

# Neighbor-Joining (NJ) Project Report

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## 1. Status of Implementation

Our NJ implementation produces the correct tree for 'example\_slide4.phy' as shown on Slide 4. The output matches the expected Newick tree structure, confirming correctness.

## 2. NJ Implementation Summary

We implemented the Neighbor-Joining algorithm in Python 3. A custom class (NJTreeNode) was used to construct the tree and export it in Newick format. Dictionaries and matrix caching were used to optimize merging and distance updates. The algorithm reads PHYLIP-formatted input and writes Newick-formatted output.

## 3. Machine and Timing Details

- Operating System: Windows 10 (64-bit)
- CPU: Intel(R) Core(TM) i5 / i7
- RAM: 8 GB
- Timing method: Python's `time` module for NJ, PowerShell's `Measure-Command` for QuickTree.

## 4. RF-Distance Computation

We used 'rfdist.py' to compute RF-distances between the trees generated by QuickTree and our NJ implementation. For each pair of trees, we recorded RF distance, max RF, and normalized RF. RapidNJ was not used due to OS compatibility issues.

## 5. Experimental Results Table

File	QuickTree Time (s)	Your NJ Time (s)	Speedup vs QT	Speedup vs RapidNJ
1347_FAINT.phy	7.8	2036.87	0.0	N/A
1493_Fe-ADH.phy	6.3	2677.2	0.0	N/A
1560_Ferritin.phy	7.1	3184.94	0.0	N/A
1640_CoA_bind.phy	5.4	3808.97	0.0	N/A
1707_Cys_knot.phy	4.9	4265.69	0.0	N/A

1732_Histidine_kinase.phy	6.5	4817.17	0.0	N/A
1756_FAD_binding_3.phy	9.0	3.15	2.86	N/A
1772_FAD_binding_6.phy	6.9	16.05	0.43	N/A
1806_NAD_binding_1.phy	7.6	43.06	0.18	N/A
1815_Lig_chan.phy	6.4	84.22	0.08	N/A
1830_Glyco_hydro_18.phy	6.2	160.14	0.04	N/A
1849_PAS.phy	7.5	340.35	0.02	N/A
1849_PBP.phy	7.3	492.27	0.01	N/A
89_Adeno_E3_CR1.phy	1.5	0.52	2.88	N/A