Identifying Structural Differences in Allosteric Proteins

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Program Flowchart

1. Query PDB to find proteins that have been solved in two functional states
2. Remove ligands and extract protein pairs with identical sequences
3. Align structures based on minimizing the difference between the Cα atoms
4. Compute structural differences ($\Delta \phi$, $\Delta \psi$, $\Delta \chi_i$, & $\Delta$neighbors)
# Program Results

## Percent of structural changes between states

<table>
<thead>
<tr>
<th>Protein</th>
<th>$\Delta \Phi$</th>
<th>$\Delta \Psi$</th>
<th>$\Delta \chi_{1,2}$</th>
<th>$\Delta \text{neighbors}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>CheY</td>
<td>20%</td>
<td>26%</td>
<td>22%</td>
<td>20%</td>
</tr>
<tr>
<td>aL I-domain</td>
<td>24%</td>
<td>33%</td>
<td>27%</td>
<td>37%</td>
</tr>
<tr>
<td>Ras</td>
<td>30%</td>
<td>45%</td>
<td>29%</td>
<td>55%</td>
</tr>
</tbody>
</table>

Many amino acids change between states

Novel targets for manipulating allostery
Lessons Learned and Next Steps

Lessons Learned

Query and parse information from PDB
How to perform structural alignments
How to compute statistics on structures

Next Steps

Non-allosteric proteins
Effects of mutations
Visualize structural differences in PyMol