**BioFEL toolbox documentation**

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# About

BioFEL is an analogue of the CCP4 suite in crystallography, for biological imaging using X-ray free electron lasers.

BioFEL exists to produce and support an integrated suite of common programs, tools and utilities for biological structure determination using X-ray Free Electron Lasers. By sharing common programs and utilities, we hope to promote a user community sharing common analysis software, promote interaction amongst users and enable researchers to freely interact with each other. BioFEL aims to avoid the unnecessary duplication and re-creation of core software in multiple research groups, and thereby avoid the growth of a confusing labyrinth of incompatible software tools. BioFEL aims to be a resource for the XFEL imaging community that supports the widest possible researcher and user community across all FEL facilities worldwide. It encourages the wide dissemination of new ideas, techniques and practice.

If all that sounds similar to the CCP4 goals, it is because the idea is to create a similar resource for a distinct user community.

# fel\_browser

## Setting up to run

# IDL utilities

# Shell scripts

Cheetah can be run on its own, but is most easily used in conjunction with the crystfinder script – which does a lot of useful housekeeping. We should describe how to set this up somewhere

## Setting up cheetah and the crystfinder script

* Set up the crystfinder script to automate everything
* Configure cheetah.ini
  + Select the right detector
  + Select background processing options

## Tuning

### Optimising crystal hit finding

* Set hitfinderADCthreshold low enough, but not too low.