Automated phase improvement and model building

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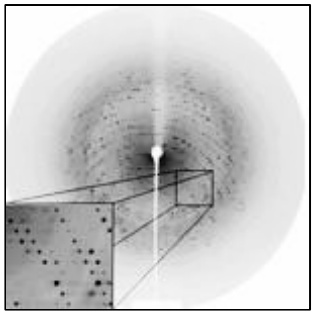
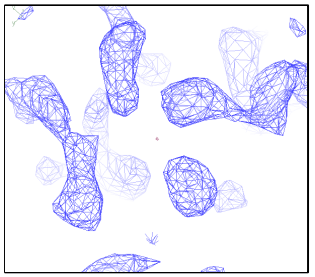
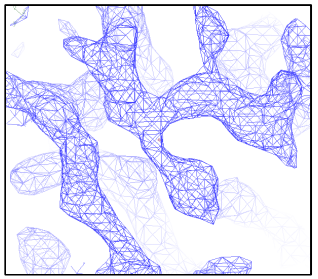
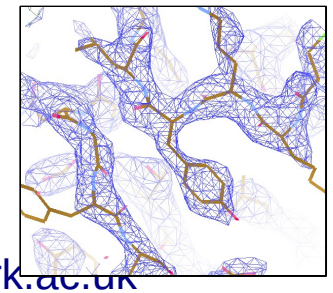
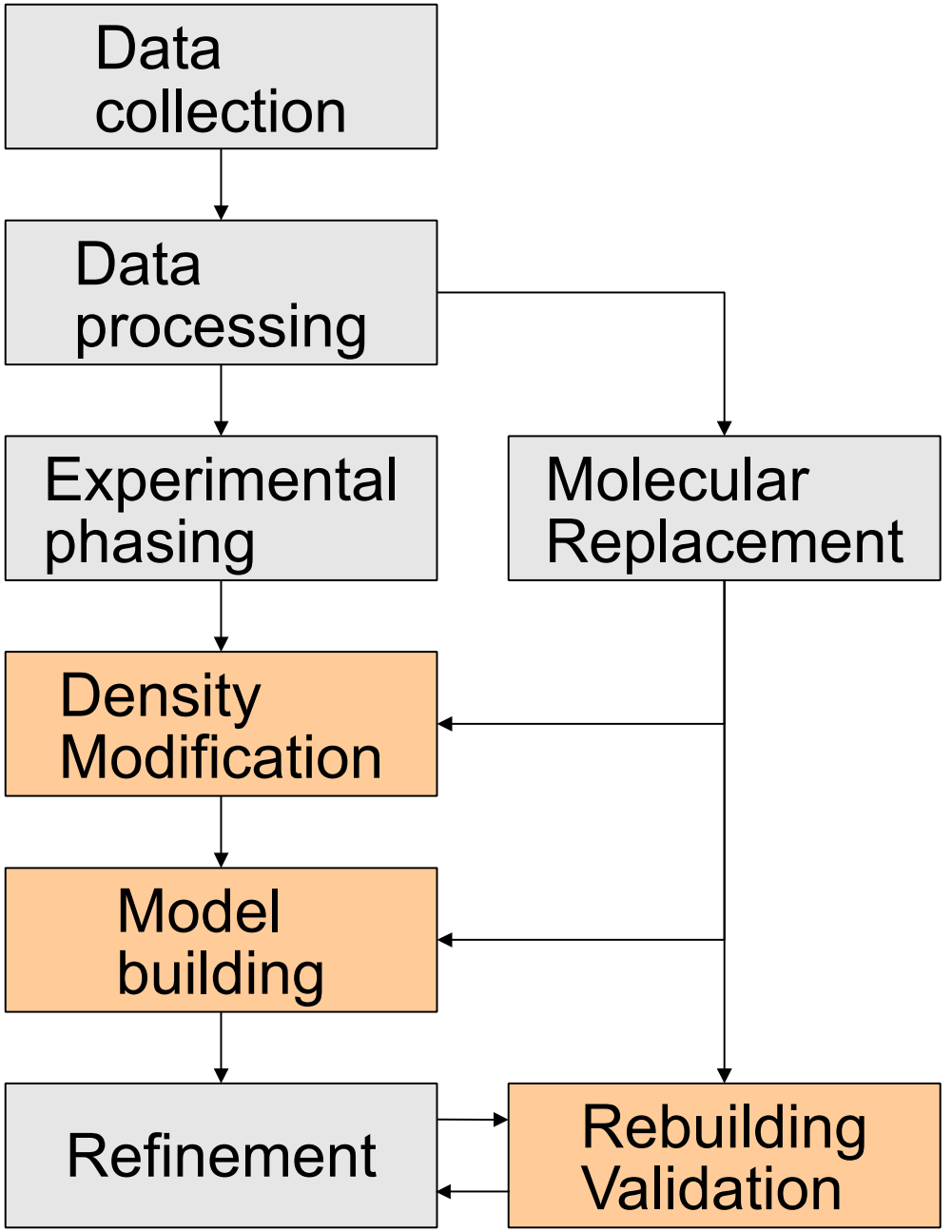
X-ray structure solution pipeline...











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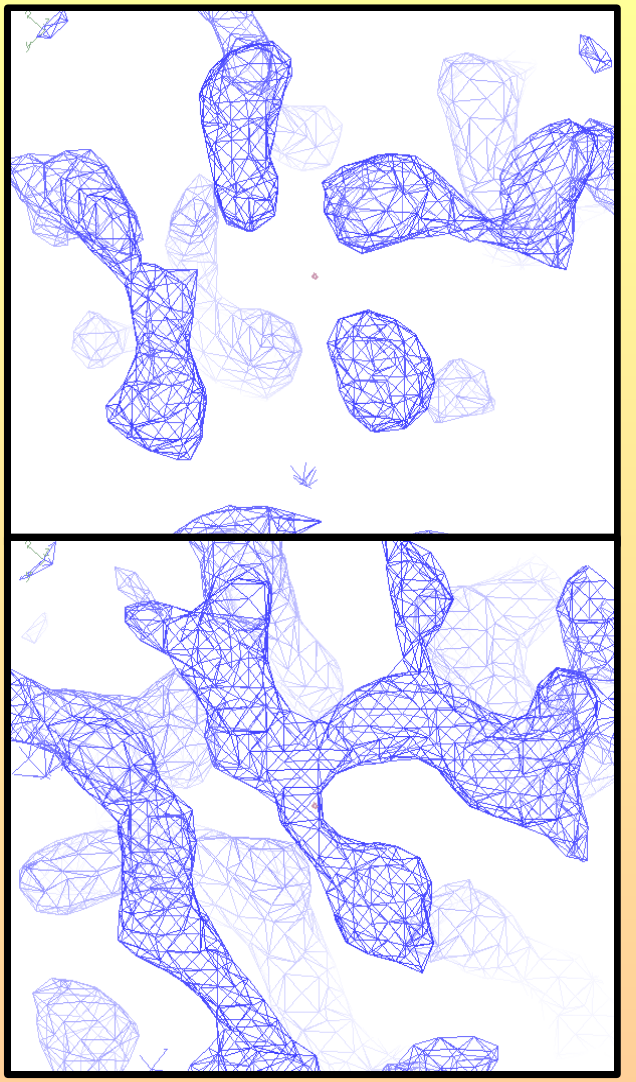
Density Modification

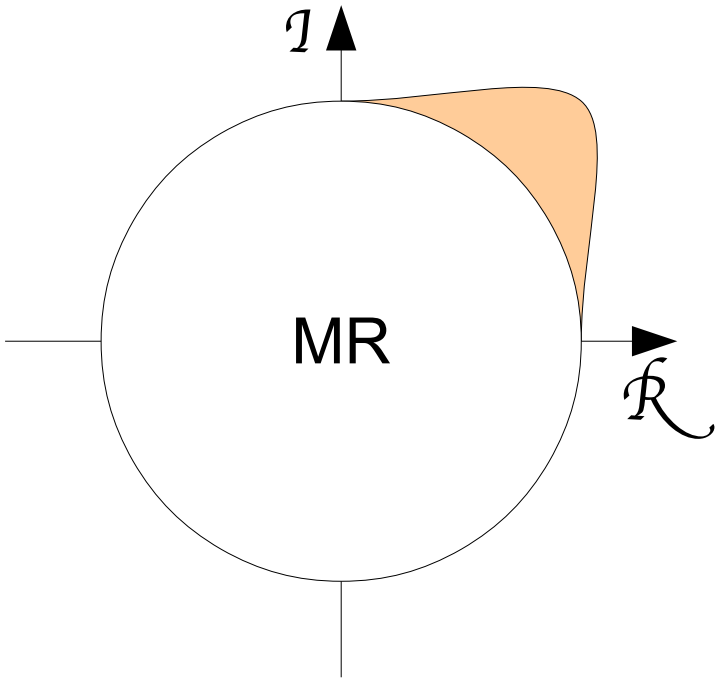
- Traditional density modification: e.g. 'dm', 'solomon', 'parrot', CNS
- Statistical density modification: e.g. 'resolve', 'pirate'

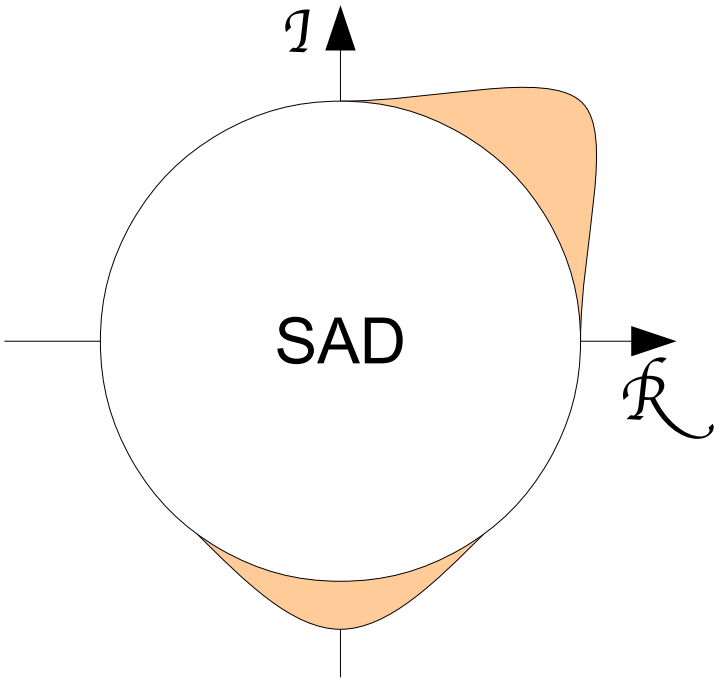


Density modification

Starting point:

- Structure factor amplitudes
- Phase estimates:
  - MR: Unimodel distribution
  - SAD: Biomodal distribution

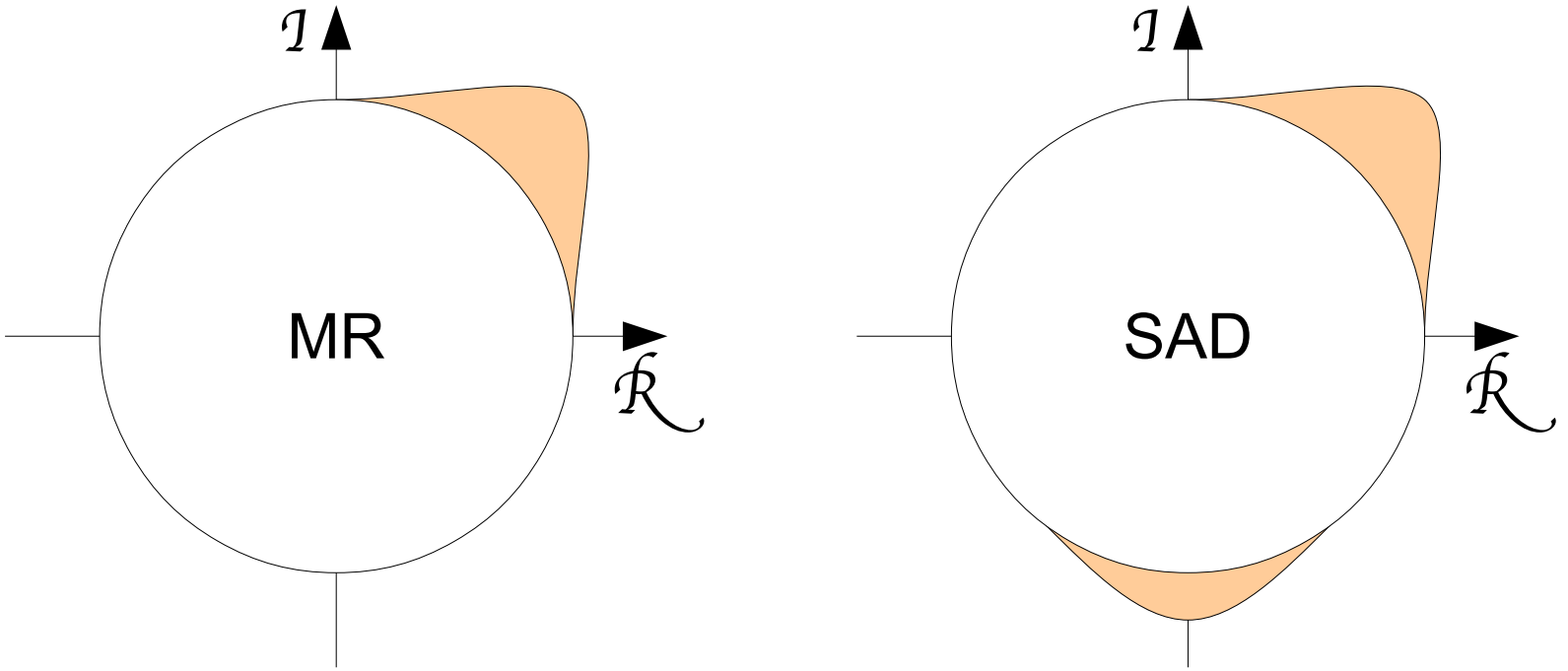




Density modification

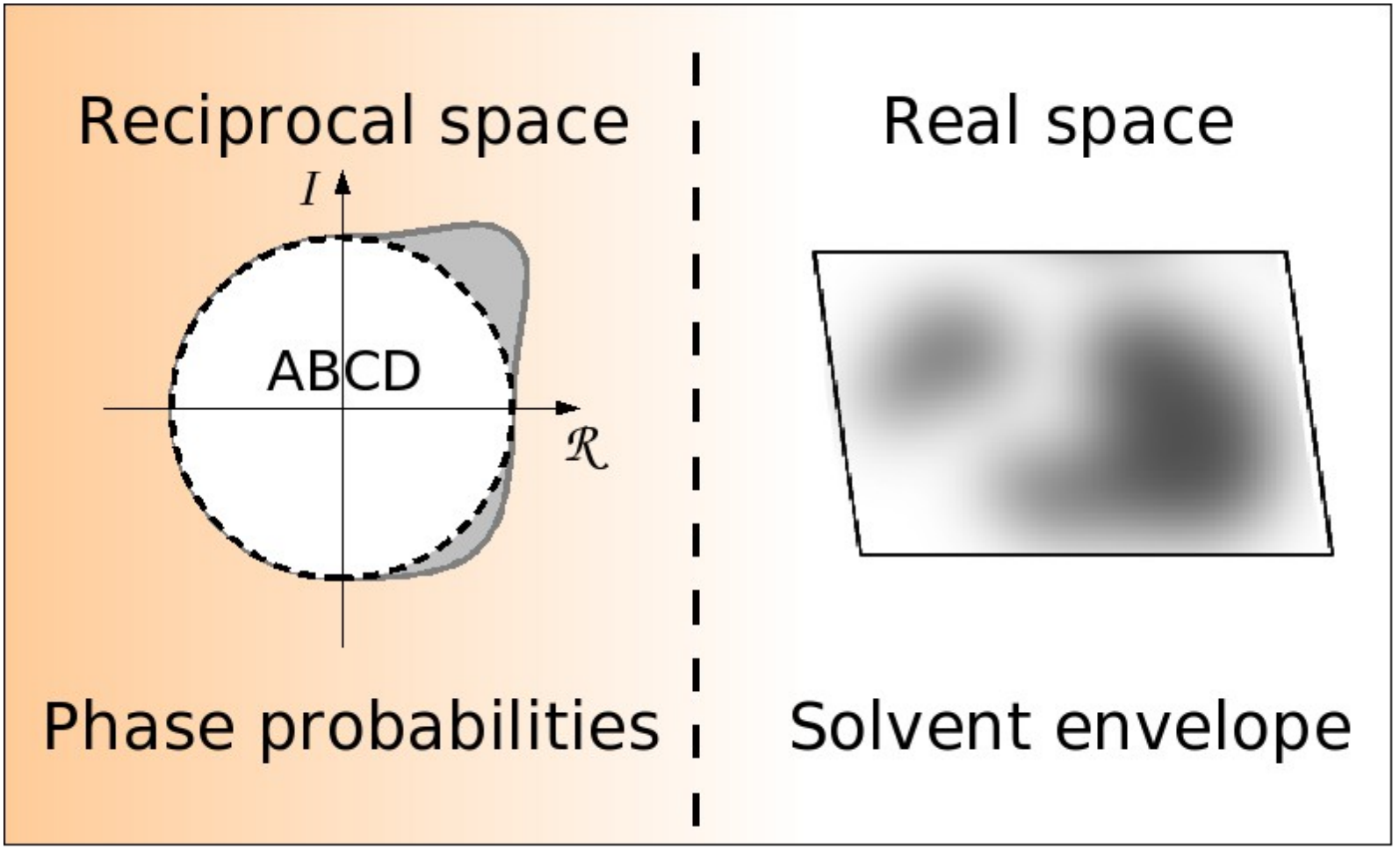
How do we represent phase probability distributions?

- Phase/figure of merit - Φ, FOM
  - (unimodel, MR only)
- Henrickson-Lattman coeffs – ABCD
  - (bimodal or unimodal, general)



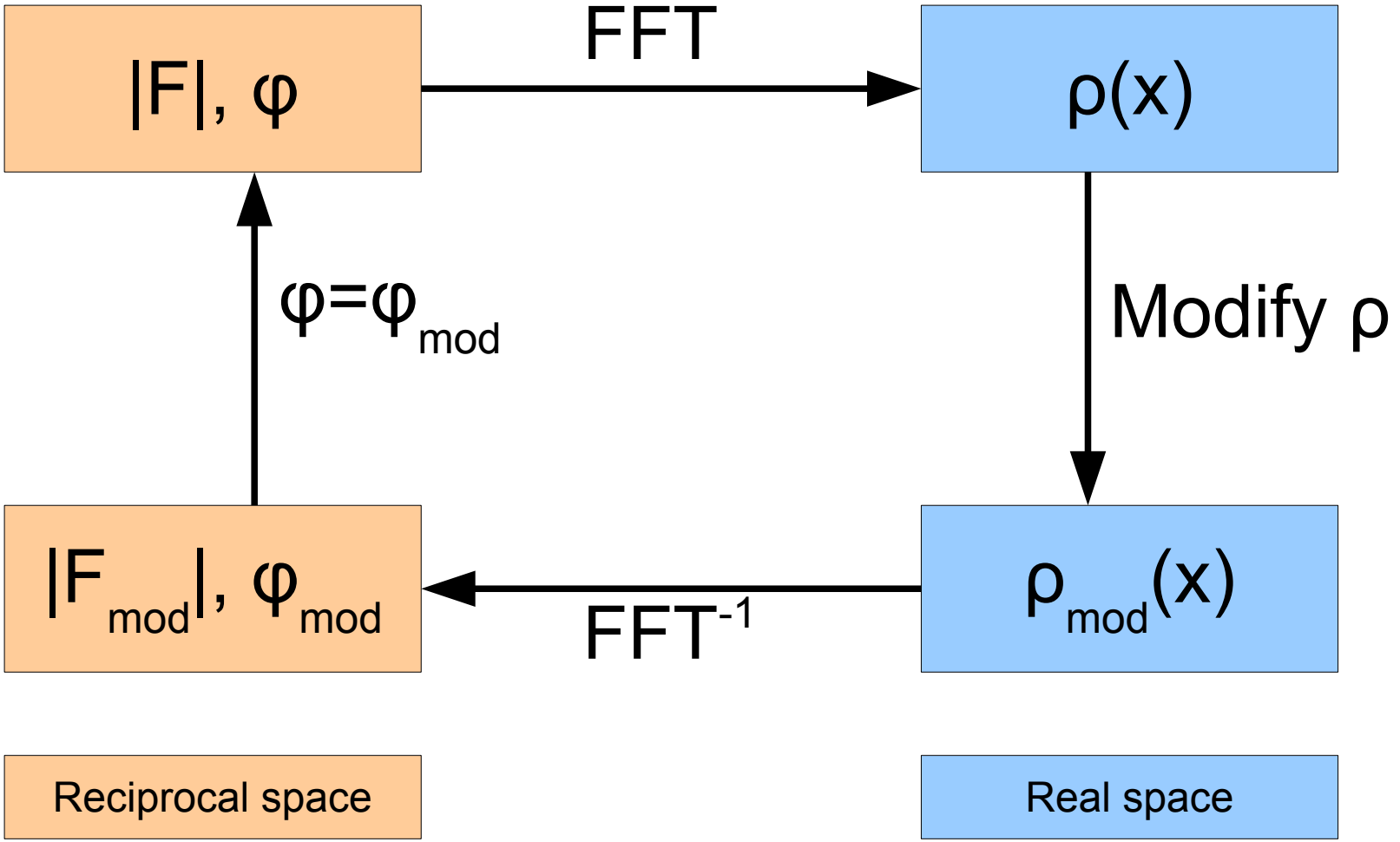
Density modification

- Density modification is a problem in combining information:



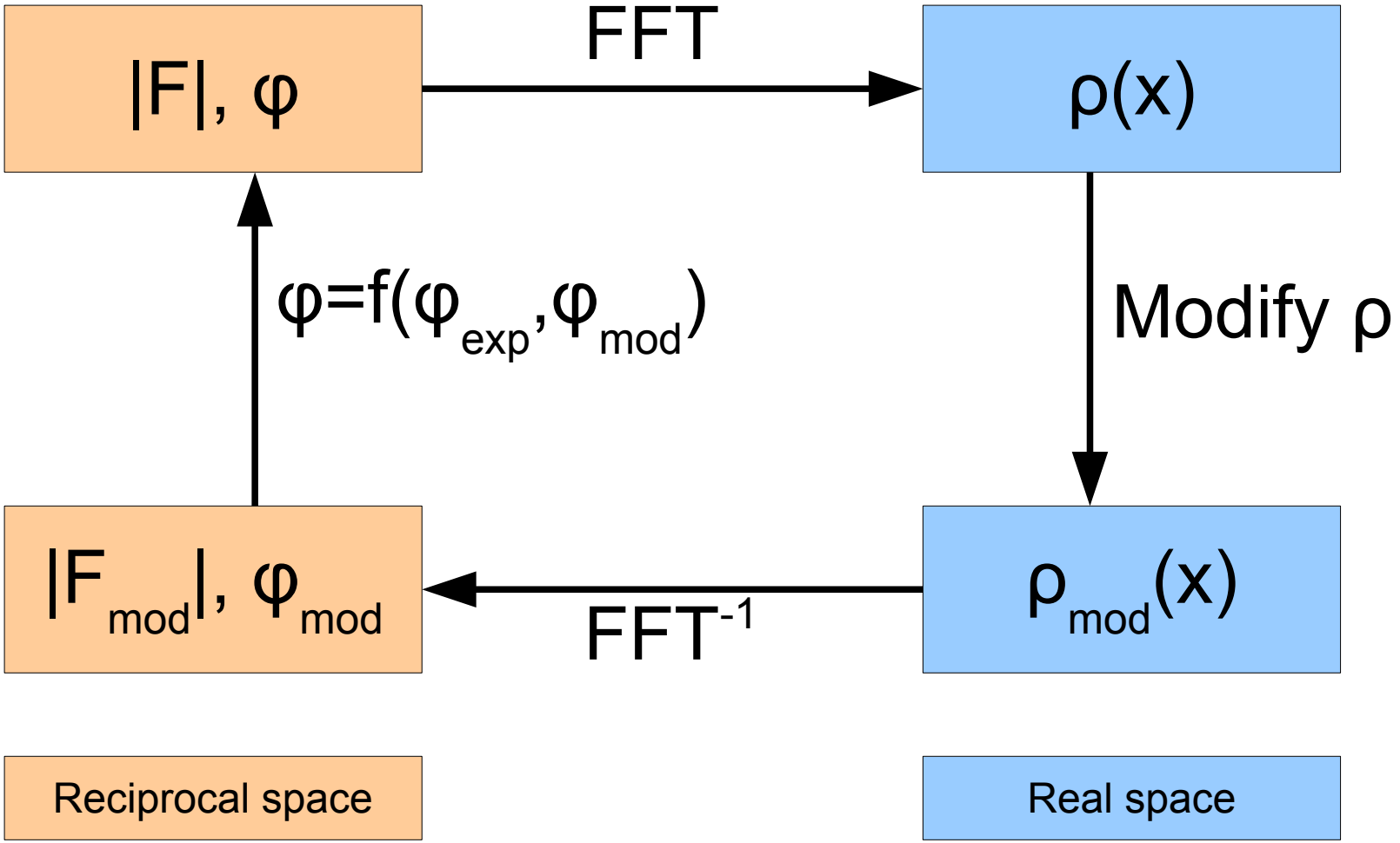
Density modification

1. Rudimentary calculation:



Density modification

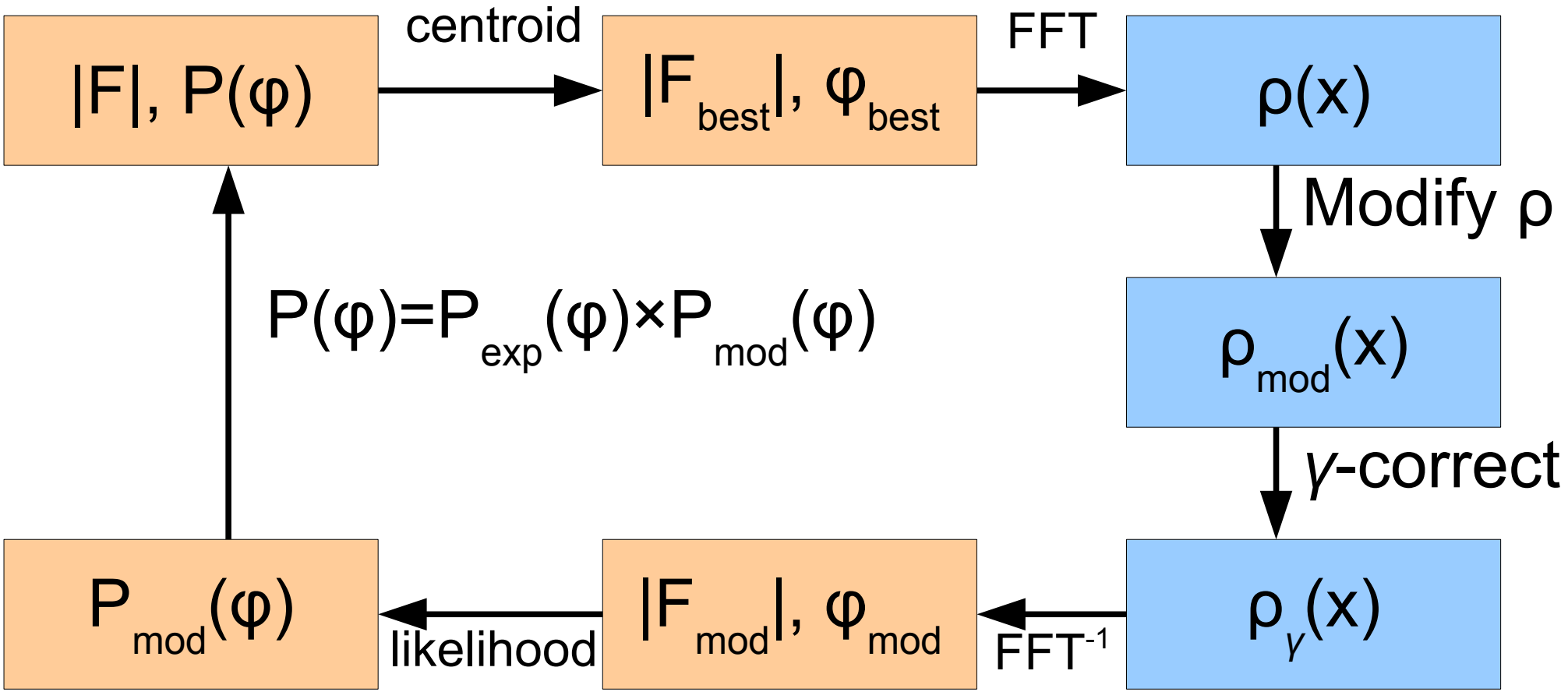
2. Phase weighting:



Density modification

DM, SOLOMON, (CNS)

4. Bias reduction (gamma-correction):

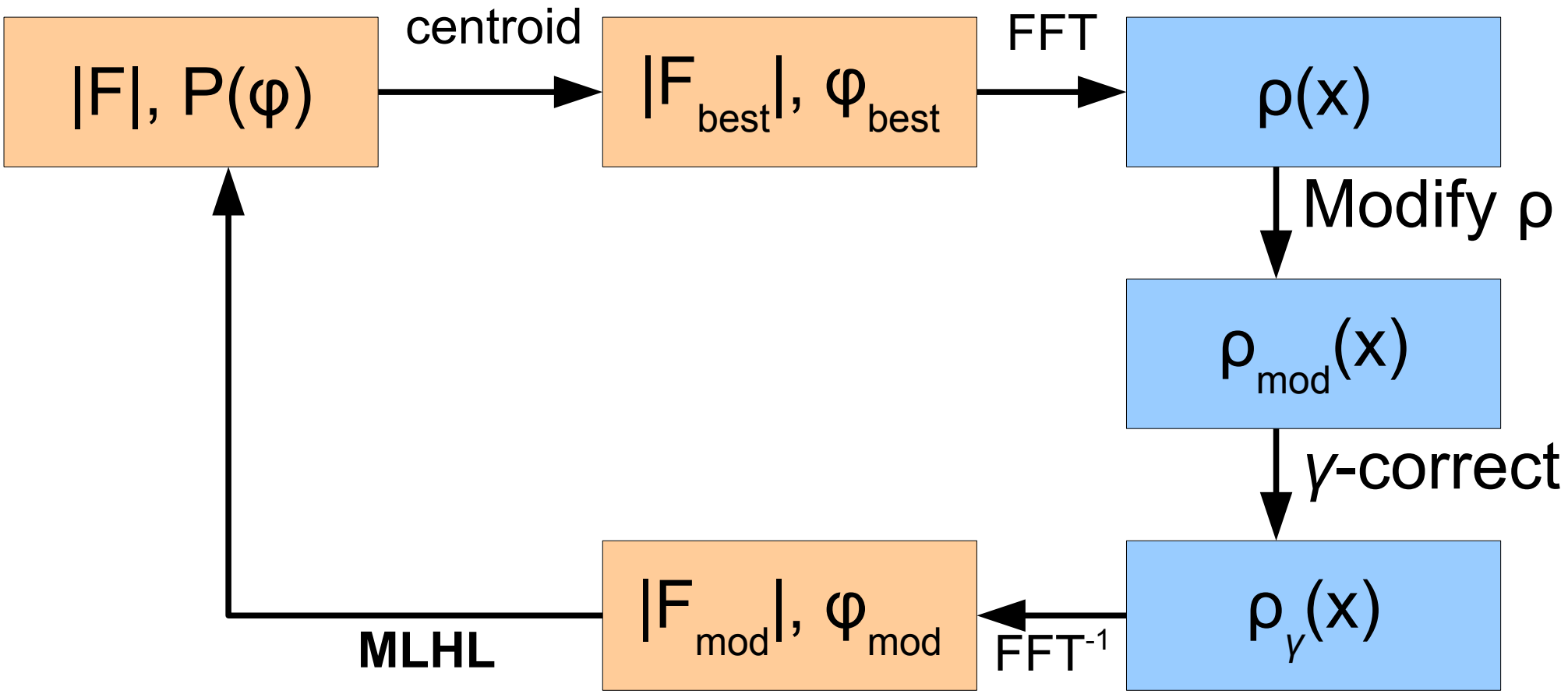


J.P.Abrahams

Density modification

PARROT

5. Maximum Likelihood H-L:



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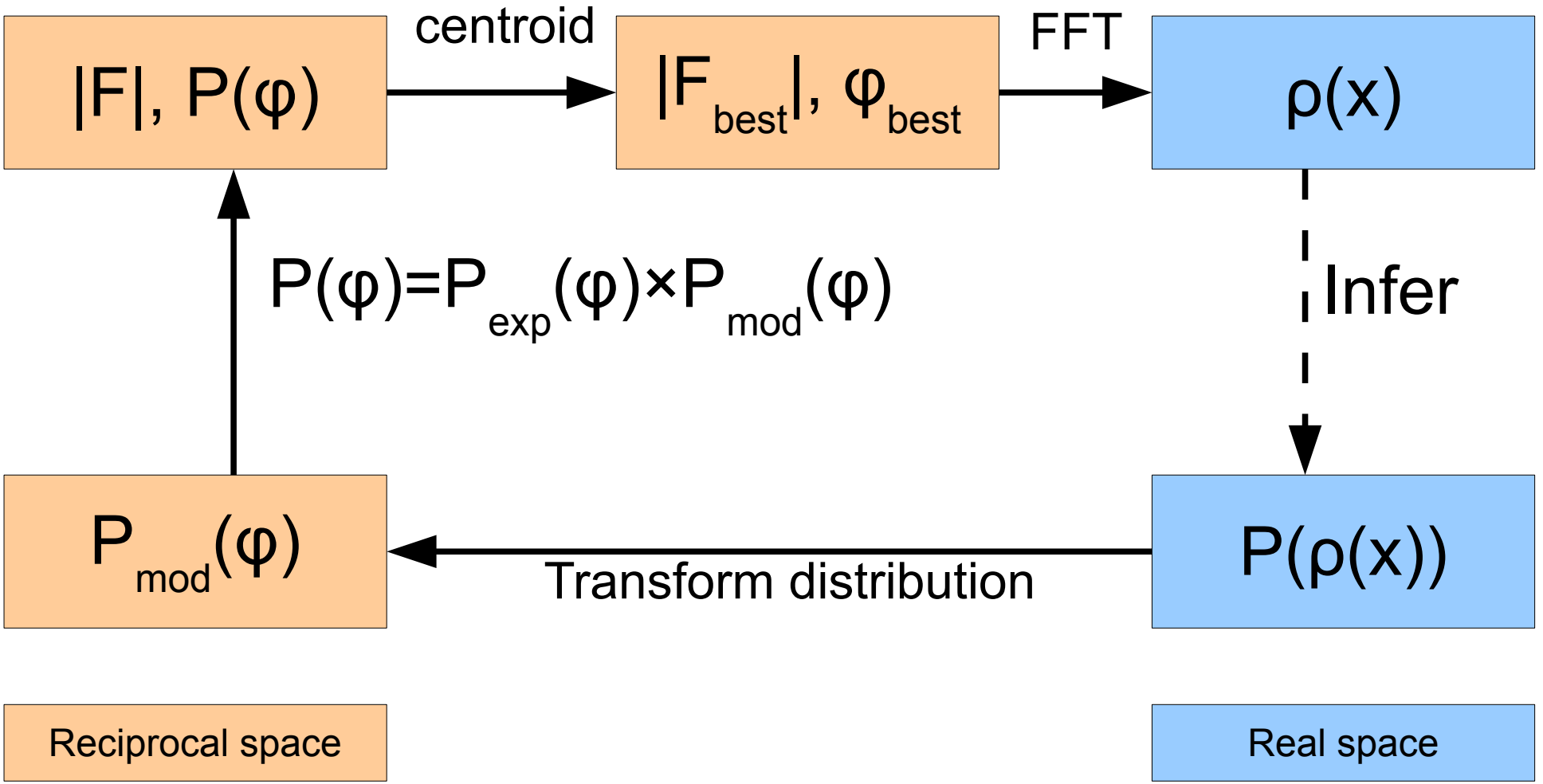
Density modification

RESOLVE, PIRATE

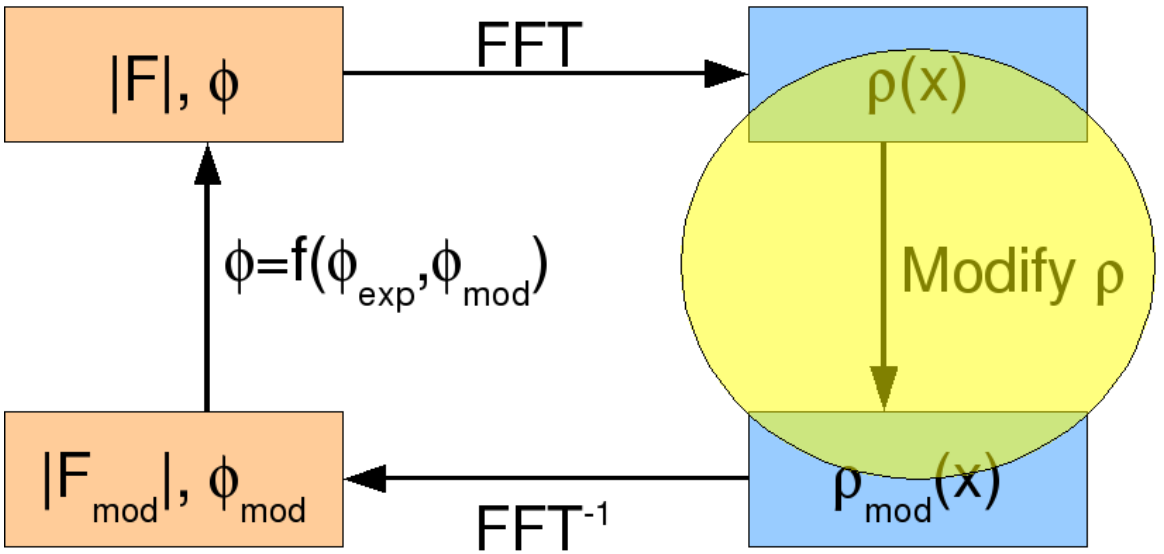
6. Statistical density modification:



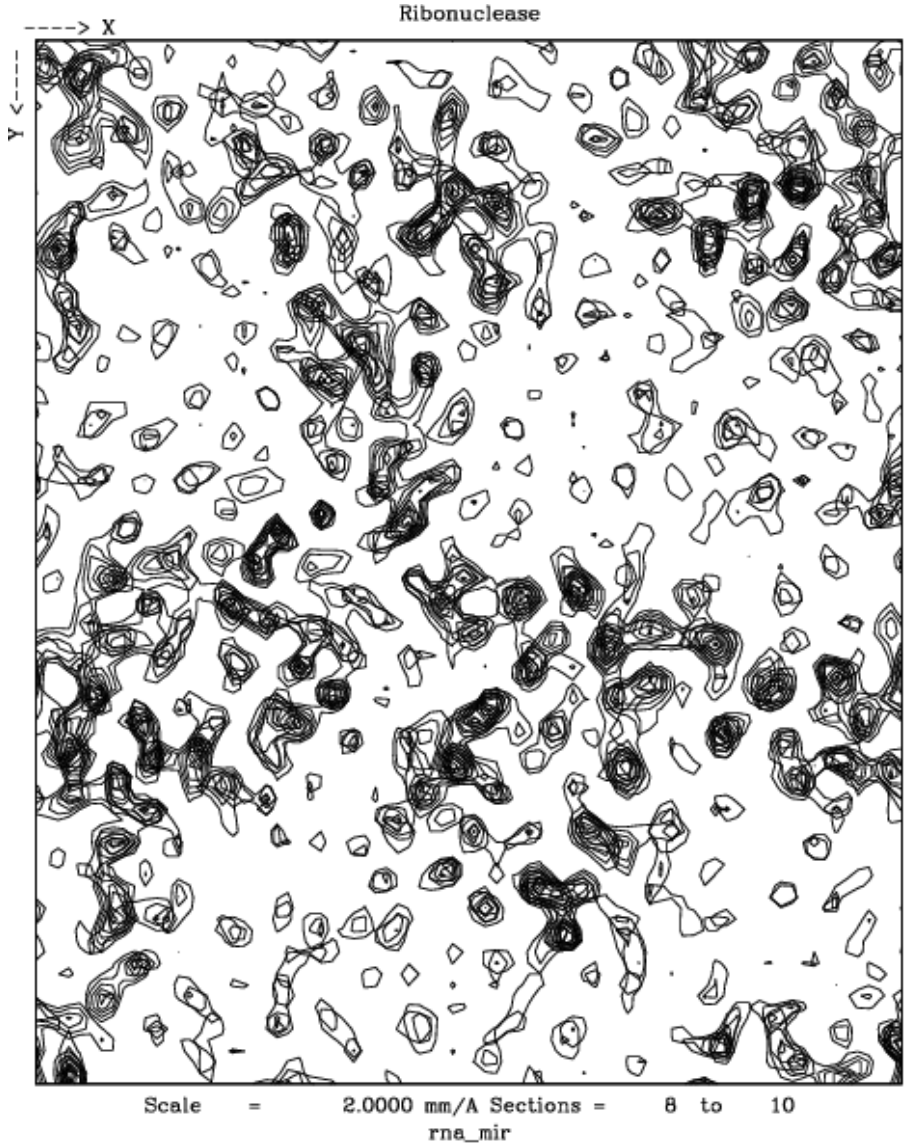
Density modification

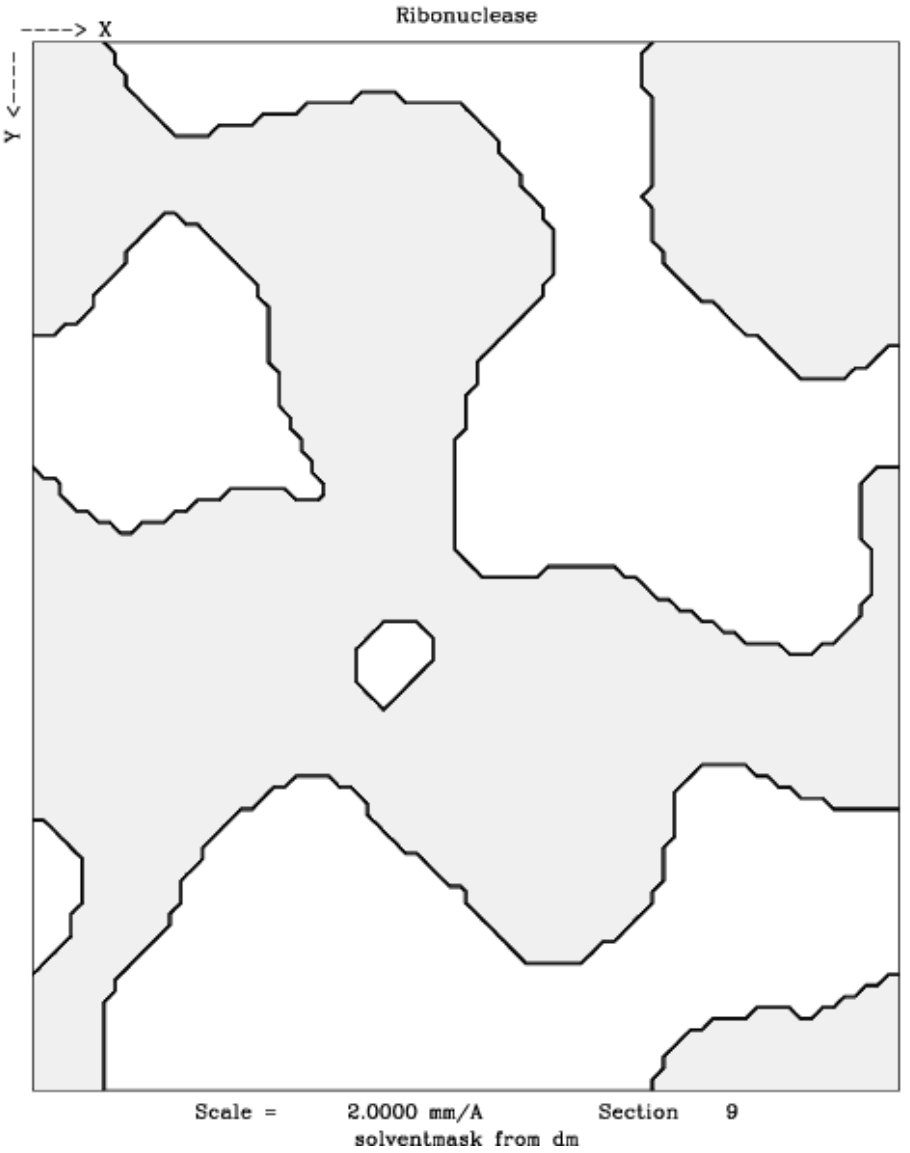
Traditional density modification techniques:

- Solvent flattening
- Histogram matching
- Non-crystallographic symmetry (NCS) averaging



Solvent flattening





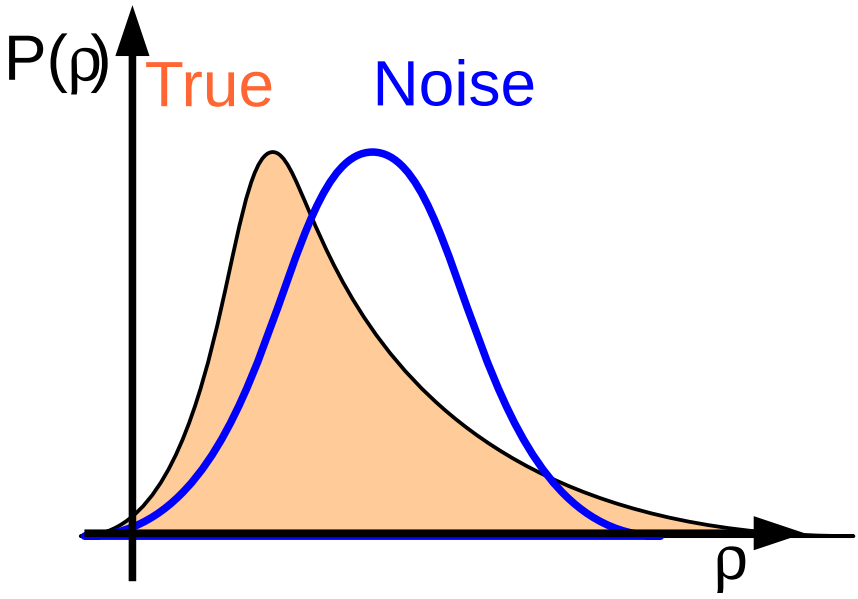
Histogram matching

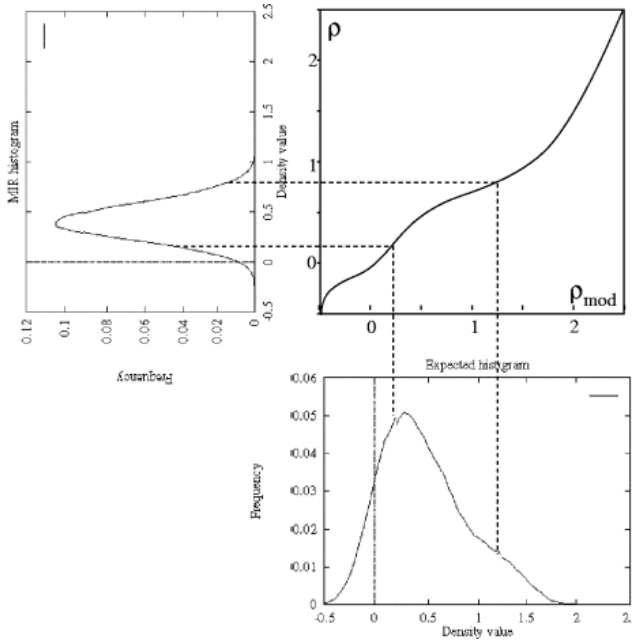
A technique from image processing for modifying the protein region.

- Noise maps have Gaussian histogram.
- Well phased maps have a skewed distribution: sharper peaks and bigger gaps.

Sharpen the protein density by a transform which matches the histogram of a well phased map.

Useful at better than 4A.





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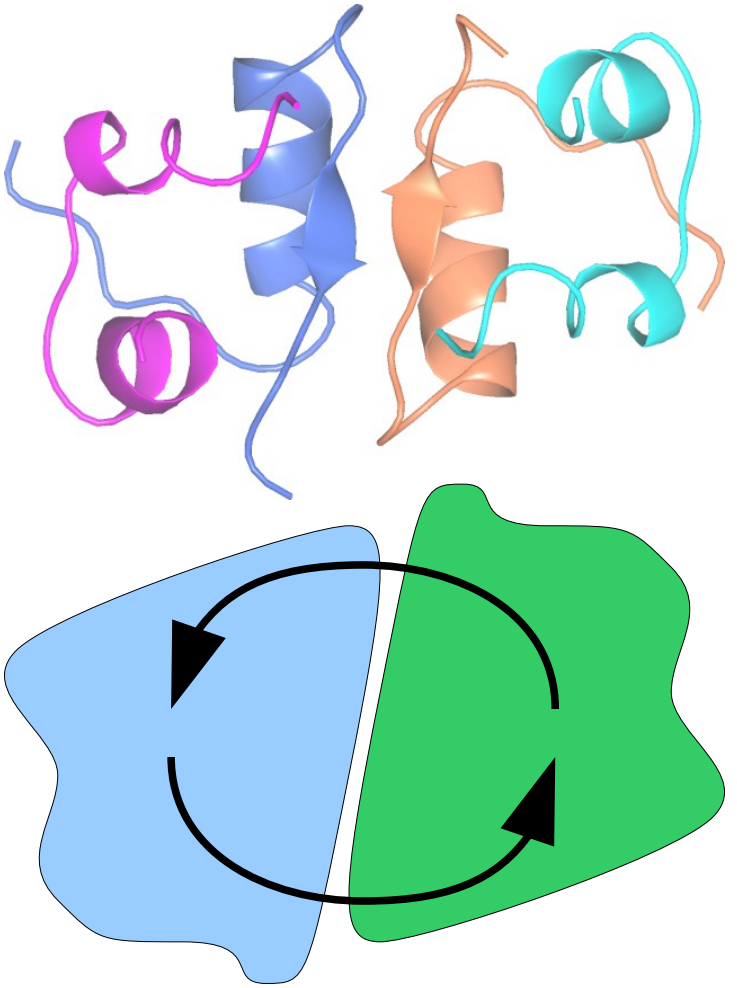
2012

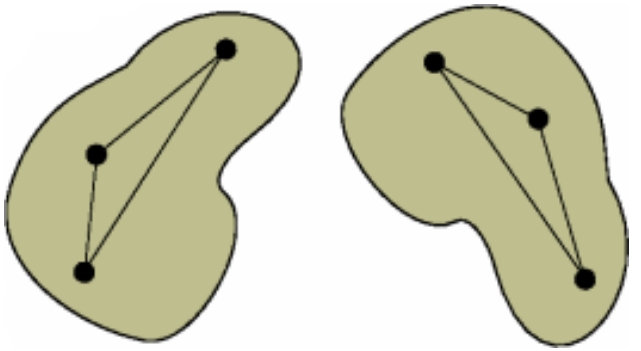
Non-crystallographic symmetry

- If the molecule has internal symmetry, we can average together related regions.
- In the averaged map, the signal-noise level is improved.
- If a full density modification calculation is performed, powerful phase relationships are formed.
- With 4-fold NCS, can phase from random!



Non-crystallographic symmetry

- How do you know if you have NCS?
  - Cell content analysis – how many monomers in ASU?
  - Self-rotation function.
  - Difference Pattersons (pseudo-translation only).
- How do you determine the NCS?
  - **From heavy atoms.**
  - From initial model building.
  - From molecular replacement.
  - *From density MR (hard).*
- Mask determined automatically.



Combining phase probabilities

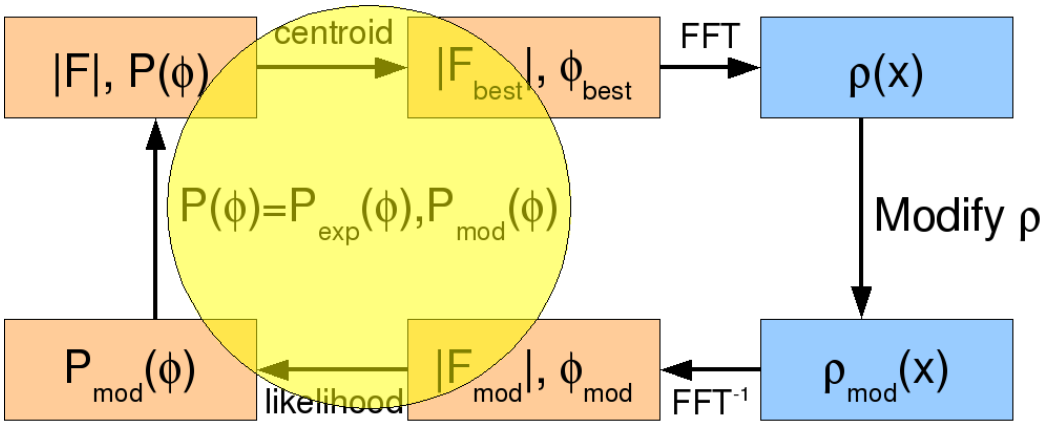
Once we have an estimate for the error in ϕ_{mod}, we can construct a probability distribution $P_{mod}(\phi)$.

The the next cycle can be started with

$$P_{new}(\phi) = P_{exp}(\phi)P_{mod}(\phi)$$

Problem: $P_{exp}(\phi)$ and $P_{mod}(\phi)$ are not independent.

The result is bias, increasing with cycle.



Density modification in Parrot

Builds on existing ideas:

- DM:
  - Solvent flattening
  - Histogram matching
  - NCS averaging
  - Perturbation gamma
- Solomon:
  - Gamma correction
  - Local variance solvent mask
  - Weighted averaging mask

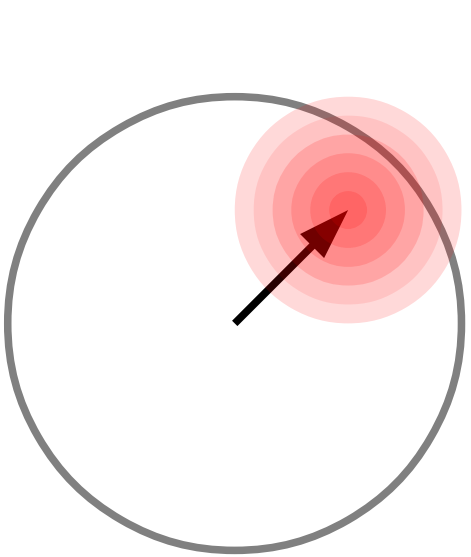
Density modification in Parrot

New developments:

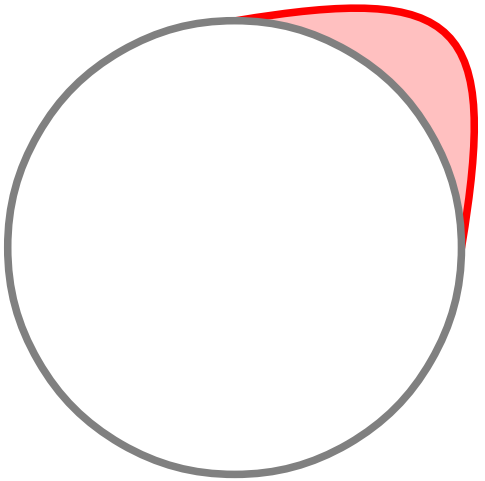
- MLHL phase combination
  (as used in refinement: *refmac, phenix.refine*)
- Anisotropy correction
- Problem-specific density histograms
  (rather than a standard library)
- Pairwise-weighted NCS averaging...

Estimating phase probabilities

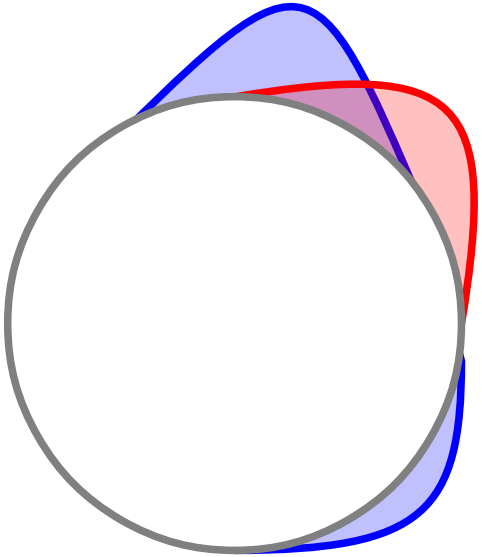
Traditional approach: Rice likelihood function



Estimate the accuracy of the modified F/phase



Turn this into a phase probability distribution

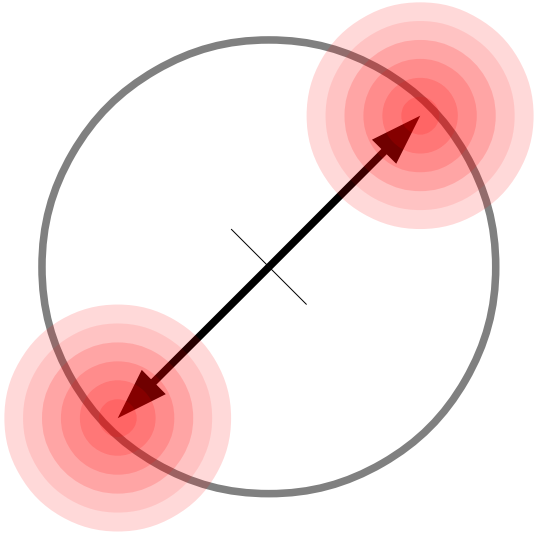


Combine with the experimental phase probability

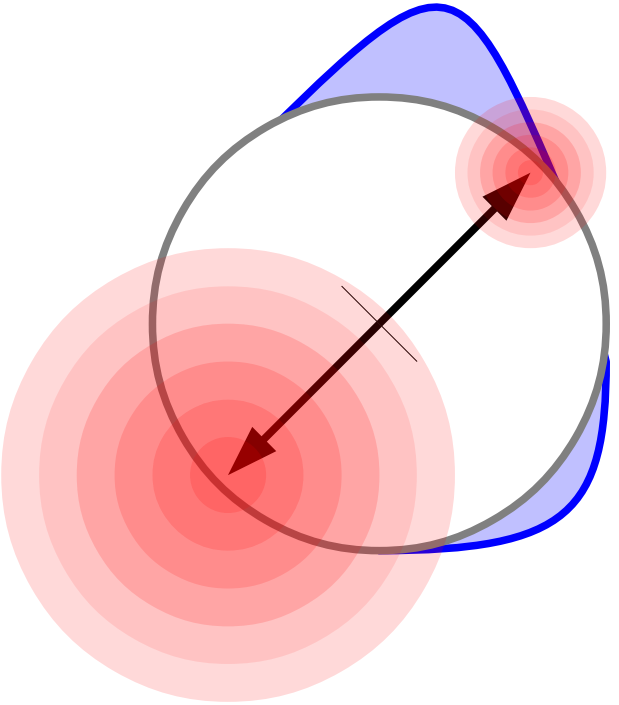
The estimate for the accuracy of the modified F/phase come from the agreement between the modified F and the observed F. **Source of bias.**

Estimating phase probabilities

Problem:



Error estimation does not take into account experimental phase information

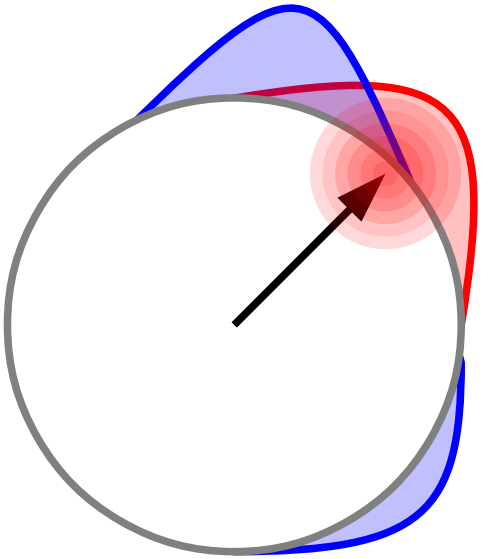


The experimental data tells us that the probable error is different in the two cases

Using the additional information from the phases improves the error model and reduces bias.

Estimating phase probabilities

Solution:
MLHL-type likelihood target function.

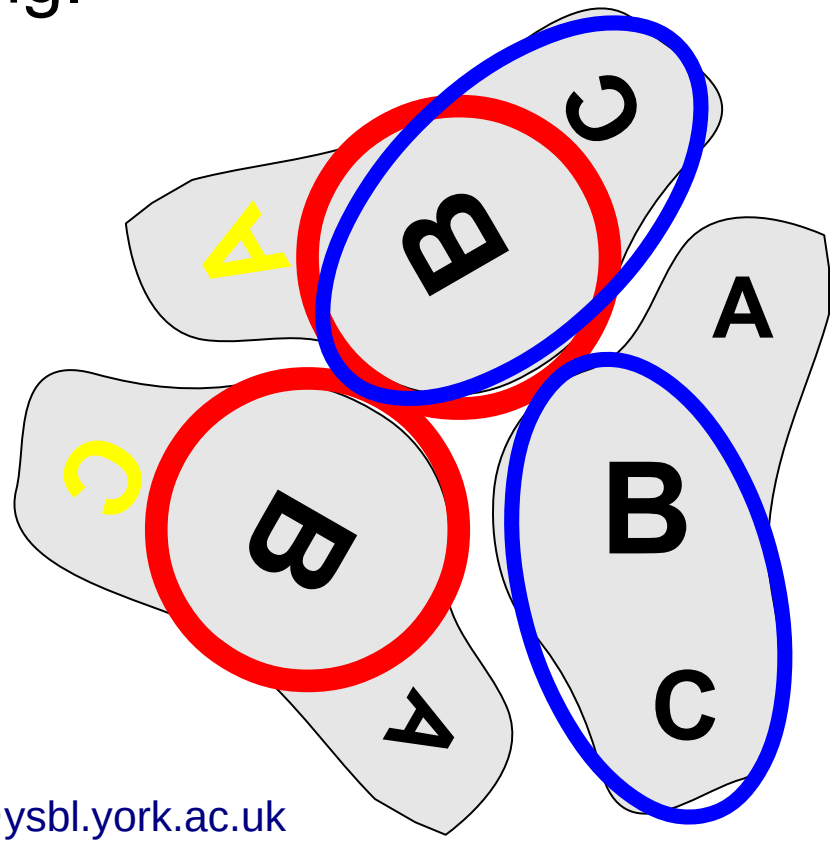


Perform the error estimation and phase combination in a single step, using a likelihood function which incorporates the experimental phase information as a prior.
This is the same MLHL-type like likelihood refinement target used in modern refinement software such as *refmac* or *phenix.refine*.

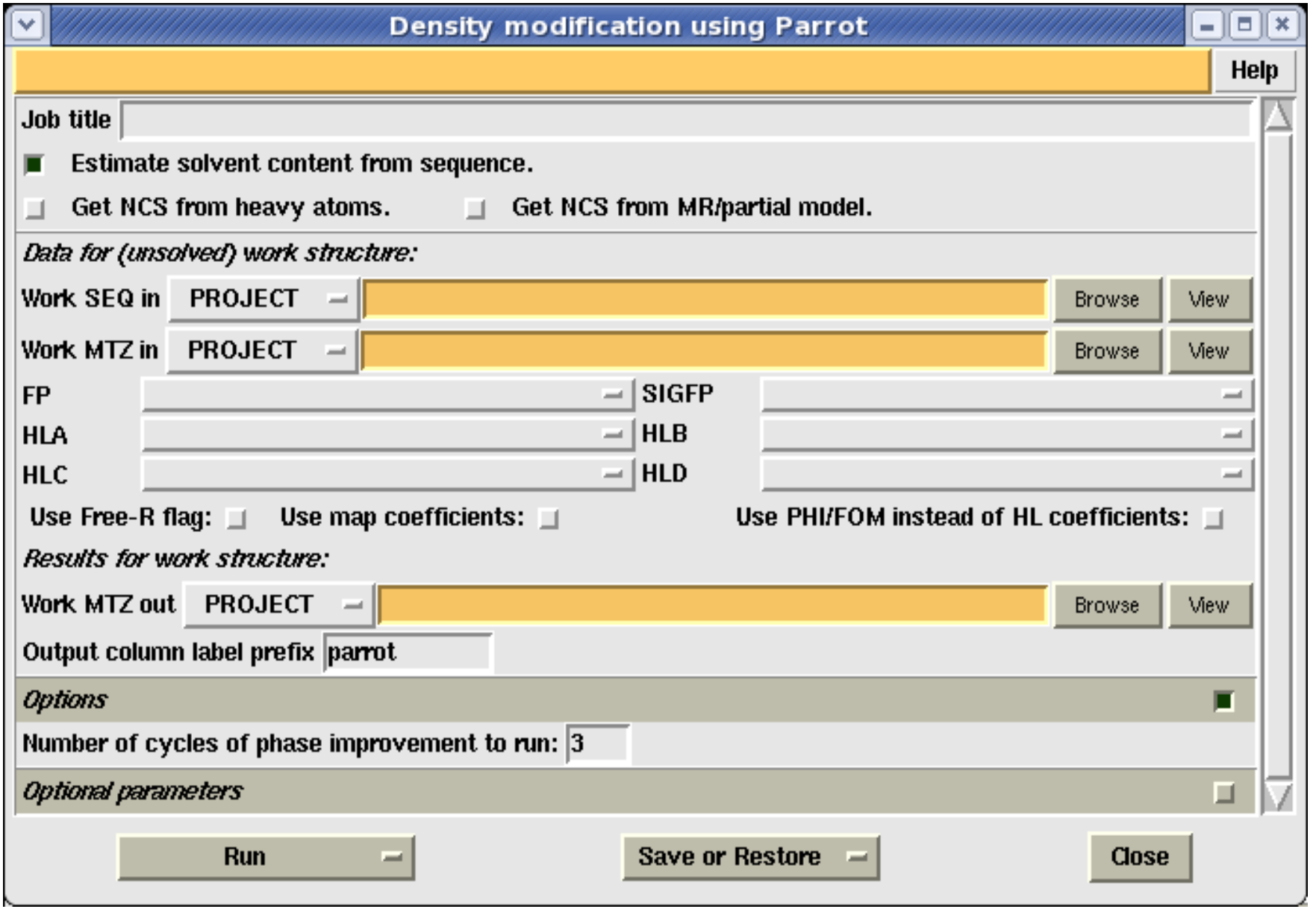
Recent Developments:

Pairwise-weighted NCS averaging:

- Average each pair of NCS related molecules separately with its own mask.
- Generalisation and automation of multi-domain averaging.



Parrot



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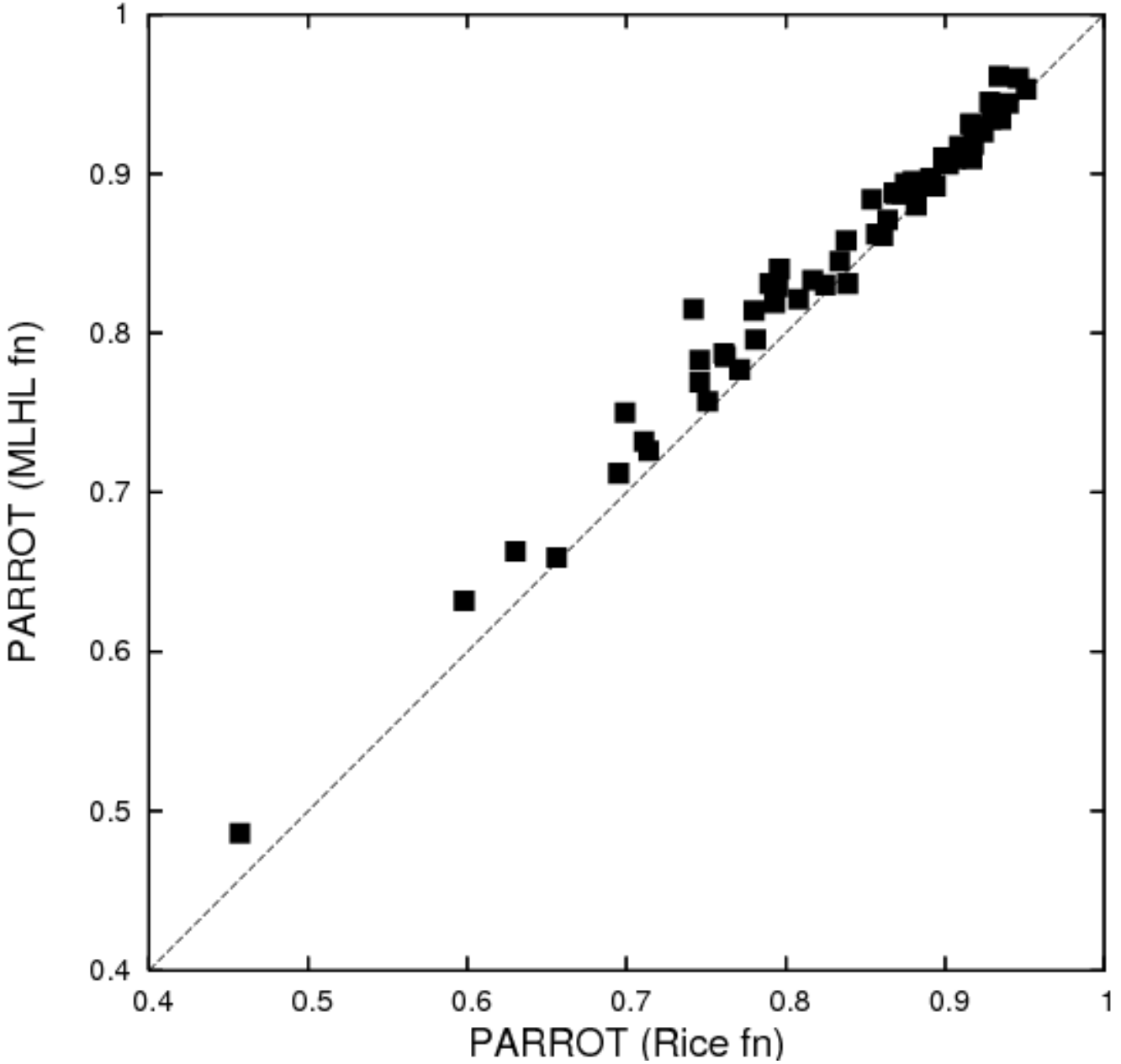
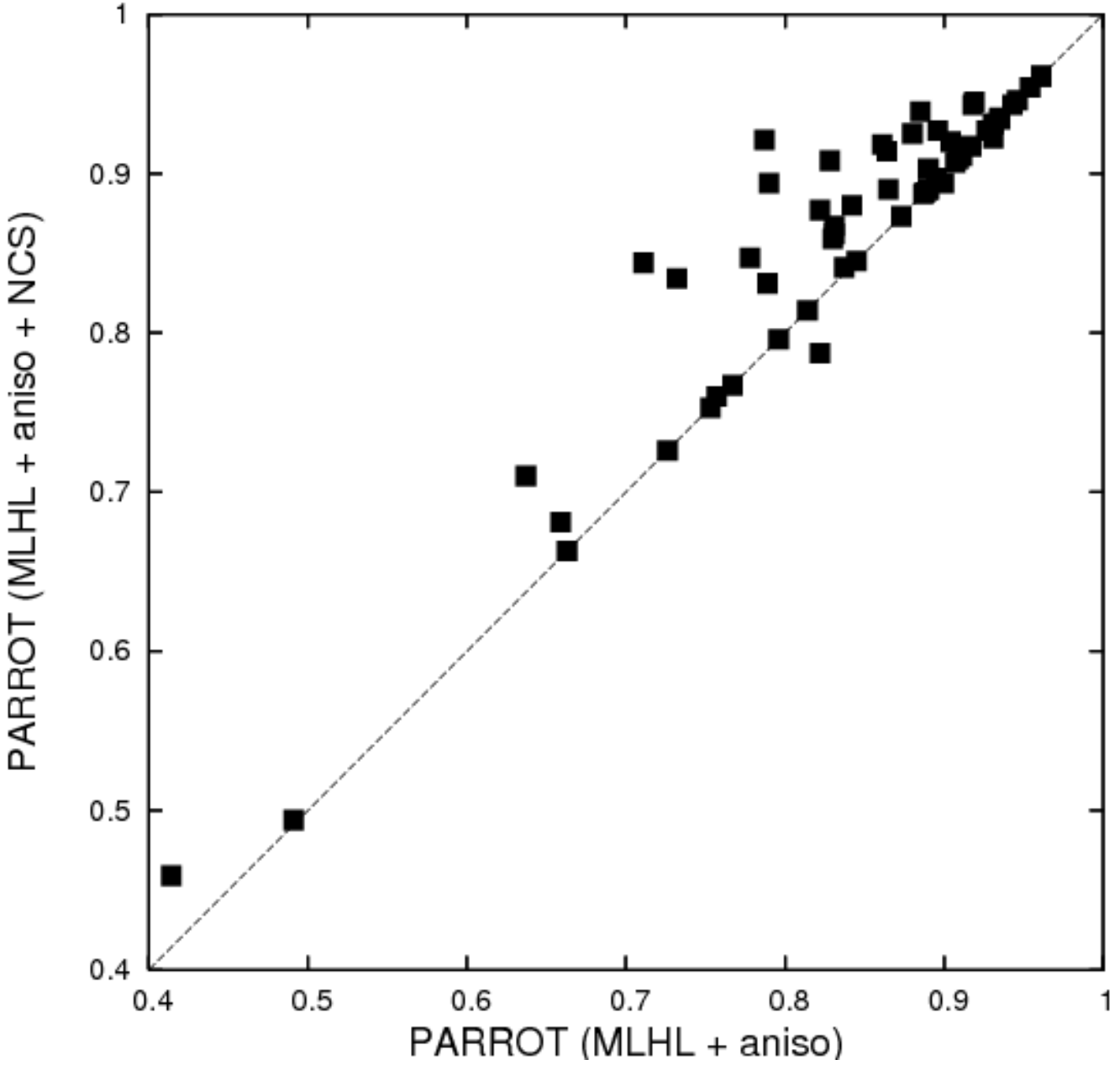
Parrot: Rice vs MLHL



Map correlations

Comparing old and new likelihood functions.

Parrot: simple vs NCS averaged



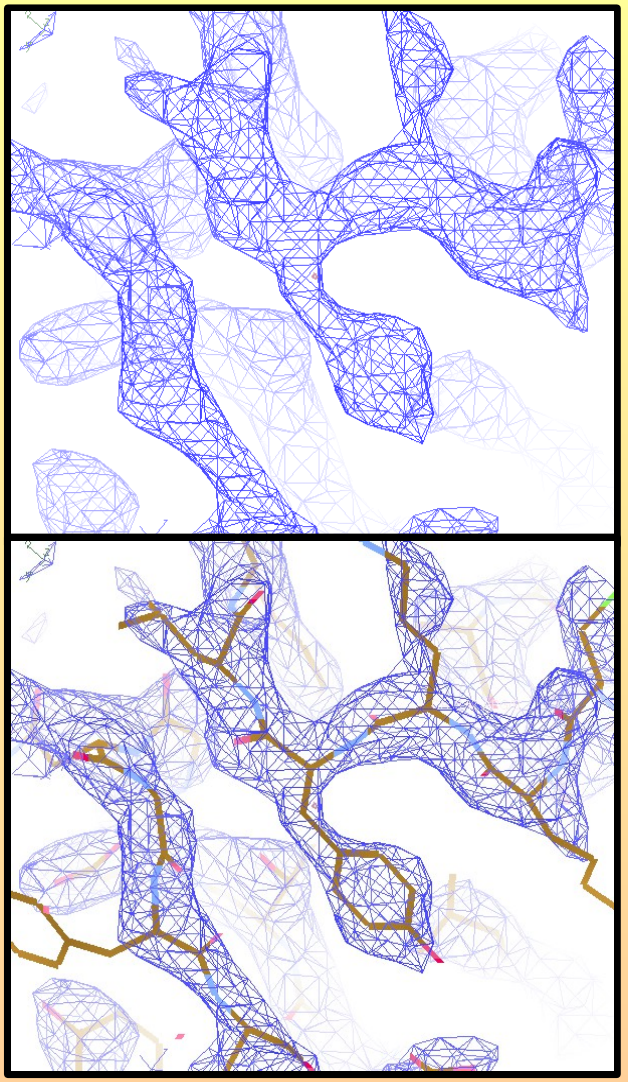
Map correlations

Comparing with and without NCS averaging.

Model Building

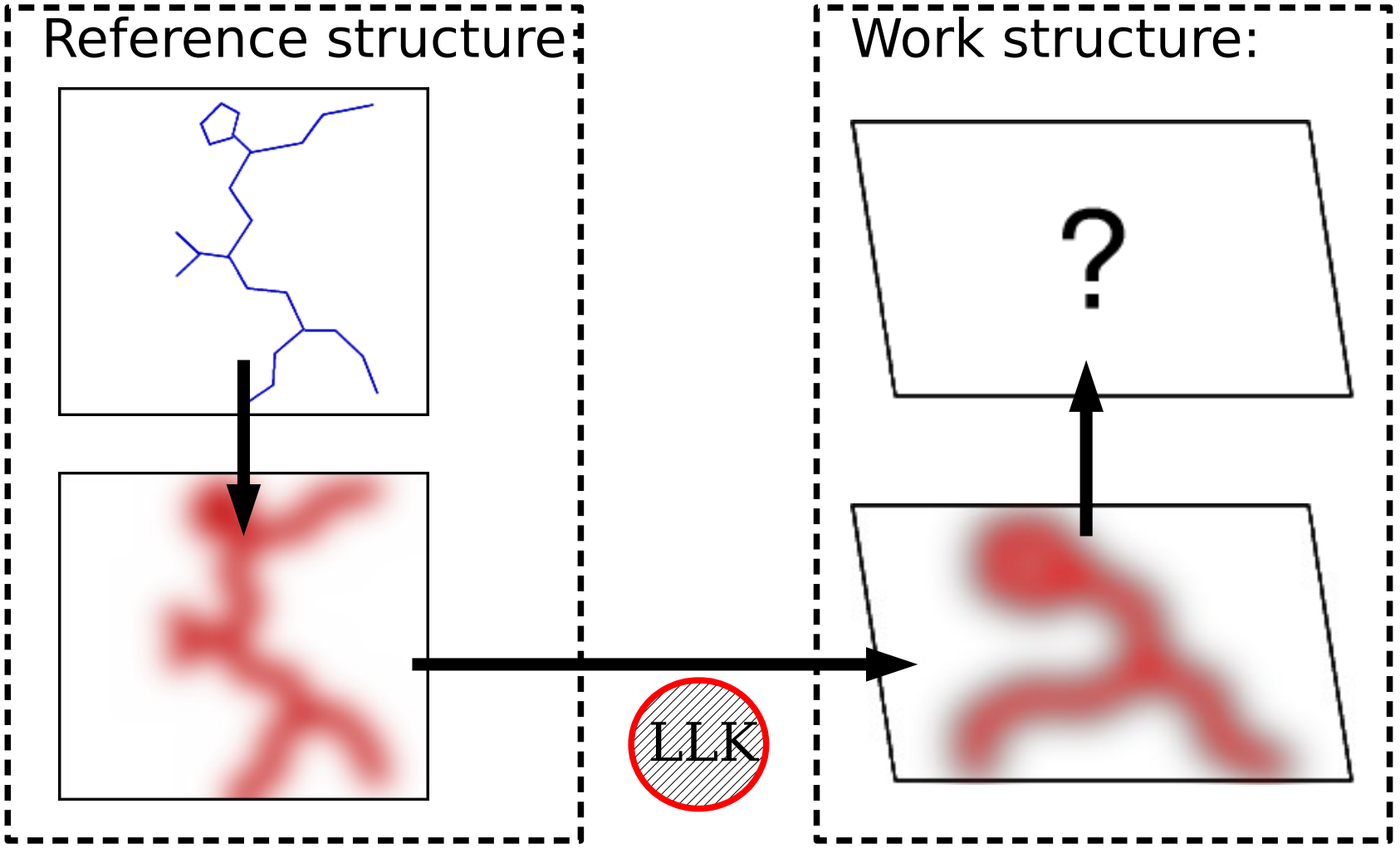
Model building software:

- Proteins:
  - Buccaneer
  - ARP/wARP
  - Phenix autobuild
- Nucleic acids:
  - Nautilus/Coot
  - ARP/wARP
  - Phenix autobuild



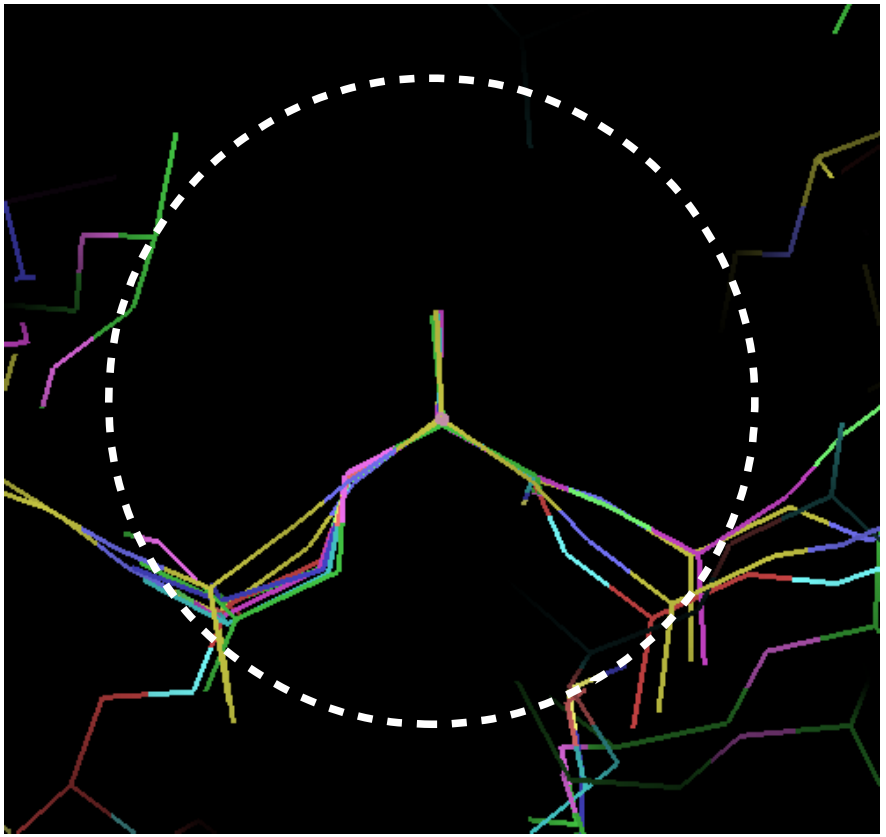
Buccaneer: Method

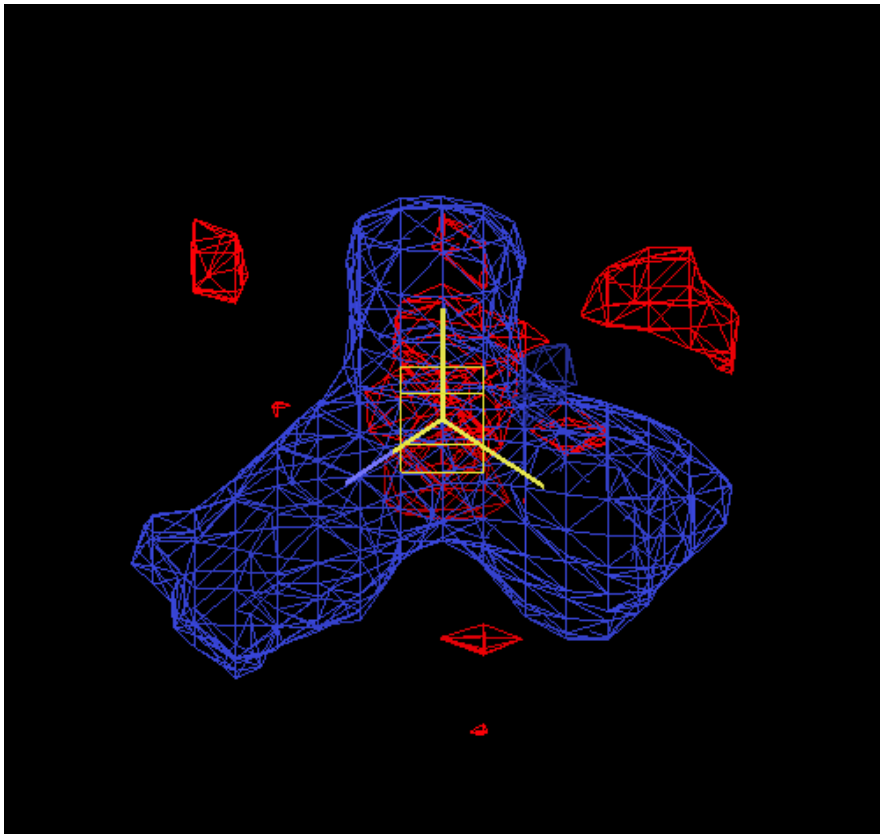
- Compare simulated map and known model to obtain likelihood target, then search for this target in the unknown map.



Buccaneer: Method

- Compile statistics for reference map in 4A sphere about Cα => LLK target.





- Use mean/variance.

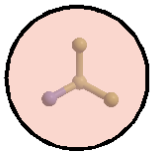
4A sphere about Ca also used by 'CAPRA' loeger et al. (but different target function).

Buccaneer

Use a likelihood function based on conserved density features.

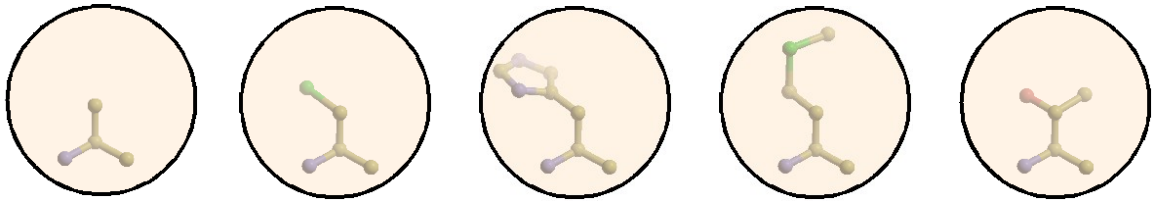
The same likelihood function is used several times. This makes the program very simple (<3000 lines), and the whole calculation works over a range of resolutions.

Finding, growing: Look for C-alpha environment



(4.0A sphere about Cα)

Sequencing: Look for C-beta environment



ALA CYS HIS MET THR ... x20

(5.5A sphere about Cβ)

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Buccaneer

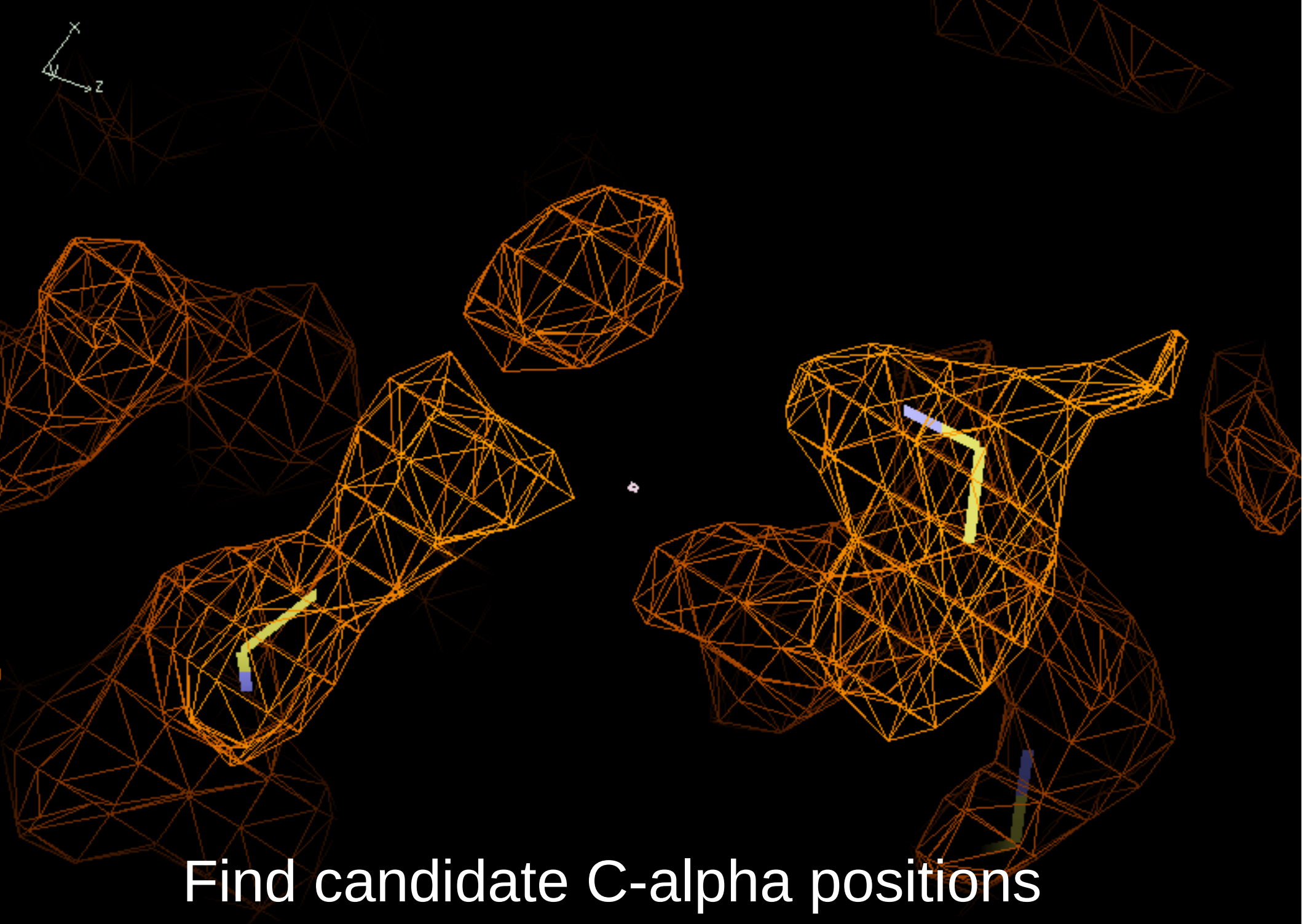
10 stages:

- **Find** candidate C-alpha positions
- **Grow** them into chain fragments
- **Join** and merge the fragments, resolving branches
- **Link** nearby N and C terminii (if possible)
- **Sequence** the chains (i.e. dock sequence)
- **Correct** insertions/deletions
- **Filter** based on poor density
- **NCS Rebuild** to complete NCS copies of chains
- **Prune** any remaining clashing chains
- **Rebuild** side chains

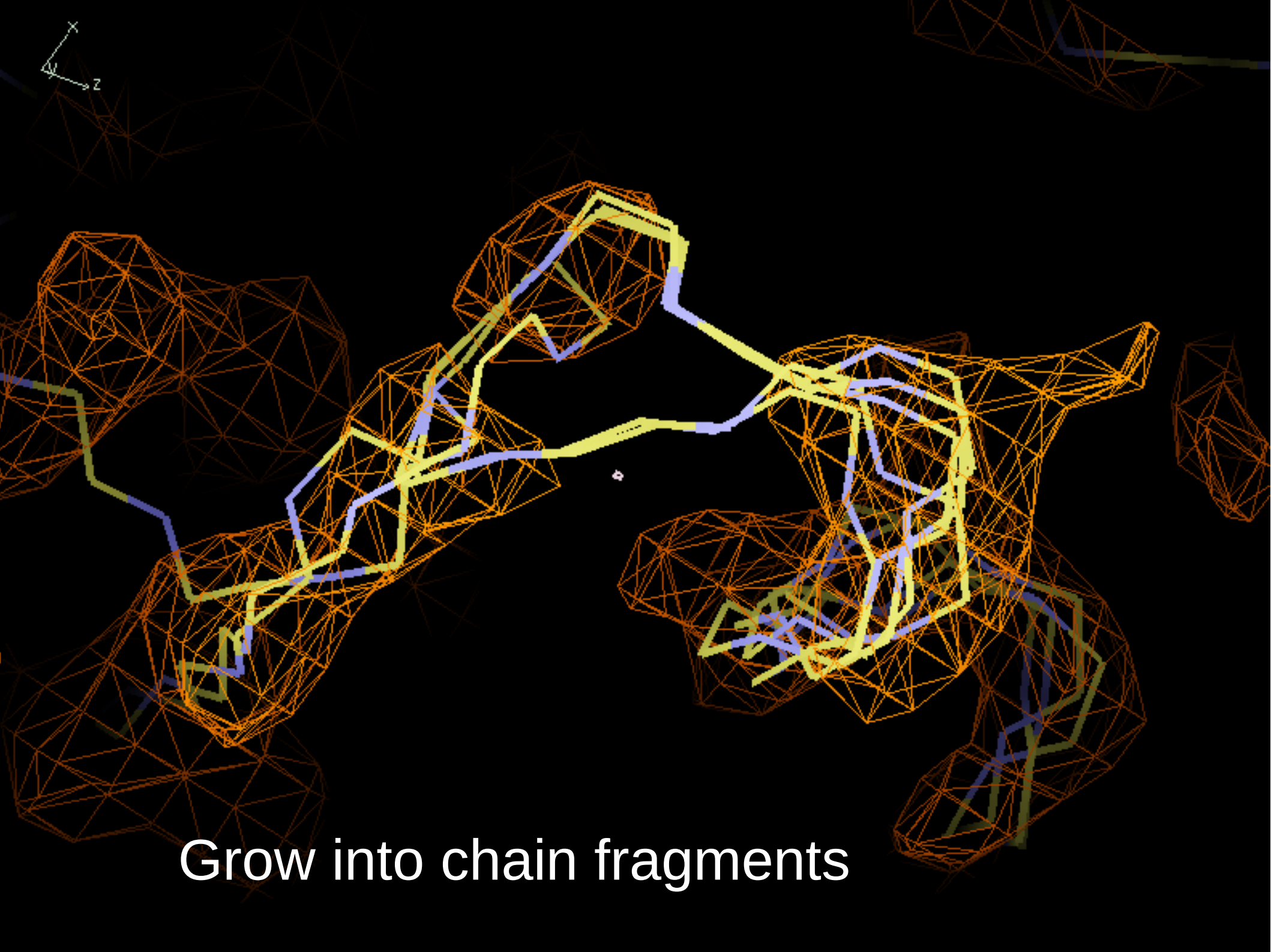
Buccaneer

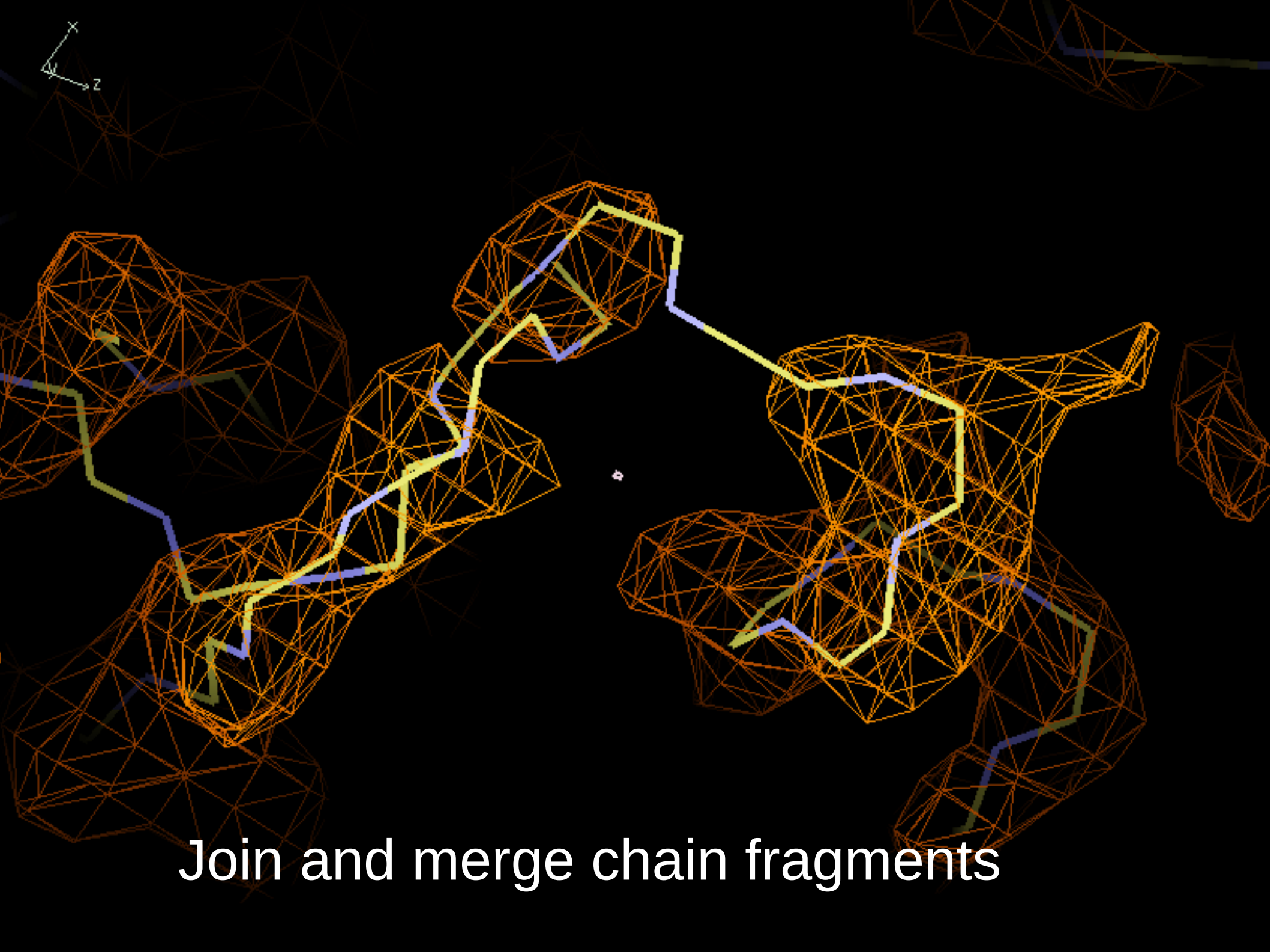
Case Study:

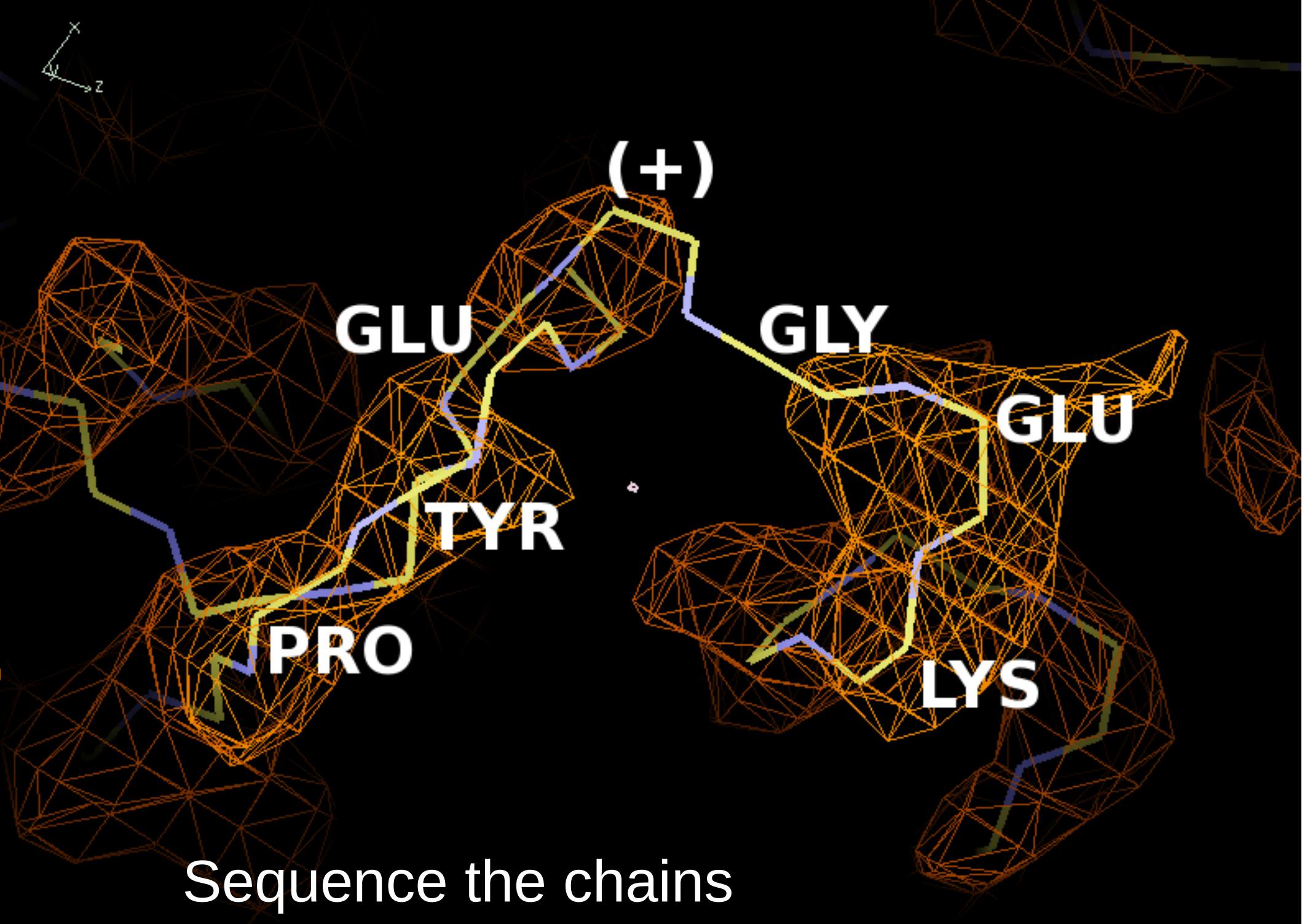
A difficult loop in a 2.9A map, calculated using real data from the JCSG.



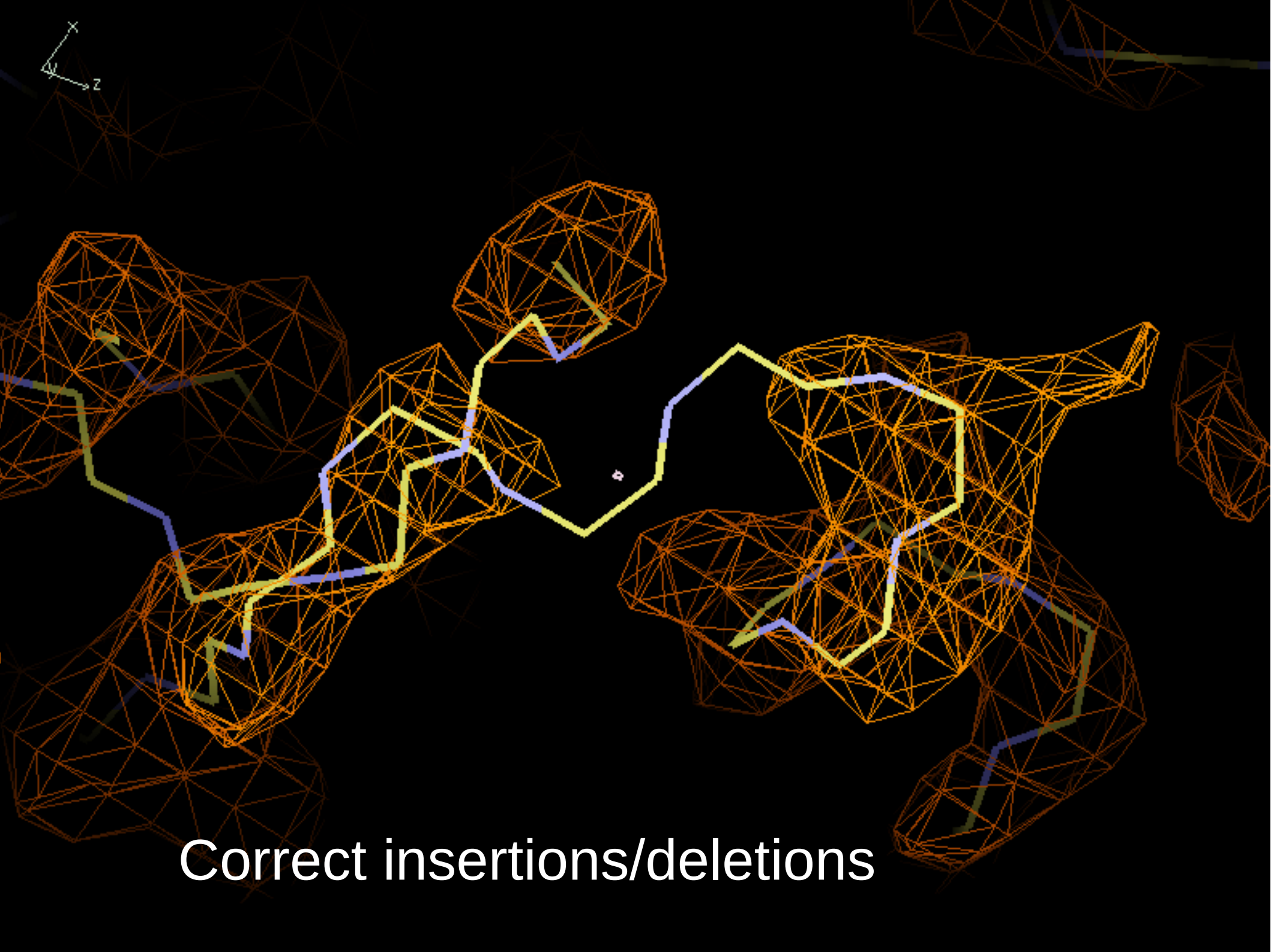
Find candidate C-alpha positions


X
Z
Grow into chain fragments

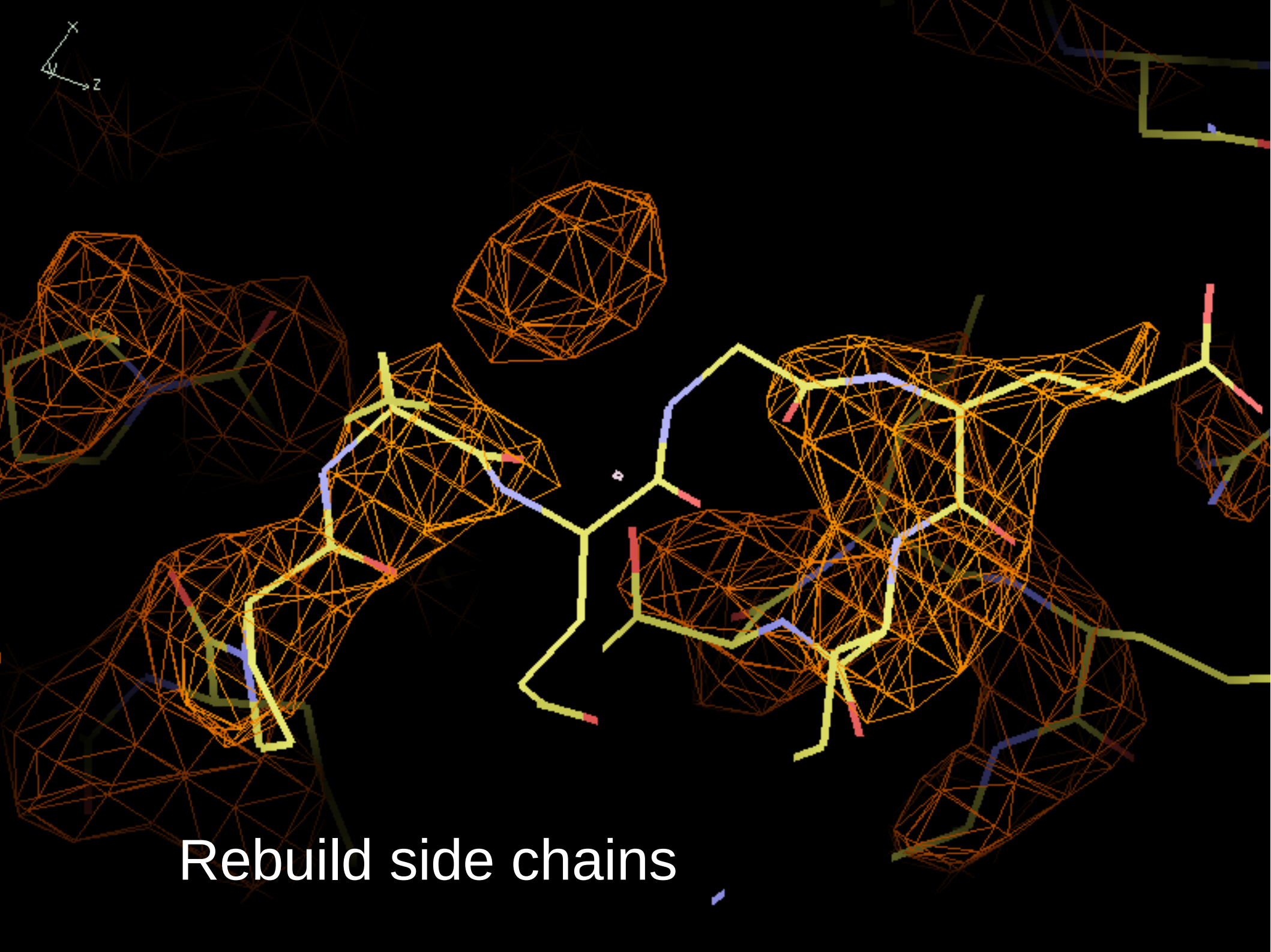

Join and merge chain fragments

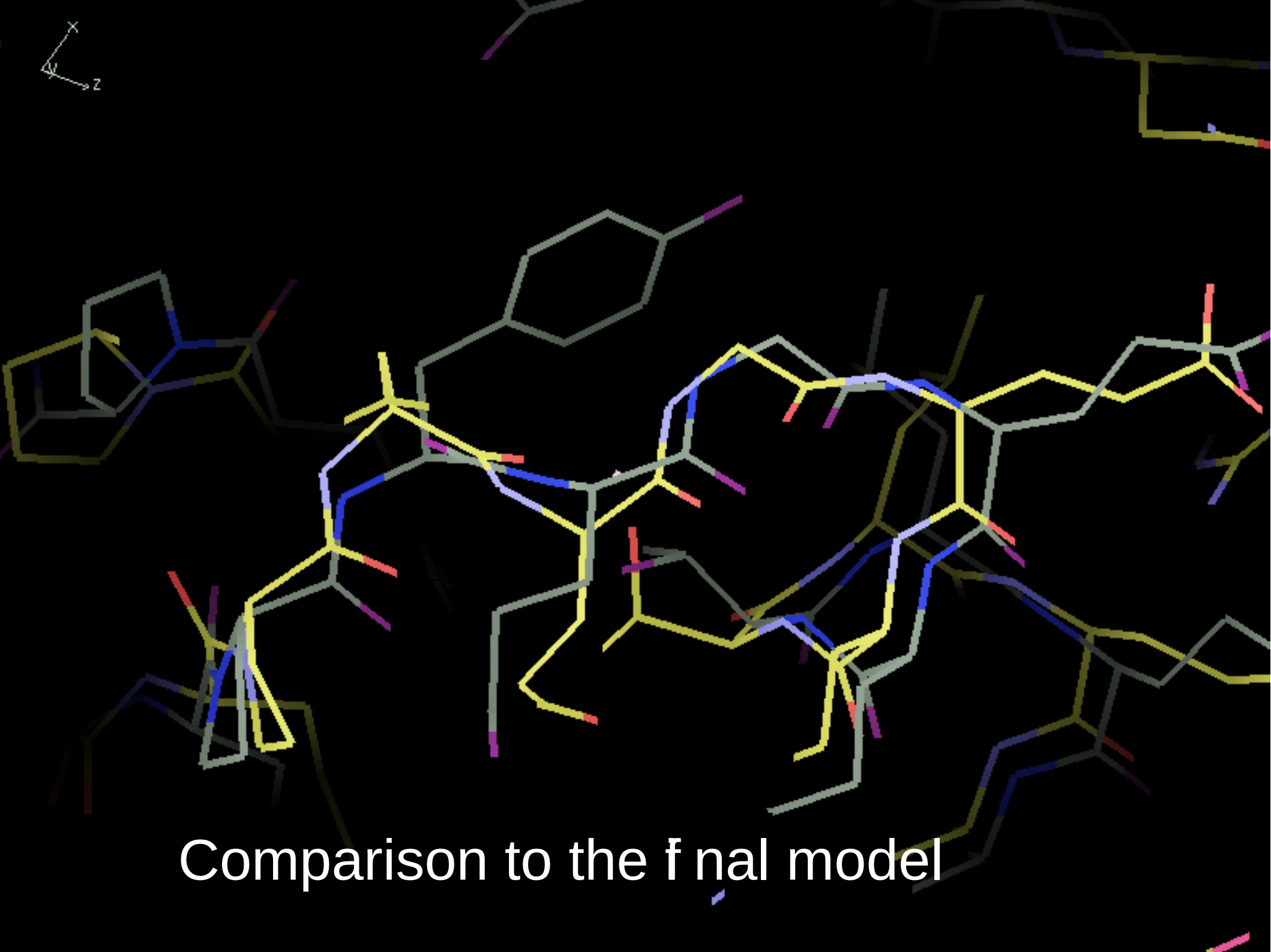


Sequence the chains


Correct insertions/deletions

Prune any remaining clashing chains

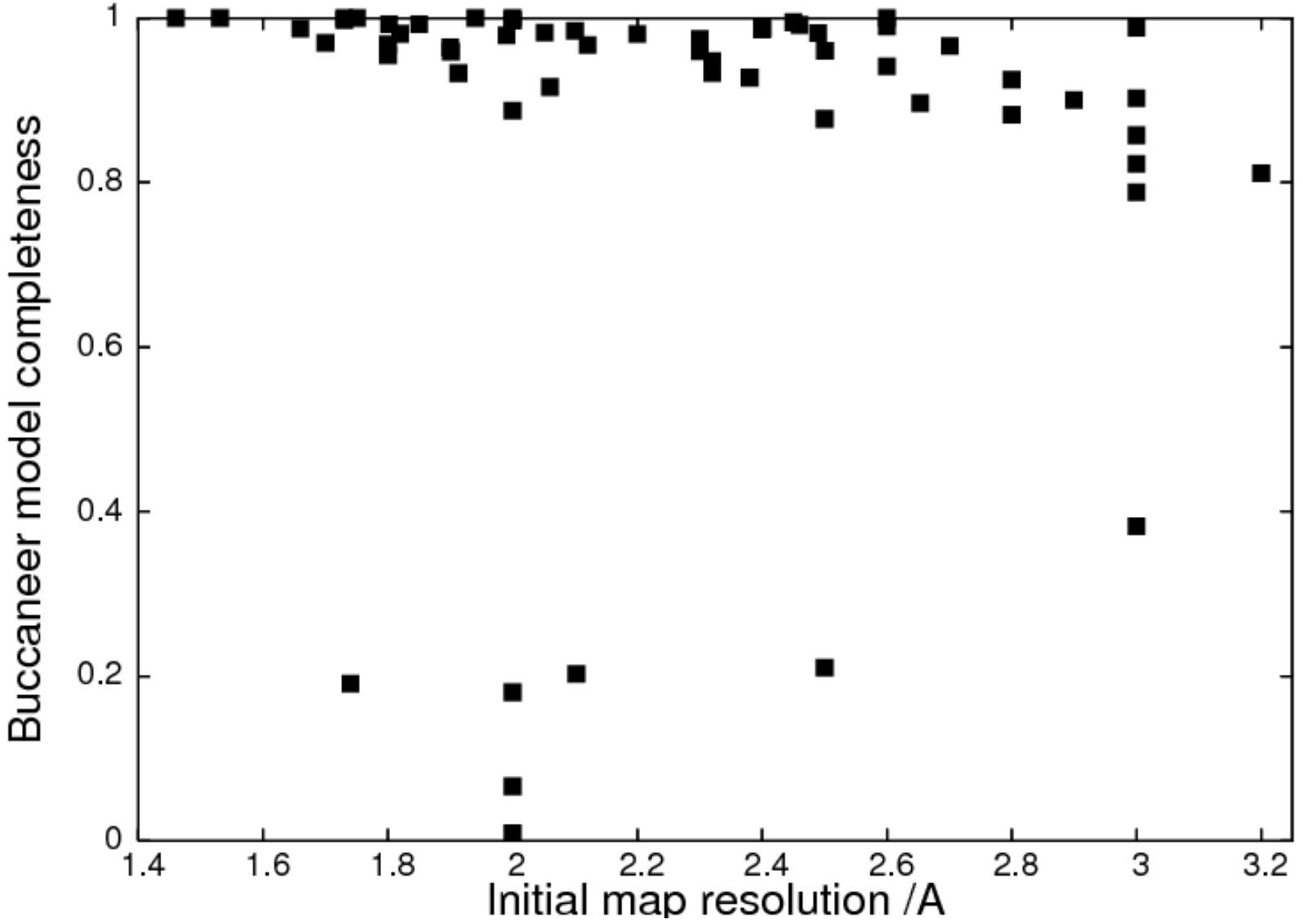

Rebuild side chains



Comparison to the final model

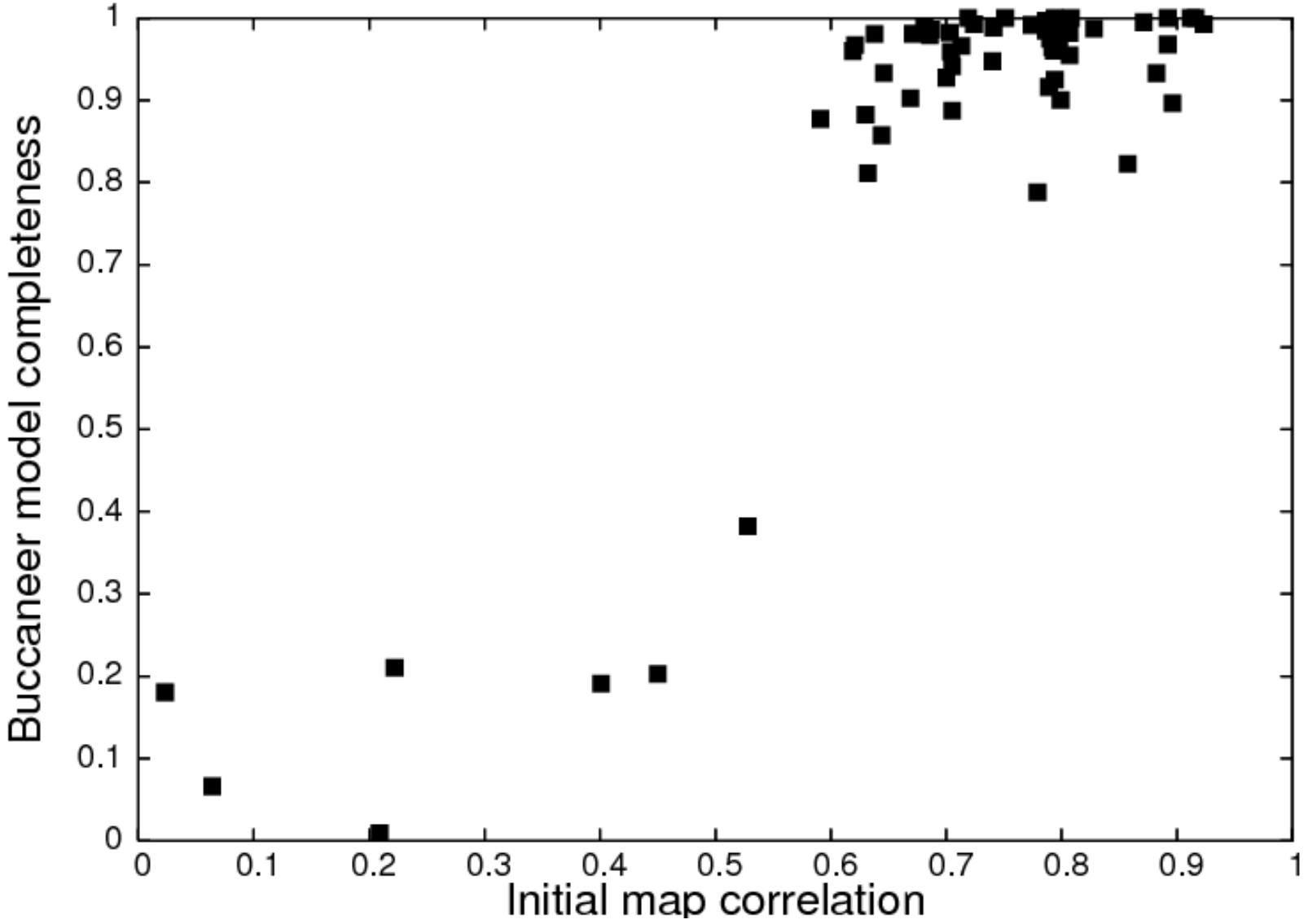
Buccaneer: Results

Model completeness not very dependent on resolution:

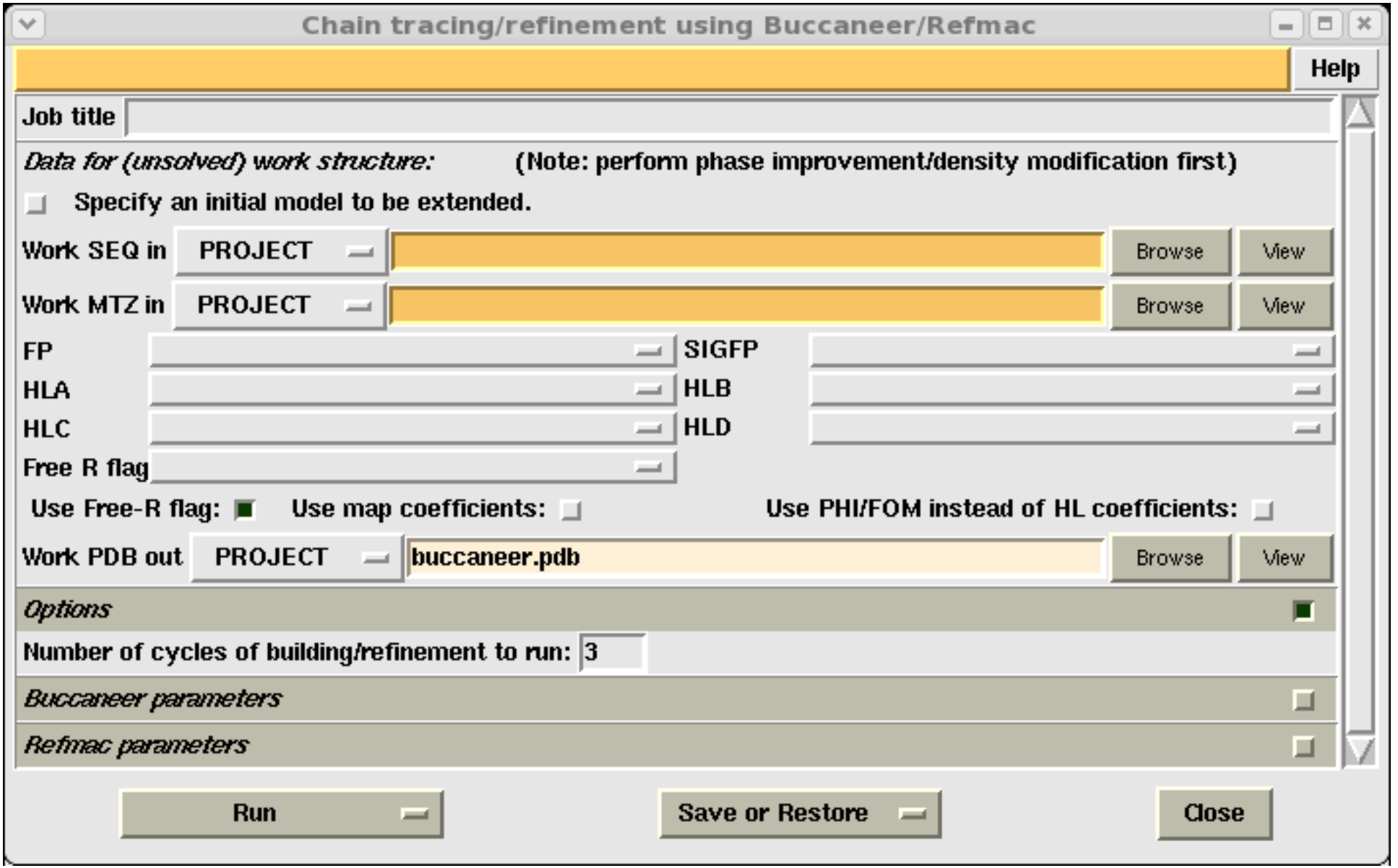


Buccaneer: Results

Model completeness dependent on initial phases:



Buccaneer


Chain tracing/refinement using Buccaneer/Refmac
Help
Job title
Data for (unsolved) work structure:
(Note: perform phase improvement/density modification first)
Specify an initial model to be extended.
Work SEQ in
PROJECT
Browse
View
Work MTZ in
PROJECT
Browse
View
FP
SIGFP
HLA
HLB
HLC
HLD
Free R flag
Use Free-R flag:
Use map coefficients:
Use PHI/FOM instead of HL coefficients:
Work PDB out
PROJECT
buccaneer.pdb
Browse
View
Options
Number of cycles of building/refinement to run:
3
Buccaneer parameters
Refmac parameters
Run
Save or Restore
Close

Buccaneer

What you need to do afterwards:

- Tidy up with Coot.
  - Or ARP/wARP when resolution is good.
  - Buccaneer+ARP/wARP better+faster than ARP/wARP.
- Typical Coot steps:
  - Connect up any broken chains.
  - Use density fit and rotamer analysis to check rotamers.
  - Check Ramachandran, molprobity, etc.
  - Add waters, ligands, check un-modeled blobs..
  - Re-refine, examine difference maps.

Buccaneer: Summary

A simple, (i.e. MTZ and sequence), very fast method of model building which is robust against resolution.

User reports for structures down to 3.7A when phasing is good.

Results can be further improved by iterating with refinement in refmac (and in future, density modification).

Proven on real world problems.

Use it when resolution is poor or you are in a hurry. If resolution is good and phases are poor, then ARP/wARP may do better. Best approach: Run both!

Nucleic Acid Building

Nautilus:

- A new tool for nucleic acid model building
- Automated (CCP4i) or interactive (Coot)
- Starting from:
  - Experimental phasing
  - Molecular replacement
  - Protein complexes

Nautilus

The task:

- To build continuous nucleic acid chains into electron density.
- To assign sequence to those chains.
- To allow addition of nucleotide chains to non-nucleotide structures.

Nautilus

'Fingerprint' detection:

- Identify high and low density features consistent with the presence of nucleic acid features.
- Very fast.
- Related to 'Essens' (Kleywegt and Jones), but with looks at both ridges and troughs.

Nautilus

Types of fingerprint:

- Sugar
- Phosphate
- Base type (A/C/G/U)

Nautilus

Use the difference between the mean of the 'high' points and the mean of the 'low' points as a score indicating how likely it is the given group is present at a given position and orientation.

Need to search positions and orientations – a more optimized version of the same target uses the minimum of the highs minus the maximum of the lows – can often stop the calculation before testing all the sample points.

Nautilus

Steps:

- Find chain seeds
- Grow into chains
- Join overlapping chains
- Link nearby chains
- Prune clashing chains
- Rebuild chains to ensure connectivity
- Assign sequence
- Build bases

Nautilus

Find:

- Optimised 6-d rotation-translation using the sugar or phosphate fingerprint.
  - ~5 seconds for whole ASU
- Sugar:
  - Build a single nucleic acid using the best matching equivalent from the database, scored by 1 x sugar + 2 x phosphate fingerprints
- Phosphate:
  - Build a pair of nucleic acids using the best matching equivalent from the database, scored by 1 x phosphate + 2 x sugar fingerprints

Nautilus

Grow:

- Try adding additional nucleic acids to either end of each fragment, scored by the sugar fingerprint and the intermediate phosphate fingerprint.
  - ~1-2 seconds

Join:

- Merge overlapping fragments into longer fragments
  - <0.1 second

Link:

- Join fragments with nearby 3' and 5' terminii
  - ~0.5 second

Nautilus

Prune:

- Eliminate clashing regions
  - <0.1 second

Rebuild chains:

- Rebuild each sugar-sugar link using a fragment from the database
  - ~0.3 seconds

Sequence:

- Score base-type fingerprints at each position and assign sequence
  - <0.1 second

Nautilus

But the real world isn't black and white. Ideally we want a probability of a base being of a particular type.

- Calculate z-scored densities for the density at each of the 6 sample positions for 200 bases (50 of each type), to form a sample database.
- Calculate z-scored densities for the 6 sample positions of the unknown base.
- Find the 50 closest matches to the unknown base from the database.
- Assign probability of being A/C/G/U on the basis of the proportion of of the 50 closest matches being of each type (+ an error term).

Google: k-NN (k-Nearest Neighbour)

Nautilus

Results:

- Good results on synthetic noisy data at 3.5A and user reports on real data at 3.8A.
  - Need more data
- Like '*buccaneer*', phases are more important than resolution.
- Failed on a quadruplex structure with good phases.
  - Try a different database?

Achnowledgements

Help:

- JCSG data archive: www.jcsg.org
- Garib Murshudov, Raj Pannu, Pavol Skubak
- Eleanor Dodson, Paul Emsley, Randy Read, Clemens Vonrhein

Funding:

- The Royal Society, BBSRC