

RhoChi:

1. Input files
2. Program structure
3. ToDo

Input files

1. Experimental data:
 - single crystal: list of hkl reflections
 - powder: 1D, 2D diffraction profiles and background

2. Model parameters:
 - “.cif” or STAR-like file (International Tables vol. G)

3. Handbook values:
 - space group
 - magnetic form-factors ($\langle j_0 \rangle$, $\langle j_2 \rangle$)
 - neutron scattering length

Experimental data

single crystal:

```
#wavelength 1.40
#field 0.000 0.000 1.000
#orientation 0.6468462 -0.6860854 0.3300297 0.2141139
-0.2557555 -0.9343334 0.7319312 0.6810804 -0.0183183
# h k l FR sFR
0 0 8 0.64545 0.01329
2 0 6 1.75682 0.04540
...
```

1D powder diffraction:

```
#wavelength 2.35
#field 0.0 0.0 5.0
# ttheta IntUP sIntUP IntDOWN sIntDOWN
7.80 0.74282 0.55201 0.24785 0.29666
8.00 0.18608 0.18170 0.16548 0.17133
...
```

2D powder diffraction:

ϕ ↓

```
#wavelength 2.35
#field 0.0 0.0 5.0
#IntUP
241 4.00000 4.20000 ...
-40.00000 -85.31322 7.54655 ...
-39.50000 -53.87826 59.90163 ...
... ... ...
```

→ 2θ

background:

```
# ttheta IntBKGR
8.20 0.11000
80.40 0.18300
...
```

Model parameters -- “.rcif”

- phase (totally correspond to .cif description)
- experiment
- refinement

global _filerhochi

data _nacaalf

_cell_length_a 9.88888773144

_cell_length_b 9.88888773144

...

loop_

_atom_site_label

_atom_site_type_symbol

_atom_site_fract_x

_atom_site_fract_y

_atom_site_fract_z

_atom_site_occupancy

_atom_site_b_iso_or_equiv

F1 F 0.13847 0.30656 0.12052 1.0 0.0

...

phase

data _ref

_refinement_file_name_output 'full.lis'

loop_

_refinement_param1

\$pnd_\$nacaalf_pd_phase_scale

...

data _pnd

_2dpd_file_name_bkg 'full.bkg'

_2dpd_file_name_input 'full.dat'

...

loop_

_2dpd_phase_name

_2dpd_phase_scale

_2dpd_phase_igsize

_2dpd_phase_extinction_radius

_2dpd_phase_extinction_mosaicity

nacaalf 0.0110321630859 0.0 0.0 0.0

refinement

experiment

It can be directly used to plot the structure

Handbook values

space group: 'itables.txt'

coefficients for $\langle j_0 \rangle$, $\langle j_2 \rangle$: 'formmag.tab'

neutron scattering length: 'bscat.tab'

```
203 Fd-3          Cubic
choice: 1
centr: true
pcentr: -0.125,-0.125,-0.125
symmetry: x,y,z
symmetry: -x,-y,z
symmetry: -x,y,-z
symmetry: x,-y,-z
symmetry: z,x,y
symmetry: z,-x,-y
symmetry: -z,-x,y
symmetry: -z,x,-y
symmetry: y,z,x
symmetry: -y,z,-x
symmetry: y,-z,-x
symmetry: -y,-z,x
```

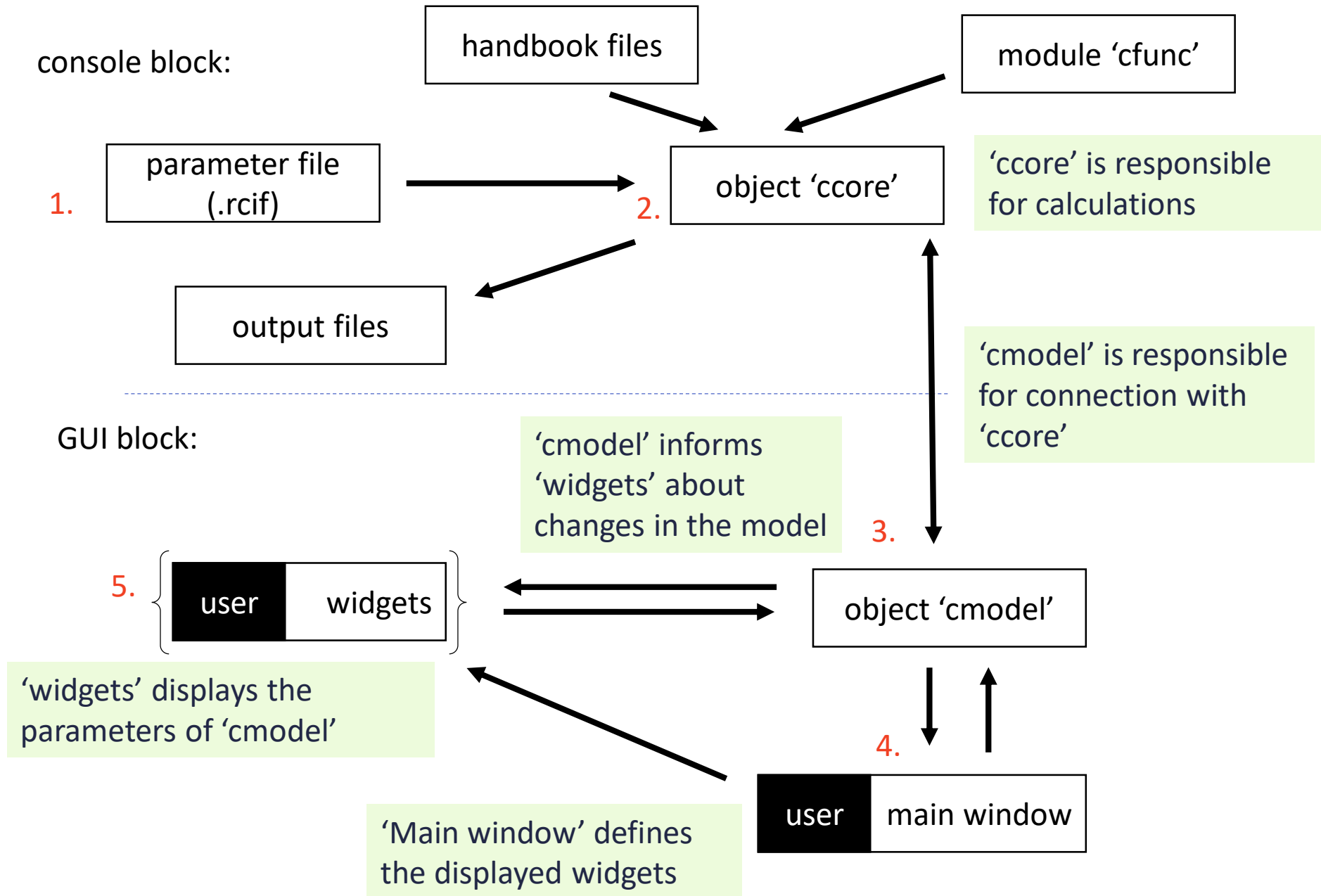
```
Z <j0> form factors for 3d transition elements and their ions
Z
F Sc0  0  0.2512 90.0296  0.3290 39.4021  0.4235 14.3222 -0.0043
F Sc1  0  0.4889 51.1603  0.5203 14.0764 -0.0286  0.1792  0.0185
F Sc2  0  0.5048 31.4035  0.5186 10.9897 -0.0241  1.1831  0.0000
F Ti0  0  0.4657 33.5898  0.5490  9.8791 -0.0291  0.3232  0.0123
...
```

#Neutron scattering lengths and cross sections

#!Isotope	conc	Coh b	Inc b	Coh xs	Inc xs	Scatt xs	Abs xs
H	---	-3.7390	---	1.7568	80.26	82.02	0.3326
1H	99.985	-3.7406	25.274	1.7583	80.27	82.03	0.3326
...							

Program structure

Principal scheme

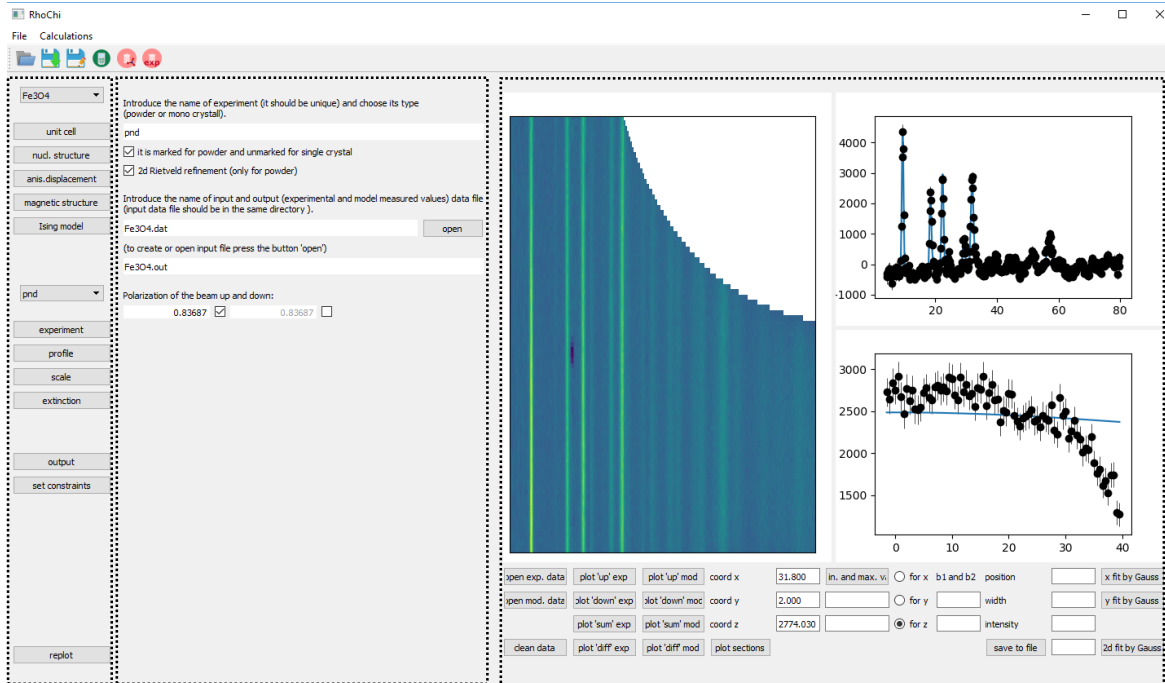


'Main window' (defined in the file 'rhochi.py')

The widgets:

- widg_cpanel
- widg_left
- widg_right

The widget description is given in separate files.



info about 'cmodel' output files

Task:

- the widgets arrangement

'Widgets' interacting with 'cmodel'

List of widgets (each in the separate file '.py'):

- widg_adp
- widg_const
- widg_exptype
- widg_extinction
- widg_magn
- widg_magn_ising
- widg_nucl
- widg_output
- widg_param
- widg_profile
- widg_results
- widg_scale
- widg_cb_exp
- widg_cb_ph
- widg_cb_ph_exp
- widg_sconstr
- widg_spgr

example: widg_spgr.py

Common elements:

- QCheckBox
- QLineEdit
- QTableWidget

Parent class:

- widg_min

(defined methods to interact with 'cmodel')

example: widg_nucl.py

On the page you can introduce information about crystal structure by loading it from the '.cif' file

press to point the '.cif' file

or by hands. Then introduce the name of phase (it should be unique) and the space groupe (example: 'P2(1)/n' or 'Fd-3m Z', 'Z' means second choice in last example).

phase

P1

1

looks on elements of symmetry for given space groupe

Unit cell parameters:

a, b, c (in angstroms) // alpha, beta, gamma (in degrees)

1.00000	<input type="checkbox"/>	1.00000	<input type="checkbox"/>	1.00000	<input type="checkbox"/>
90.00000	<input type="checkbox"/>	90.00000	<input type="checkbox"/>	90.00000	<input type="checkbox"/>

check boxex to find the optimal parameters

The position of atom and its isotropical displacement is shown in the table
press buttons to add and to delete atoms.

The handbooks values of scattering amplitude for given atoms can be loaded by pressing button 'load bsca'.

add atom delete atom load bsca

name	type_n	x	y	z	biso	occ
1	O	<input type="checkbox"/> 0.00000	<input type="checkbox"/> 0.00000	<input type="checkbox"/> 0.00000	<input type="checkbox"/> 0.00000	<input type="checkbox"/> 1.00000

Object 'cmodel' ('cmodel.py')

- cmodel
 - cmodel_ph
 - cmodel_at
 - cmodel_exp
 - cmodel_exp_ph
 - cmodel_ref:

'cmodel' has information about the model parameters

'cmodel_ph' has information about a phase

'cmodel_at' has information about an atom

'cmodel_exp' has information about an experiment

'cmodel_exp_ph' has information about a phase contributing in the experiment

(the classes are defined in the file 'cmodel.py')

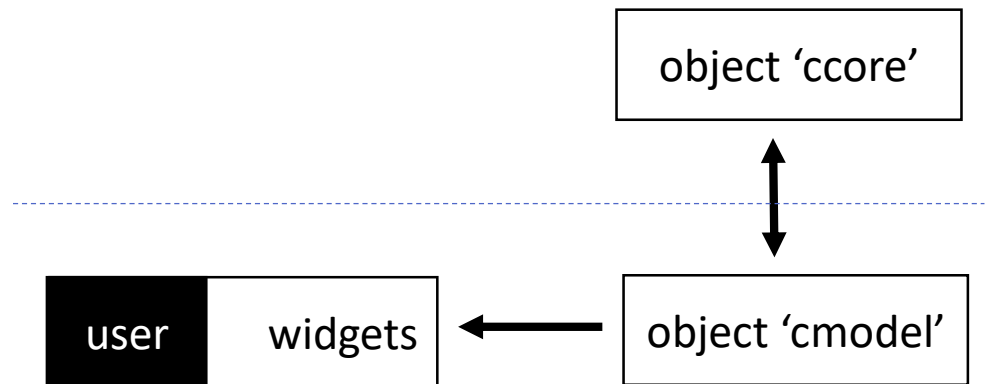
Tasks:

- interaction with 'widgets'
- interaction with 'ccore'

Parent class:

- cmodel_min

(defined methods to interact with 'widgets')



Object 'ccore' ('ccore.py')

- ccore
 - ccore_ph
 - ccore_at
 - ccore_exp
 - ccore_exp_ph
 - ccore_ref:

Tasks:

- load experimental data
- calculations

The main methods:

ccore:

- run_refinement
refinement, by simplex method
- run_errors
estimation of errorbars by calculation of Hessian

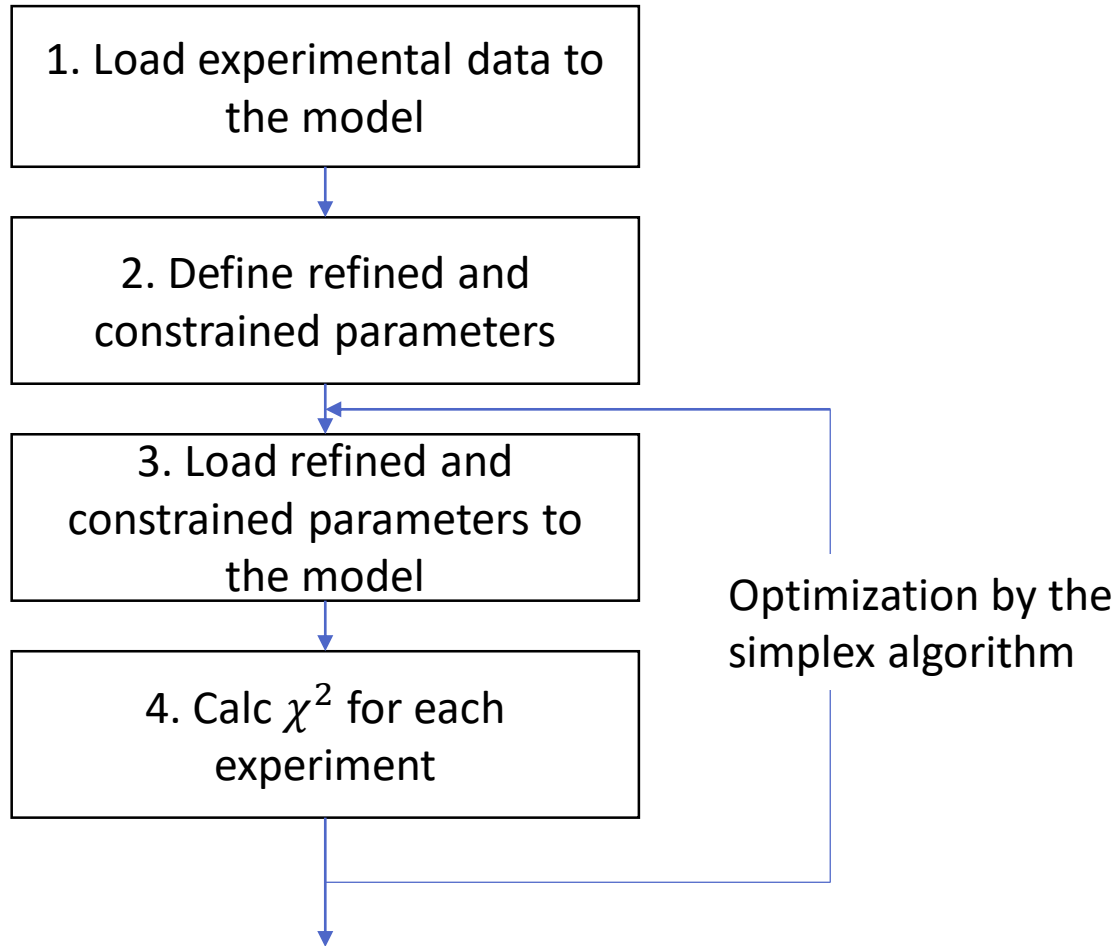
ccore_exp:

- load_exp_data
make preliminary calculations and load experimental data before refinement
- *calc_chi2*
calculation of chi2 for one experiment

ccore_ph:

- calcFNhkl
calculation of the nuclear structure factor
- calcSFThkl
calculation of the structure factor tensor

Structure of refinement



ToDo:

1. Executable file
2. Organization of file location
3. Least square refinement

Thank you for your attention.