

# CCP4 from a user perspective

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ACA Meeting 2005  
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# Overview

- File formats
- CCP4 Website
- CCP4 Help
- CCP4BB
- CCP4 Program Suite
- CCP4 Interface
- Interaction with other programs
- Example(s) of Use

# File formats

- Reflection files (mtz format)
- Coordinate files (pdb format)

Provide ways in and out of CCP4 Suite

# MTZ files

- Columns, columns, columns
- Labels
- Types
- Non-ascii
- Viewers

# PDB files

- ‘standard’
- Ascii
- Widely used

# CCP4 Website

- <http://www.ccp4.ac.uk>
- Downloads
- Problem pages
- Documentation
- Meetings
- Jobs

# CCP4 Help

- Documentation
- General crystallography
- Help in interface

# CCP4BB

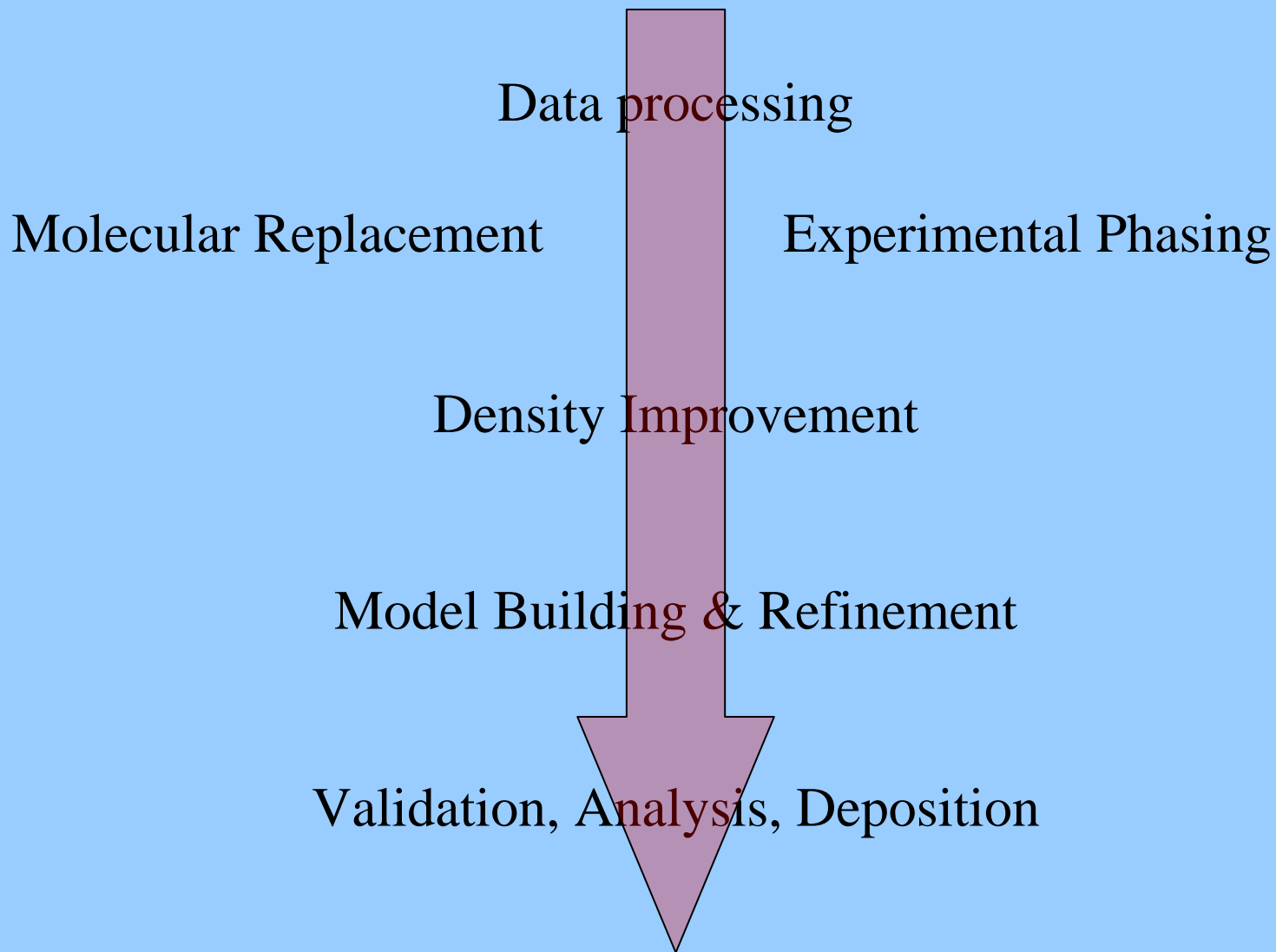
- Members from all over the world
- Fast, expert help from colleagues
- Useful tips
- Non-CCP4 topics
- Heated (entertaining) discussions



# CCP4 Program Suite

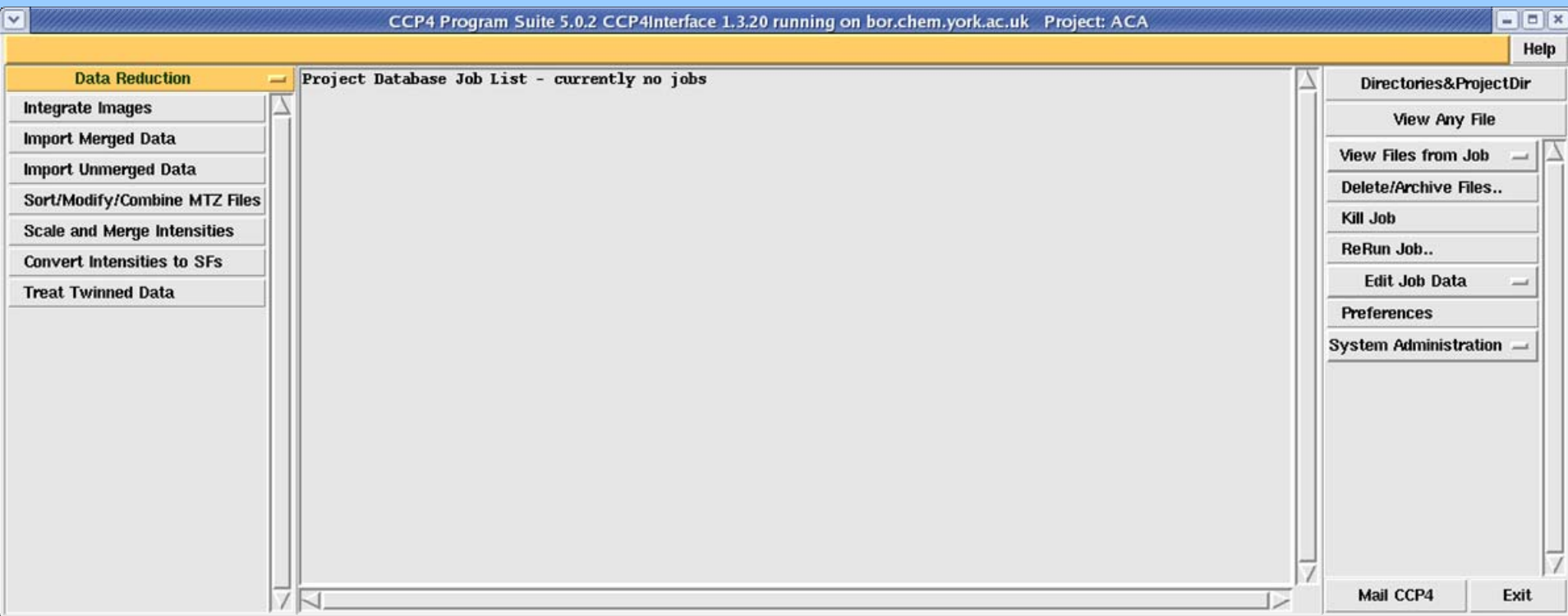
- *Many* programs
- All aspects of crystallography
- Data processing
- Molecular replacement
- Experimental Phasing
- Refinement
- Model analysis
- Utilities
- External programs

# Overview



# Interface

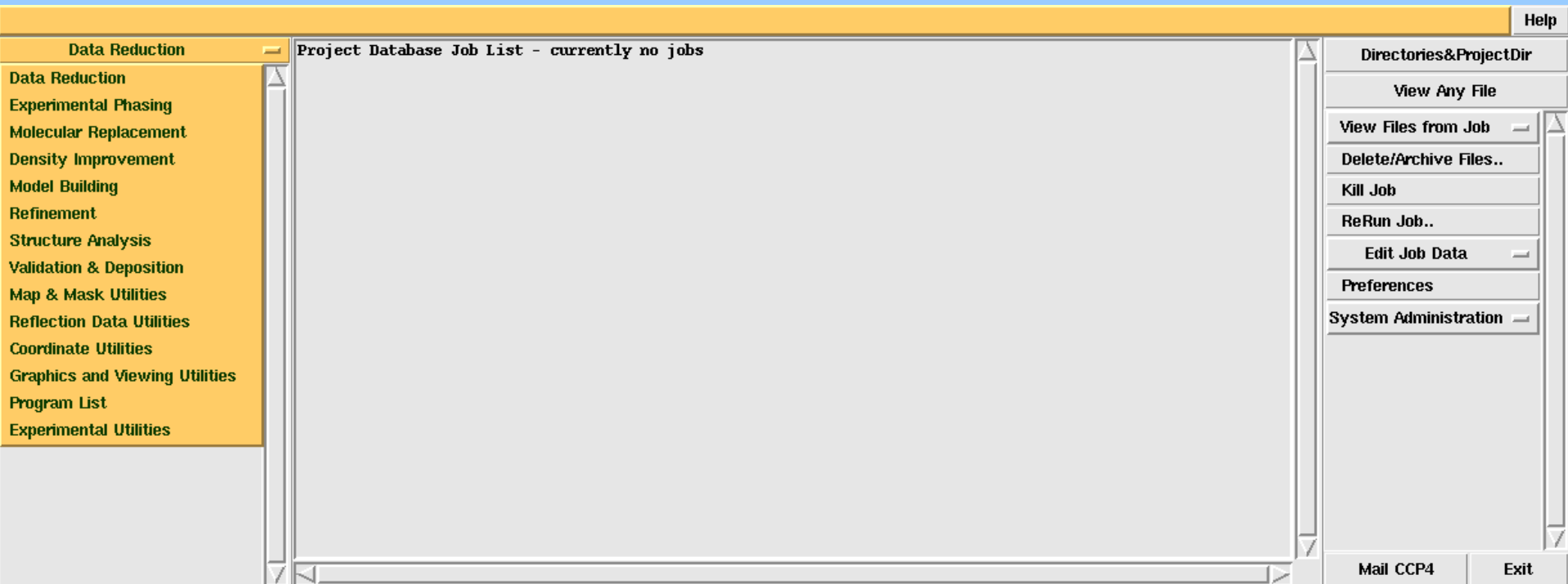
- No more typos
- Import/Export
- Help
- Defaults
- Project Management
- Tasks (logical sequence)



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# Modules



# Highlights

- Various programs will be highlighted by going through jobs run in the course of two typical projects. This will be done using the Interface.

# Example 1

- Lyase
- Se SAD
- Shelxd, MLPHARE, DM, ARP/WARP, REFMAC
- Triple helix

# Example 2

- Two related structures
- Cd SIRAS
- Shelxd, MLPHARE, DM, ARP/WARP, REFMAC
- Molecular Replacement