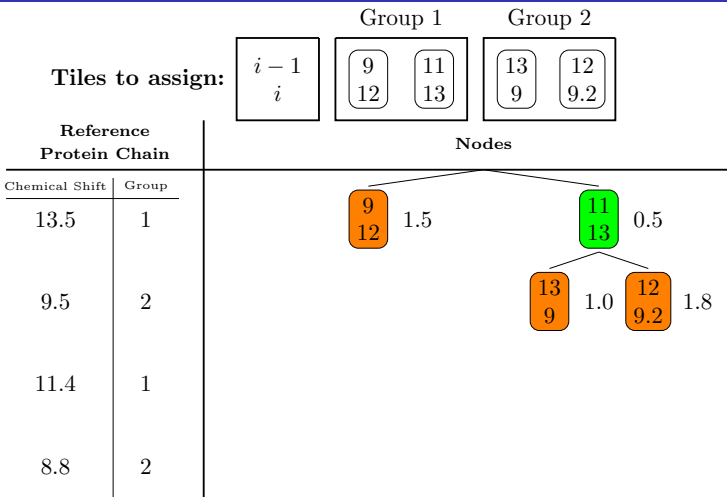
Cost Calculation

- Accuracy matching the protein chain residue
- Accuracy matching the tile above current tile
- Cost of placing all previous tiles

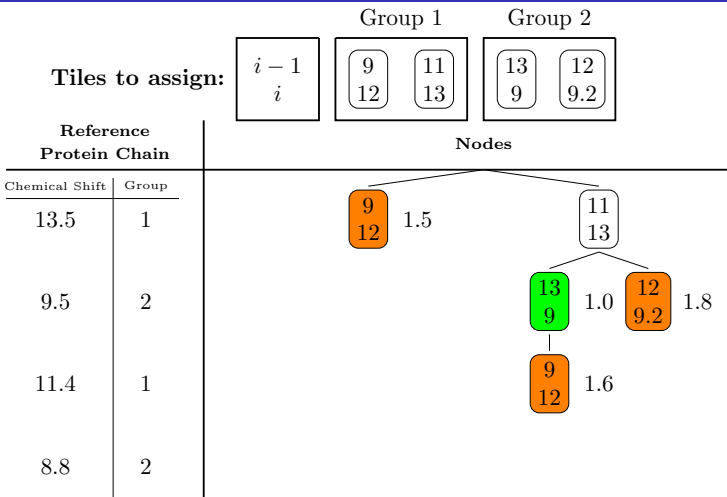
Generating child nodes



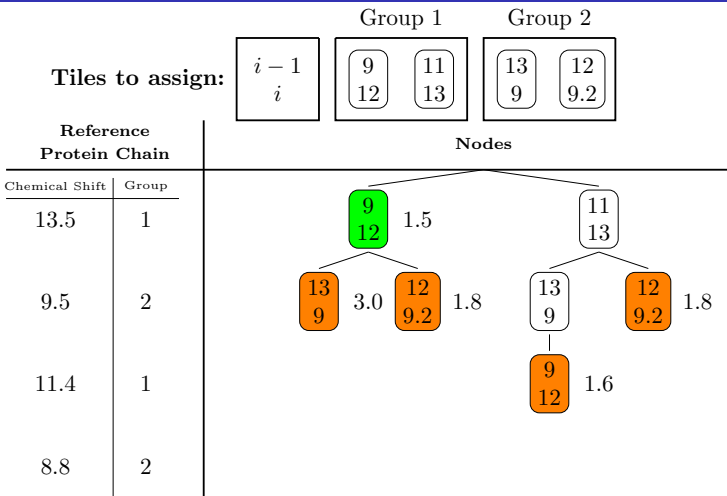
Generating child nodes



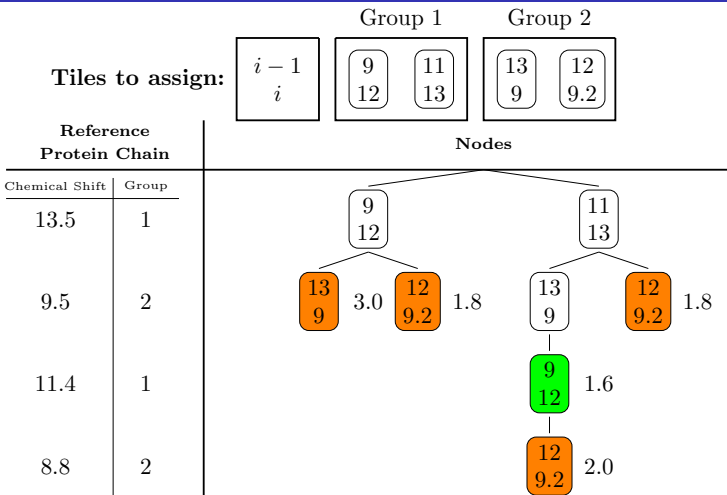
Generating child nodes



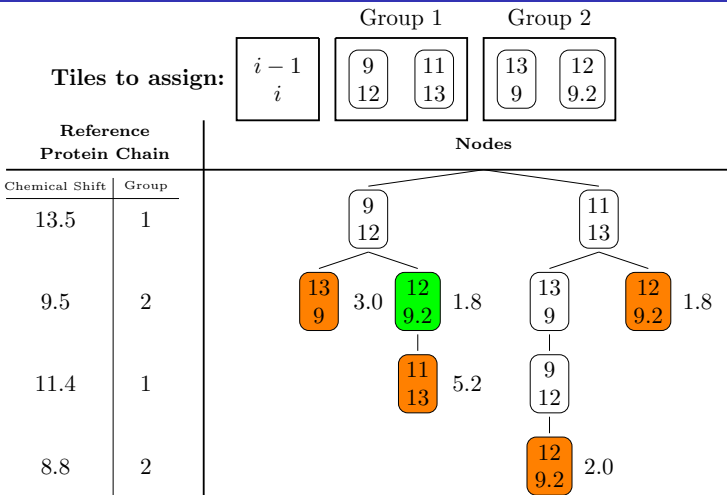
Generating child nodes



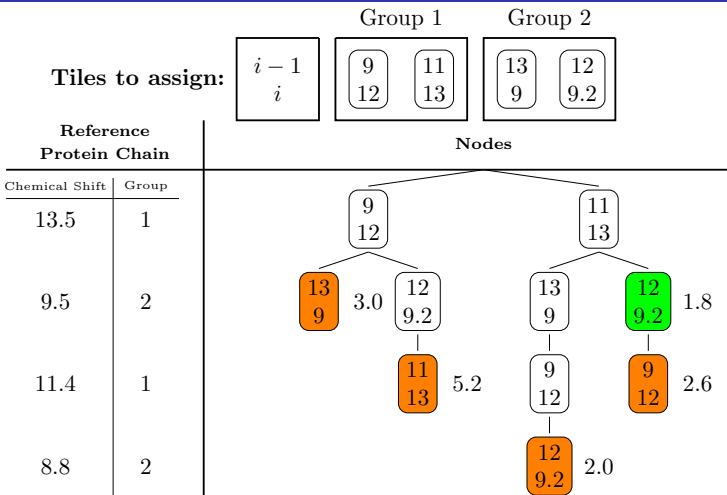
Goal State



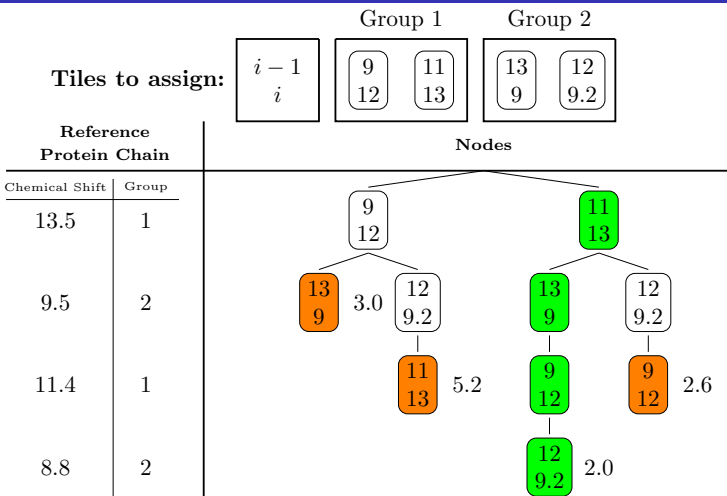
Goal State



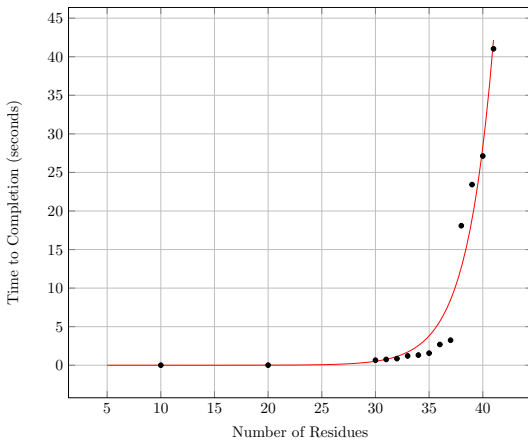
Goal State



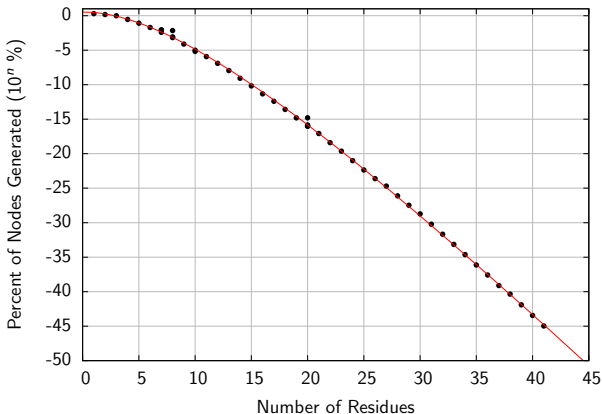
Solution State



Time of Assignment



Child Nodes Generated



Future Goals

- Parallelization
 - Decrease assignment time
 - Allow for larger data sets
- Machine learning
 - Optimize cost calculation
 - Increase accuracy of assignment

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- David Mascharka (research colleague)
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Bibliography



Babak Alipanahi, Xin Gao, Emre Karakoc, Frank Balbach, Shuai Cheng Li, Guangyu Feng, Logan Donaldson and Ming Li, *Error tolerant NMR backbone resonance assignment and automated structure generation.*, Journal of bioinformatics and computational biology, **9** (2011), 15–41.



Sean Cahill and Mark Girvin.
Introduction to 3d triple resonance experiments.
2012.



Peter Guntert, *Automated structure determination from NMR spectra*, European Biophysics Journal, **38** (2009), 129–143.



Flemming M. Poulsen.
A brief introduction to nmr spectroscopy of proteins.

Thank You

