



Workshop „Rietveld Refinement with Profex“

# Lesson 3: Basics of Rietveld Refinement

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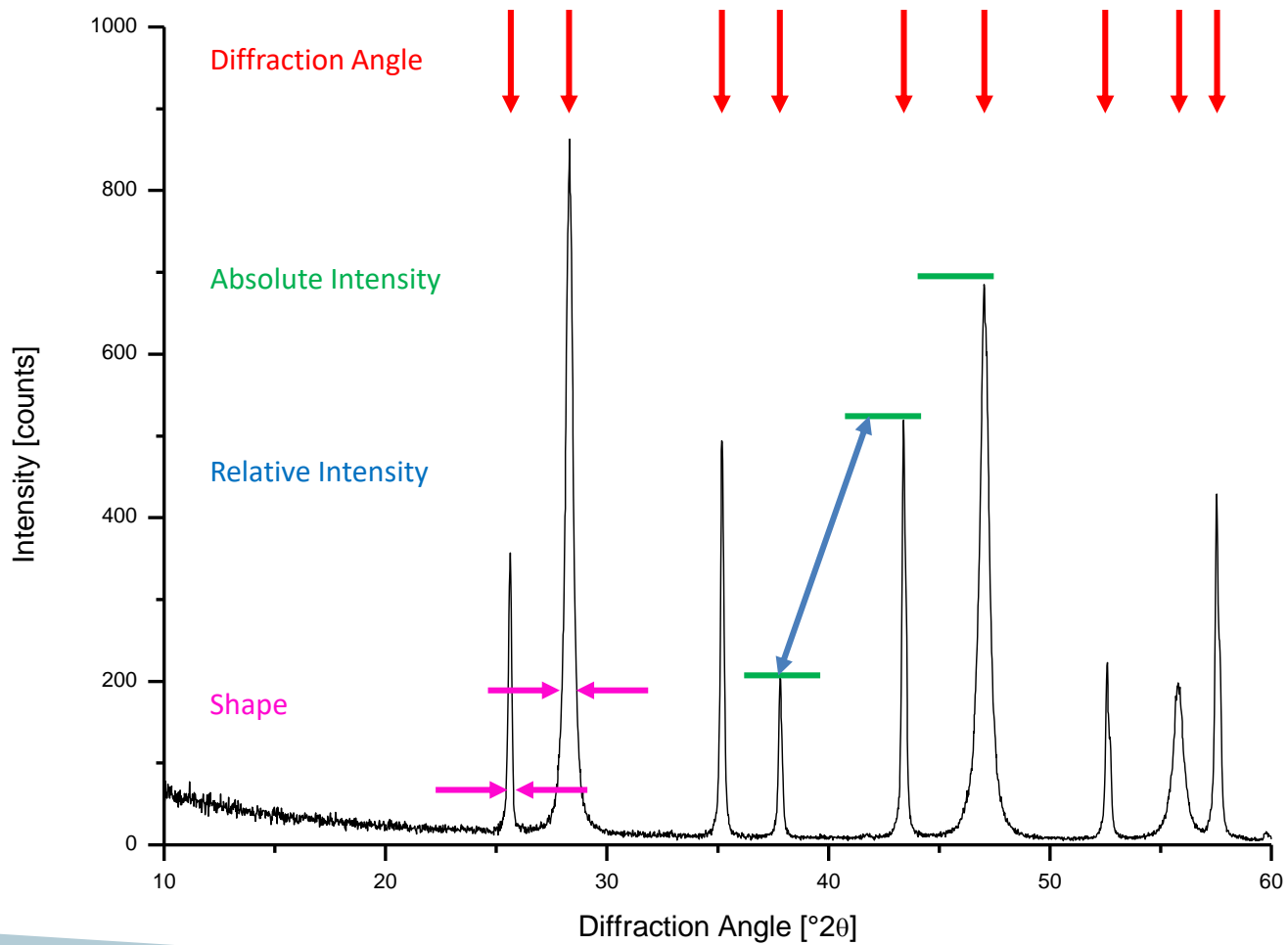
RMS Foundation, Switzerland

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Forschungszentrum Jülich, Germany



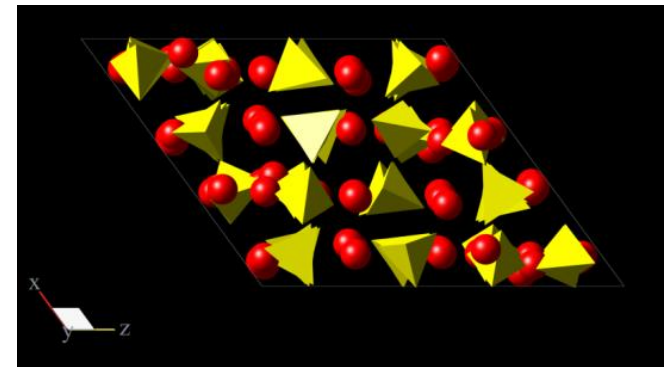
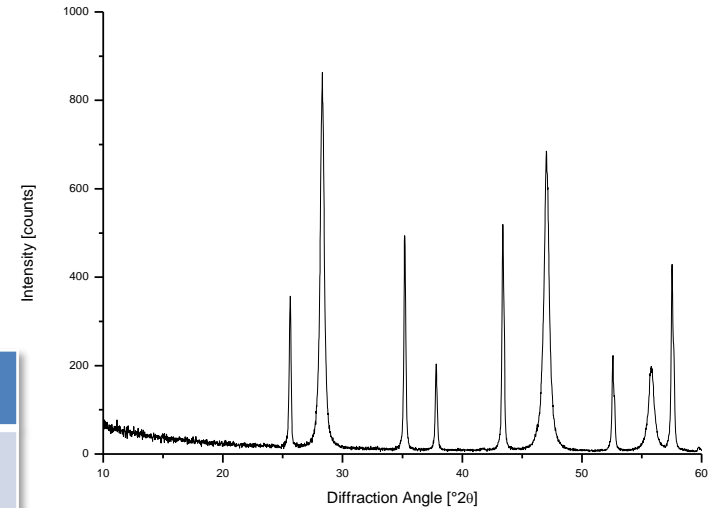
# Diffraction Pattern Features



# Diffraction Pattern Features

«Pattern Features» originate from crystallographic properties:

| Pattern Feature           | Origin  |
|---------------------------|---|
| Peak positions            | <ul style="list-style-type: none"><li>- Symmetry of the unit cell (space group)</li><li>- Dimensions of the unit cell</li></ul> |
| Relative peak intensities | <ul style="list-style-type: none"><li>- Coordinates of atoms in unit cell</li><li>- Species of atoms</li></ul>                  |
| Absolute peak intensities | <ul style="list-style-type: none"><li>- Abundance of phase</li></ul>  |
| Peak width                | <ul style="list-style-type: none"><li>- Crystallite size</li><li>- Micro-Strain in crystal lattice</li></ul>                    |



# Rietveld Refinement

Concept: Fit crystallographic parameters to XRD data

- Unit cell dimensions
- Phase quantities
- Crystallite sizes / shapes
- Atomic coordinates / bond lengths
- Micro-strain in crystal lattice
- Texture effects
- Substitutions / Vacancies



Prof. Hugo Rietveld (1932 – 2016)

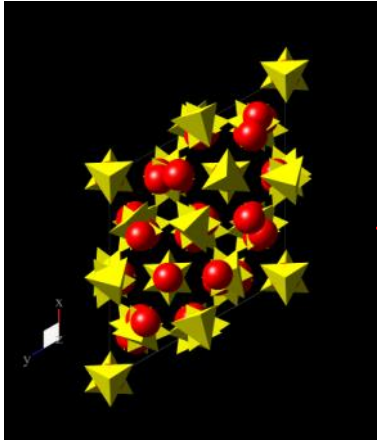
**No phase identification!**  
**All phases must be identified first**  
(unknown phase → no Rietveld refinement)

**No structure solution!**  
(all crystal structures must be known)

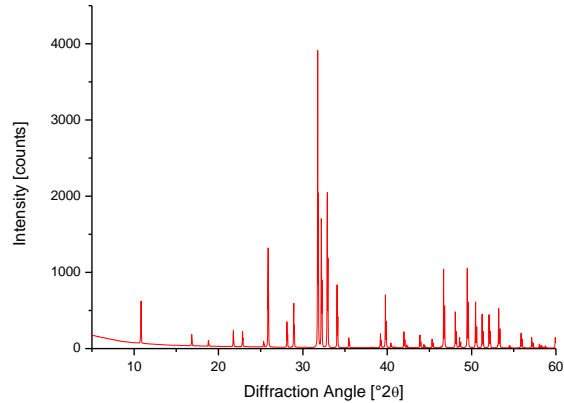
Needs excellent data quality!

# Rietveld Refinement

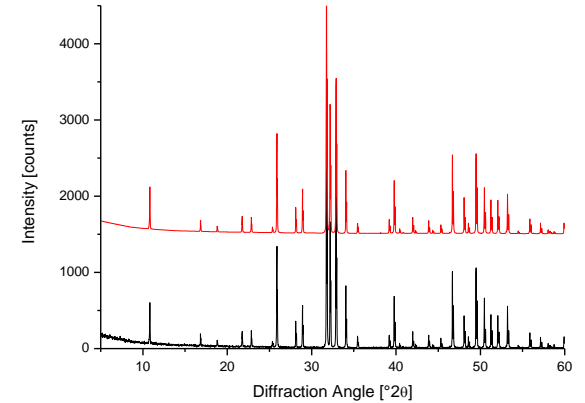
Known structure model



Calculate theoretical diffraction pattern



Compare with measured pattern

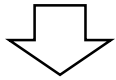


Optimize structure model, repeat calculation

Minimize differences between calculated and observed pattern by least-squares method

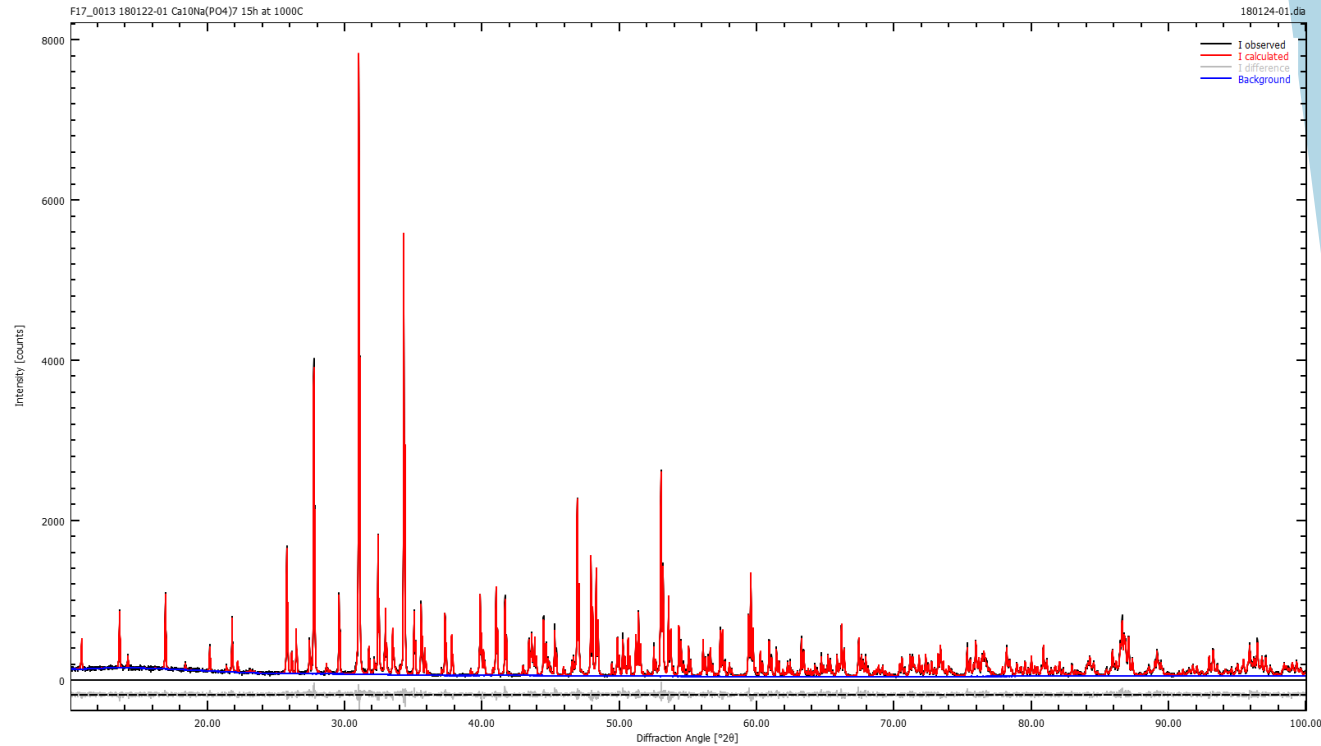
# Rietveld Refinement

Calculated pattern = Measured pattern



Optimized (refined) crystal structure models = Sample phases

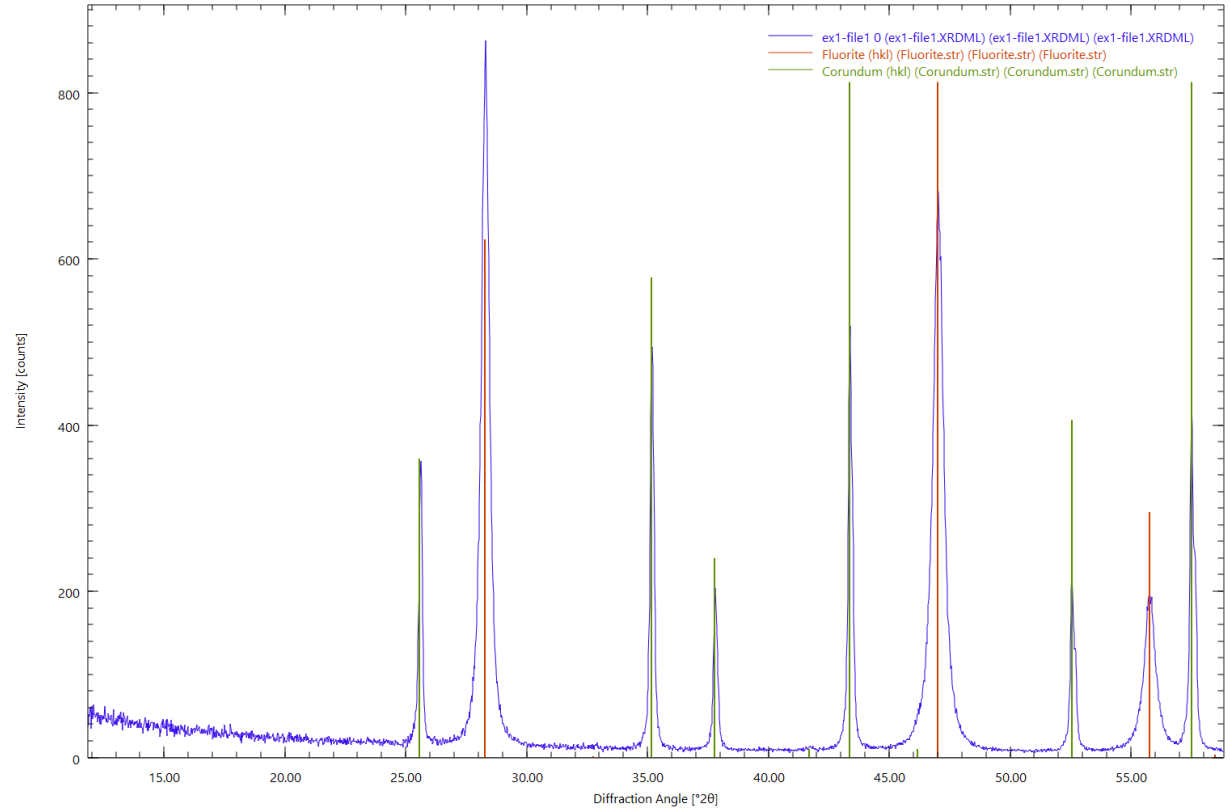
Starting models for all phases required  
→ Start with phase identification



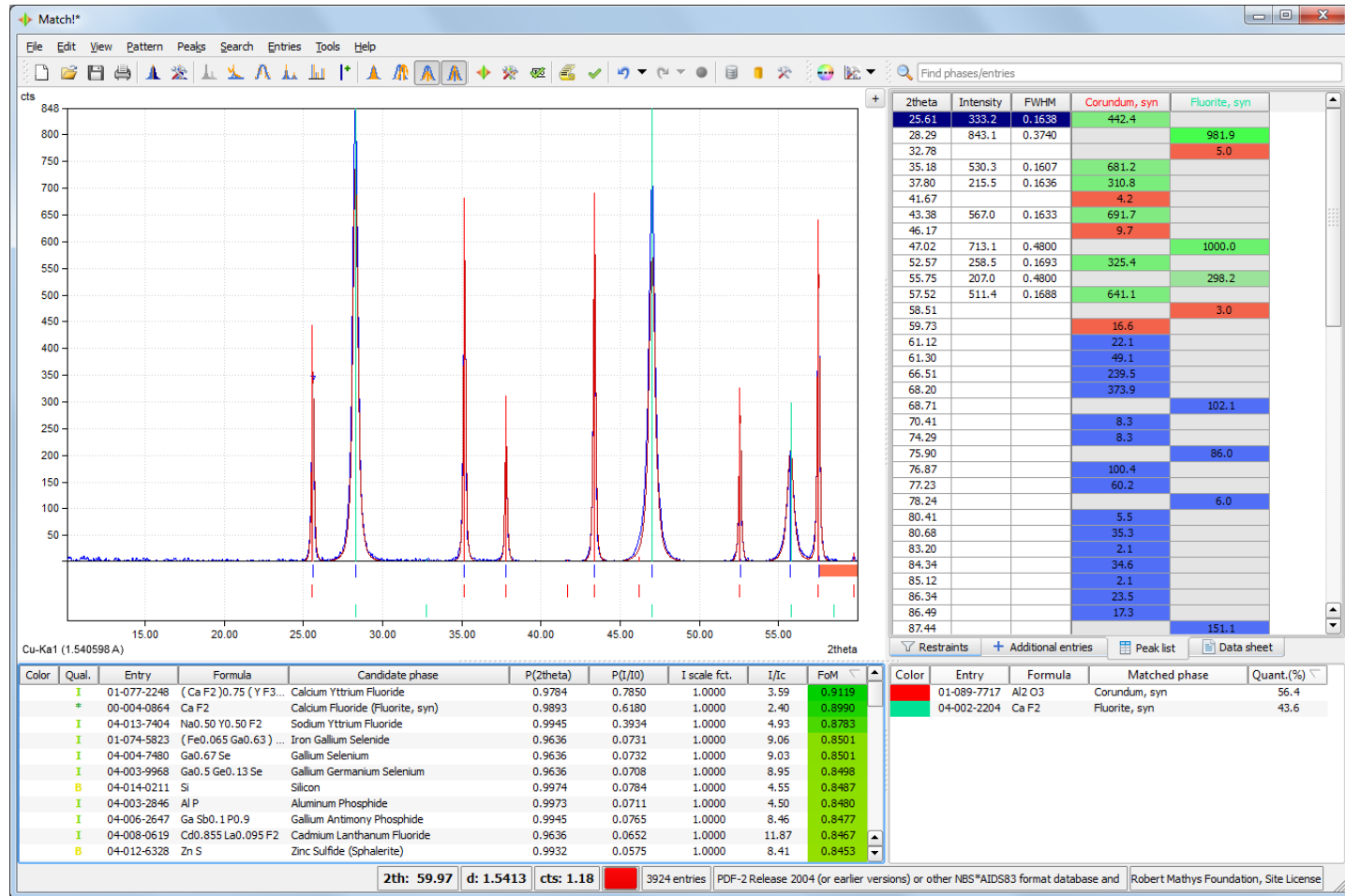
# Step 1: Phase Identification

Every crystal structure produces a unique set of diffraction peaks (angle and intensity)

Compare measured peak positions and intensities with a database



# Step 1: Phase Identification





## Step 2: Obtain Crystal Structure Models

For each phase, a structure model must be obtained.

The model contains:

- Space group
- Cell parameters
- Atomic positions:
  - Scattering factor
  - Fractional coordinates
  - Thermal displacement parameter

```
data_04-004-2852
#Copyright 2024 International Centre
#for Diffraction Data. All rights reserved.

_chemical_name_systematic      'Aluminum Oxide'
_chemical_formula_sum          'Al2 O3'
_chemical_formula_weight       101.96

_cell_length_a                 4.7602(2)
_cell_length_b                 4.7602(2)
_cell_length_c                 12.9933(17)
_cell_angle_alpha              90
_cell_angle_beta               90
_cell_angle_gamma              120
_cell_formula_units_Z          6
_cell_volume                   254.98
_symmetry_cell_setting         hexagonal
_symmetry_space_group_name_H-M R-3c
_symmetry_Int_Tables_number    167

loop_
_atom_site_label
_atom_site_type_symbol
_atom_site_fract_x
_atom_site_fract_y
_atom_site_fract_z
_atom_site_U_iso_or_equiv
_atom_site_symmetry_multiplicity
_atom_site_Wyckoff_symbol
_atom_site_occupancy
Al1 Al 0.0 0.0 0.35216 0.00284 12 c 1.0
O2 O 0.30624 0.0 0.25 0.00343 18 e 1.0
```

```
data_04-002-2191
#Copyright 2024 International Centre
#for Diffraction Data. All rights reserved.

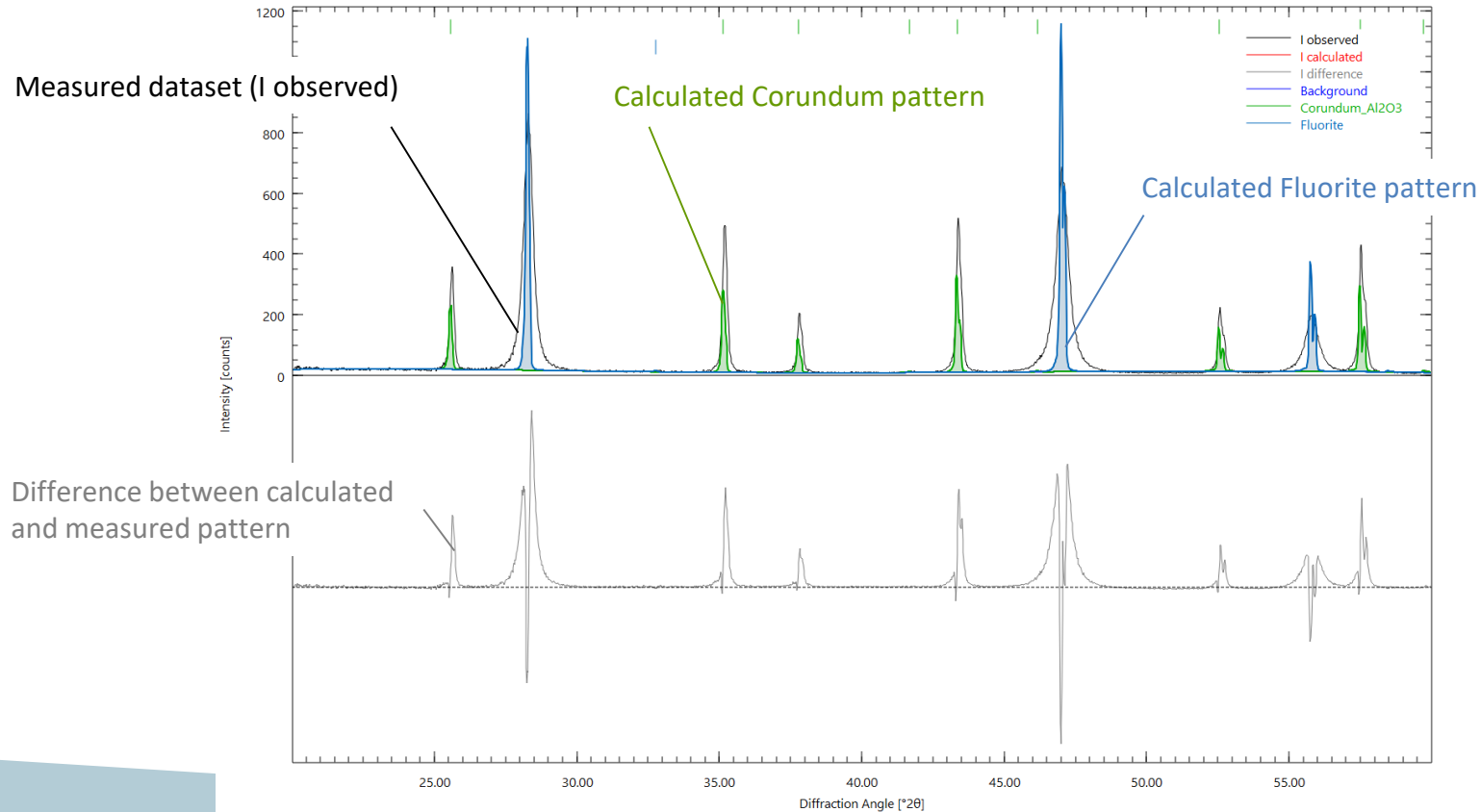
_chemical_name_systematic      'Calcium Fluoride'
_chemical_formula_sum          'Ca F2'
_chemical_formula_weight       78.07

_cell_length_a                 5.463
_cell_length_b                 5.463
_cell_length_c                 5.463
_cell_angle_alpha              90
_cell_angle_beta               90
_cell_angle_gamma              90
_cell_formula_units_Z          4
_cell_volume                   163.04
_symmetry_cell_setting         cubic
_symmetry_space_group_name_H-M Fm-3m
_symmetry_Int_Tables_number    225

loop_
_atom_site_label
_atom_site_type_symbol
_atom_site_fract_x
_atom_site_fract_y
_atom_site_fract_z
_atom_site_U_iso_or_equiv
_atom_site_symmetry_multiplicity
_atom_site_Wyckoff_symbol
_atom_site_occupancy
Ca1 Ca 0.0 0.0 0.0 . 4 a 1.0
F2 F 0.25 0.25 0.25 . 8 c 1.0
```

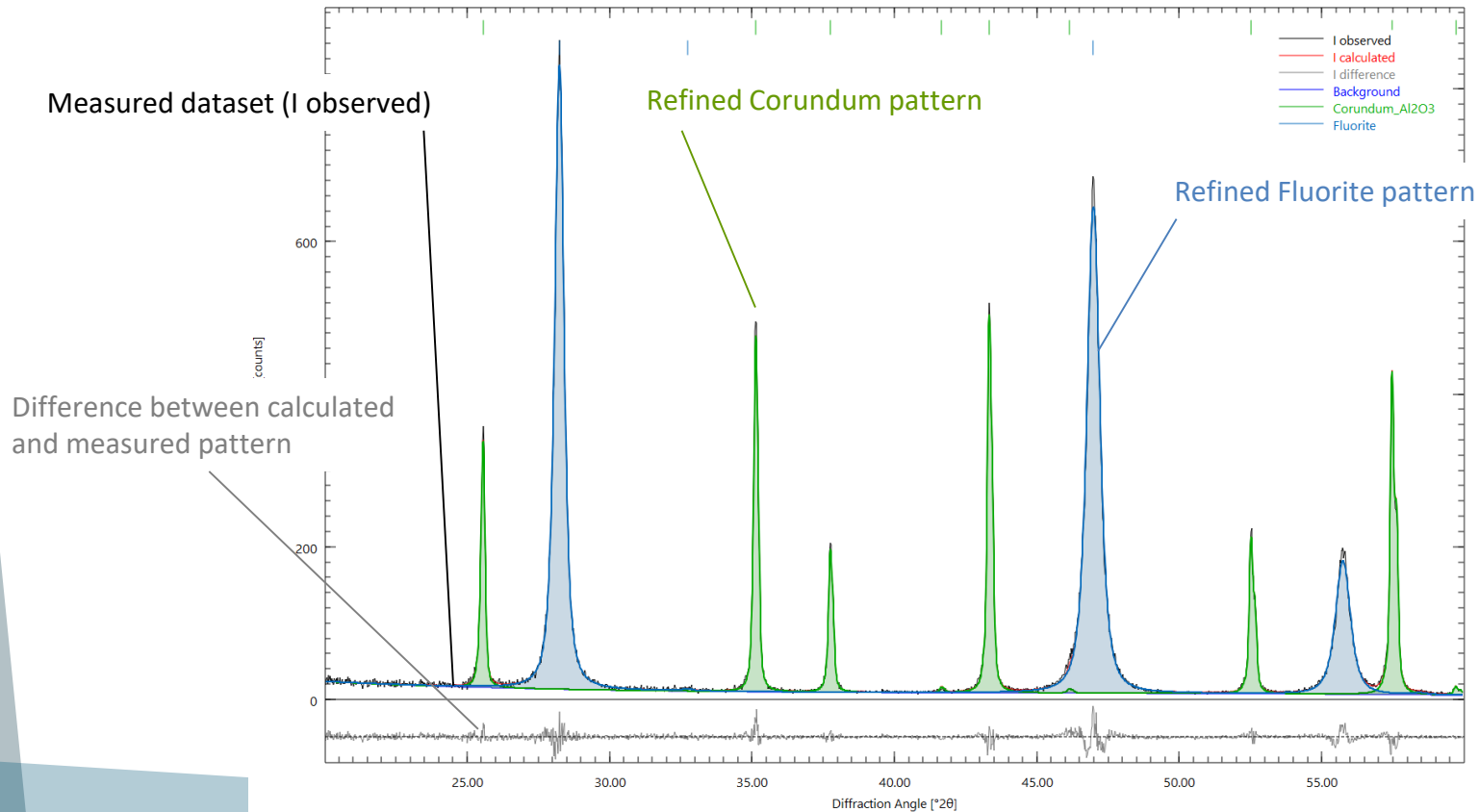
## Step 3: Rietveld Refinement 1<sup>st</sup> Iteration

- Calculate theoretical diffraction pattern from structure models
- Compare with measured pattern



## Step 3: Rietveld Refinement Curve Fitting

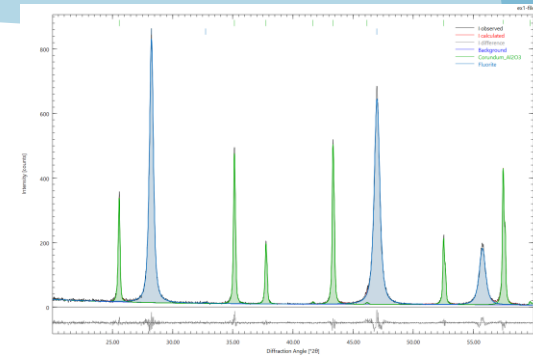
- Optimize crystallographic parameters in structure models
- Minimize difference between observed and calculated pattern



## Step 3: Rietveld Refinement Curve Fitting

Optimize crystallographic parameters in structure models represent sample composition:

- Phase quantities
- Cell parameters
- Crystallite size
- Lattice strain
- Atomic coordinates
- Atomic site occupancy factors
- Thermal displacement parameters



| Refined Parameters      |          |         |
|-------------------------|----------|---------|
| Parameter               | Value    | ESD     |
| ▼ Statistics            |          |         |
| Rwp                     | 7.58     |         |
| Rexp                    | 14.01    |         |
| $\chi^2$                | 0.29     |         |
| GoF                     | 0.54     |         |
| Background Coefficients | 6        |         |
| ▼ Global GOALS          |          |         |
| corundum/sum            | 0.4958   | 0.0041  |
| fluorite/sum            | 0.5042   | 0.0041  |
| ▼ Local GOALS           |          |         |
| ▼ Corundum_Al2O3        |          |         |
| Refined Composition     | Al12 O18 |         |
| A                       | 0.47610  | 0.00003 |
| C                       | 1.29960  | 0.00008 |
| UNIT                    | NM       |         |
| GrainSize(1,1,1)        | 124.1    | 5.0     |
| UNIT                    | NM       |         |
| ▼ Fluorite              |          |         |
| Refined Composition     | Ca4 F8   |         |
| A                       | 0.54677  | 0.00003 |
| UNIT                    | NM       |         |
| GrainSize(1,1,1)        | 42.4413  |         |
| UNIT                    | NM       |         |

# Modelling the Peak Profile

Mathematical model to describe the peak profile is needed.

Two different approaches:

➤ Use empirical function

➤ Pseudo-Voigt

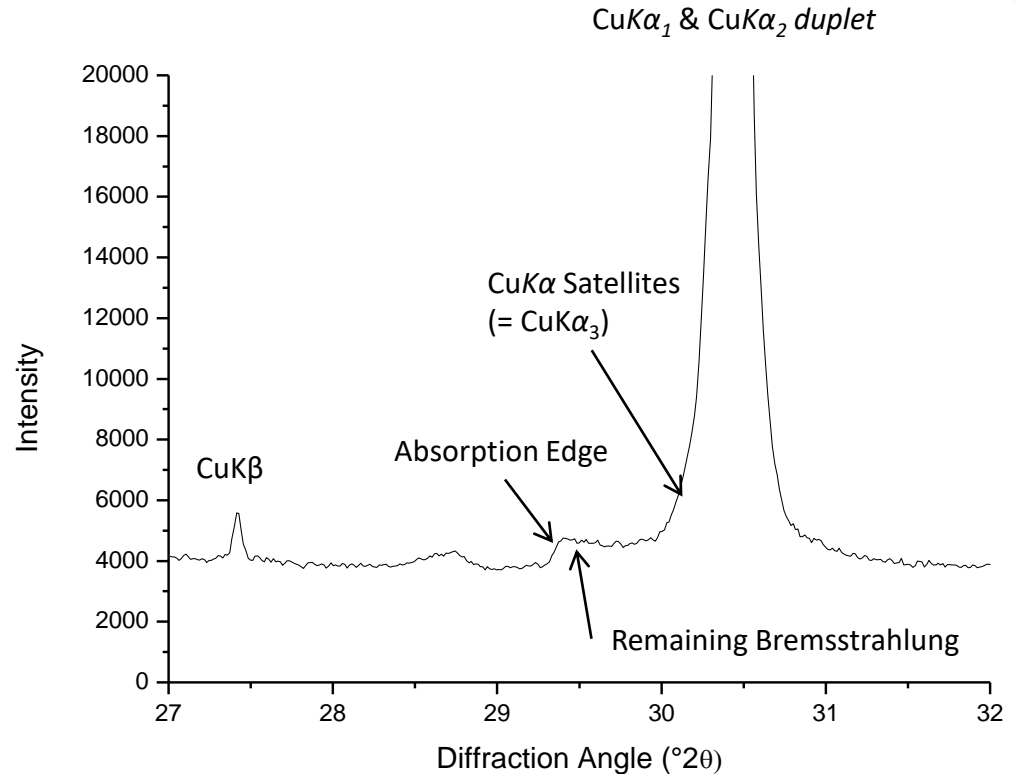
➤ Pearson-IIV

➤ ...

➤ Simulate peak profile from instrument configuration

➤ Convolute the effect of every optical element

= Fundamental Parameters Approach (FPA)

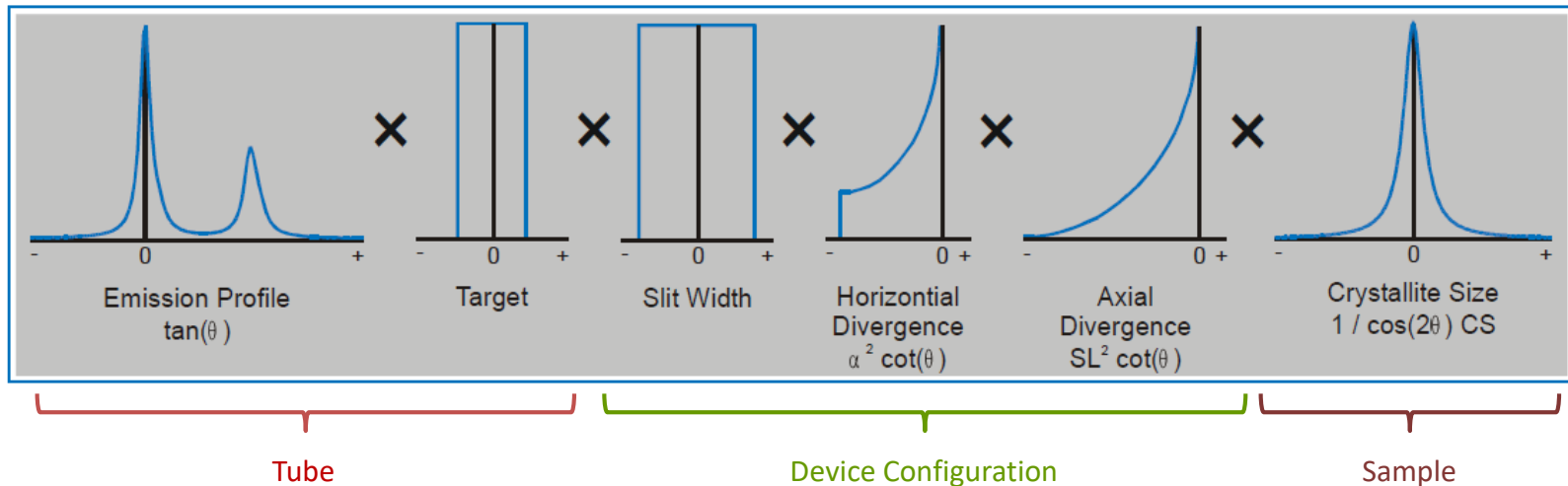


# Fundamental Parameters Approach (FPA)

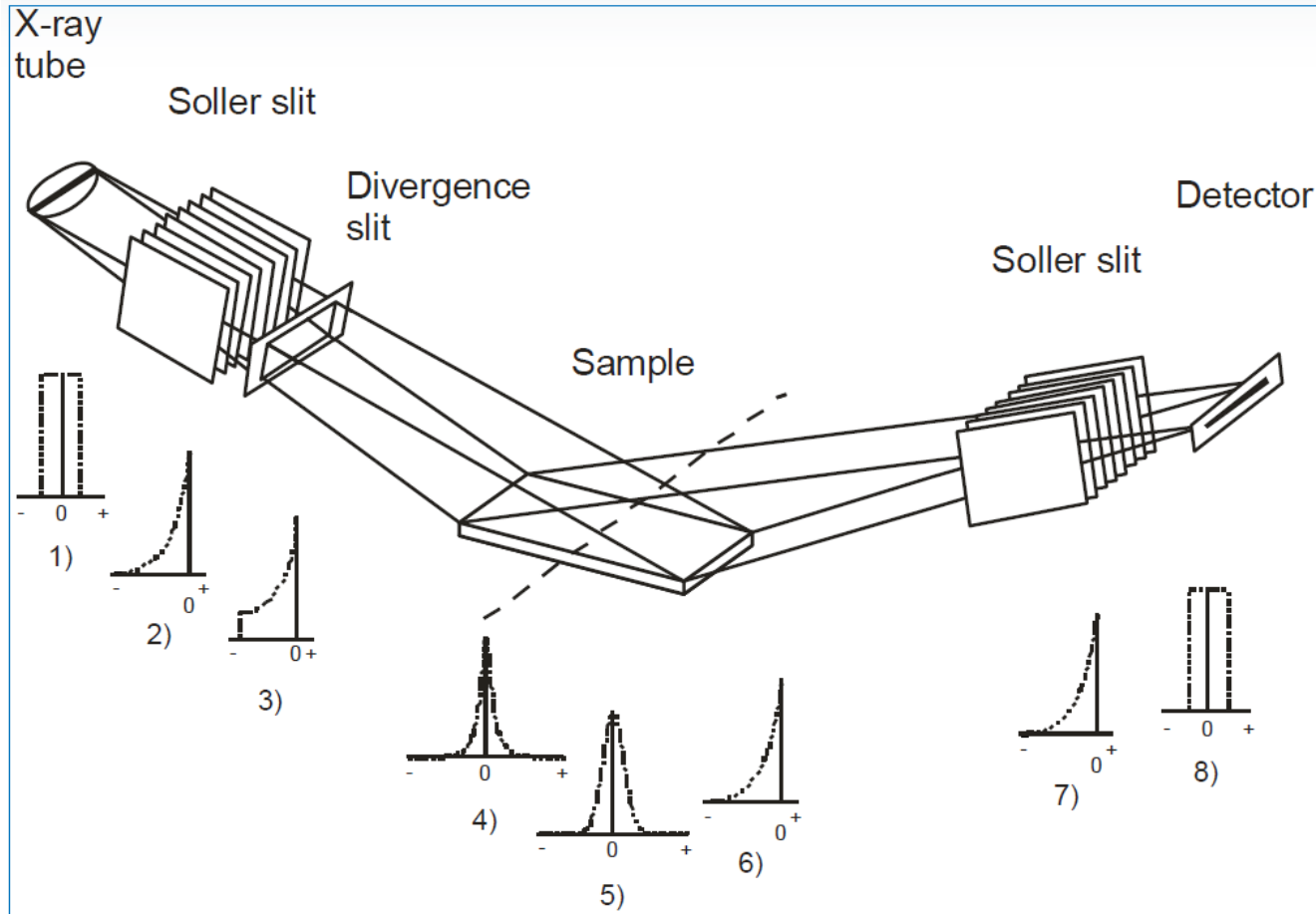
Calculate the peak profile from the device configuration

Take into account the contributions of:

- Source emission profile (X-ray wavelength distribution from Tube)
- Every optical element in the beam path (position, size, etc.)
- Sample contributions (peak broadening due to crystallite size & strain)

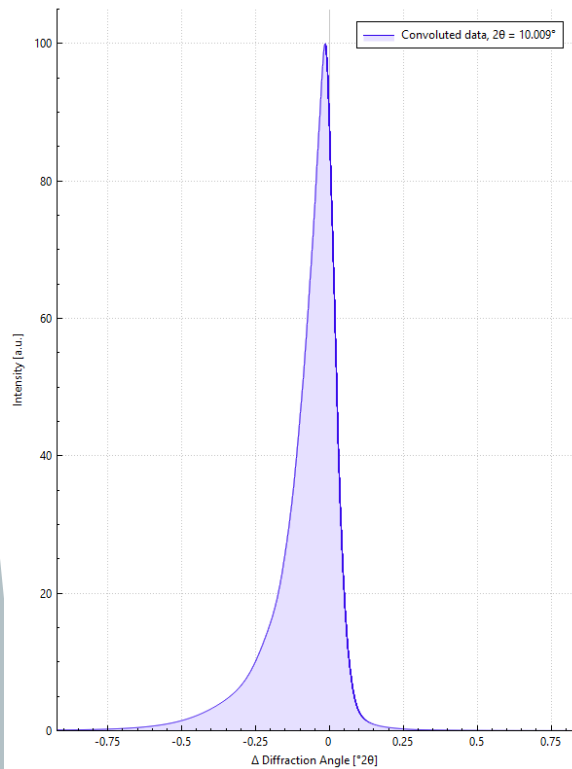


# Fundamental Parameters Approach (FPA)

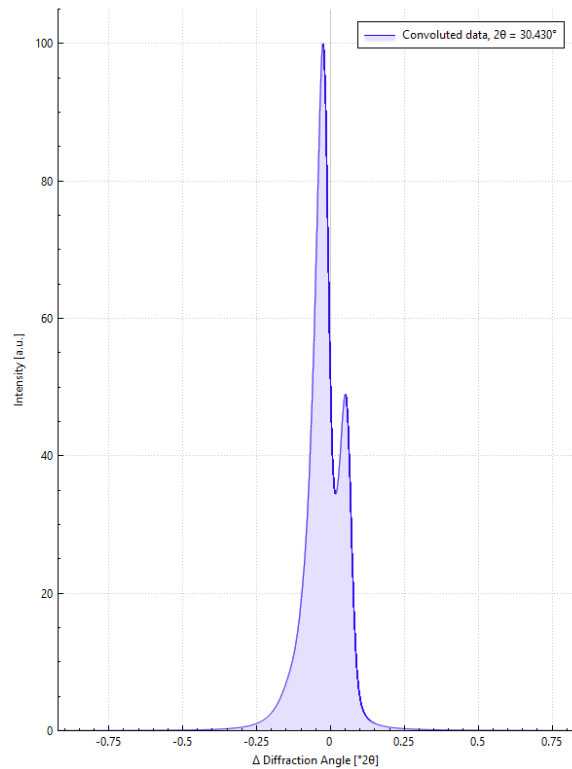


# Fundamental Parameters Approach (FPA)

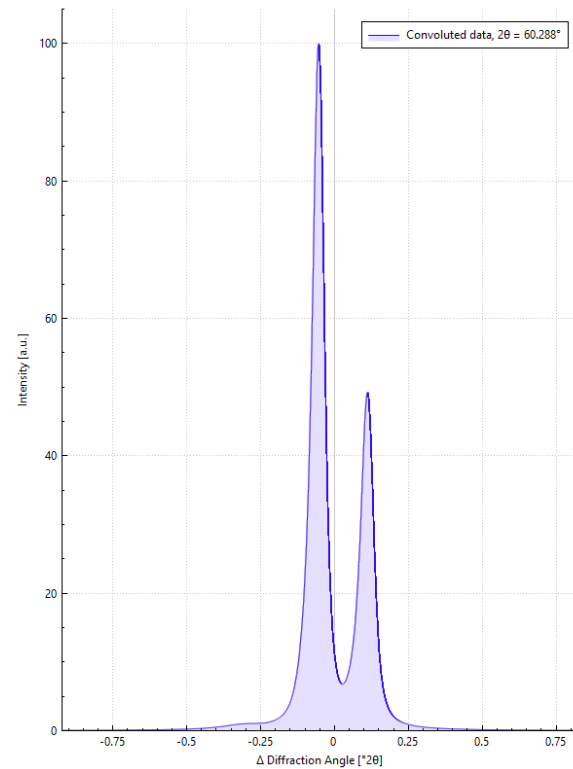
## Calculated Peak Profiles



$2\theta=10^\circ$



$2\theta=30^\circ$

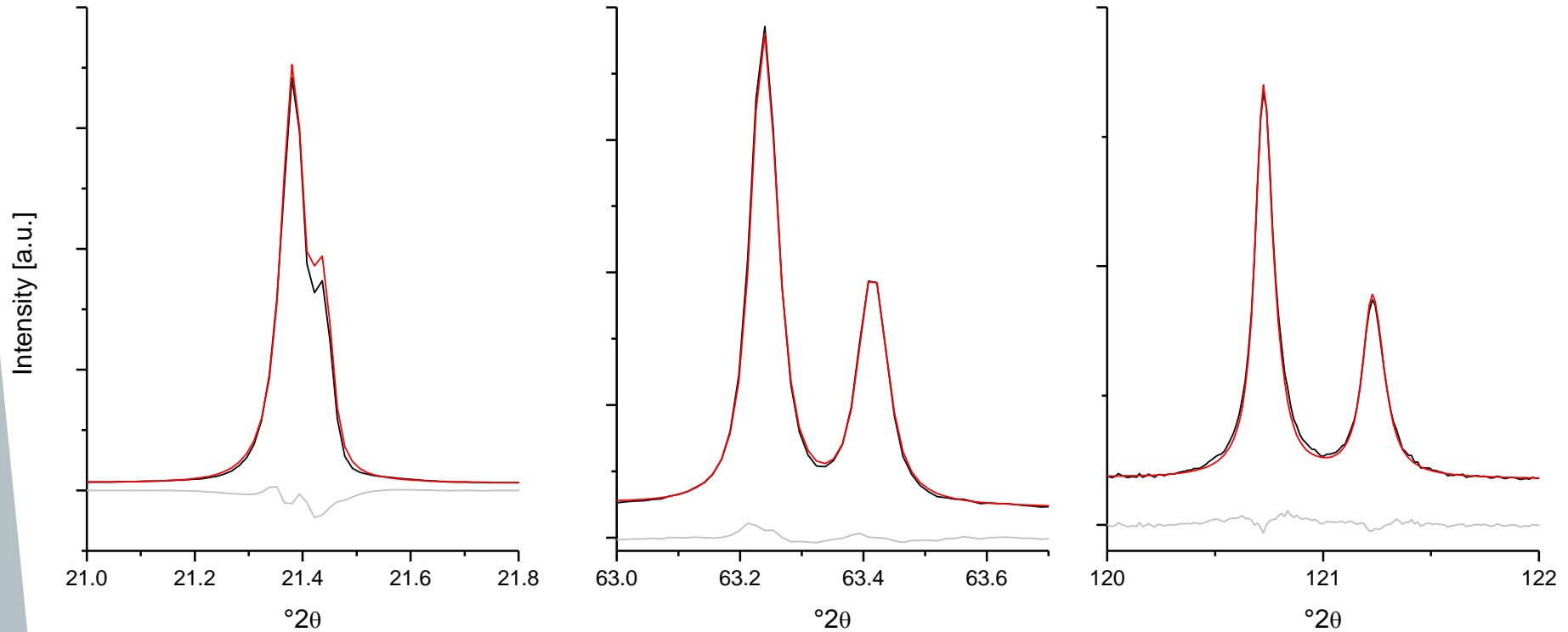


$2\theta=60^\circ$



# Fundamental Parameters Approach

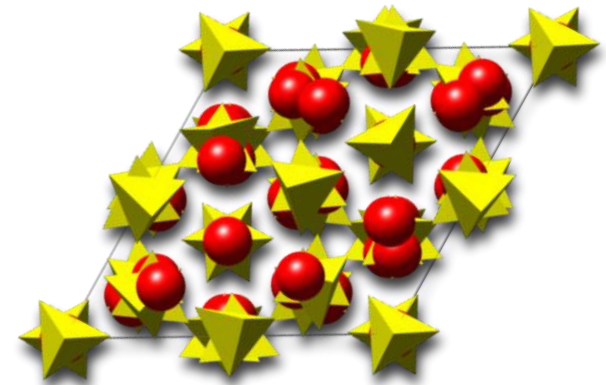
If done properly:



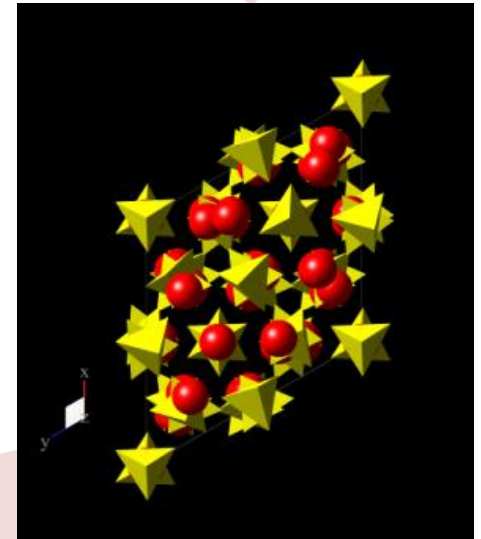
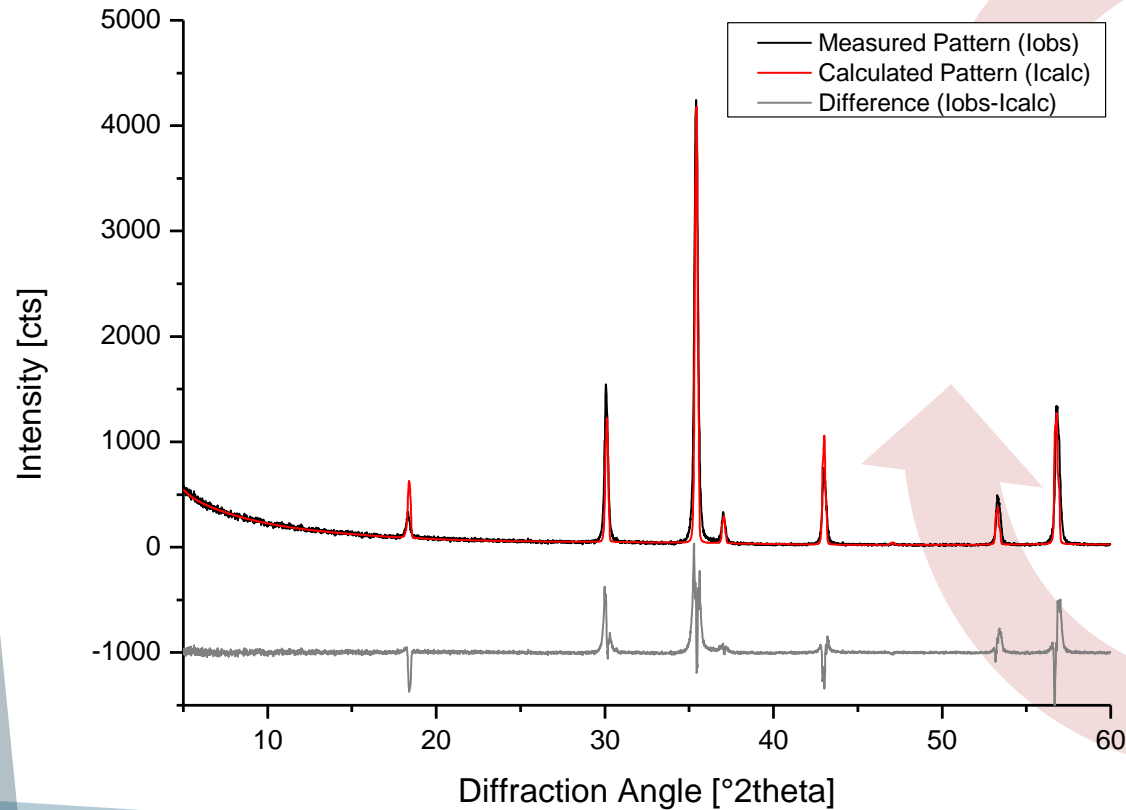
Very good description of the peak profile

# Summary: Rietveld Refinement Basics

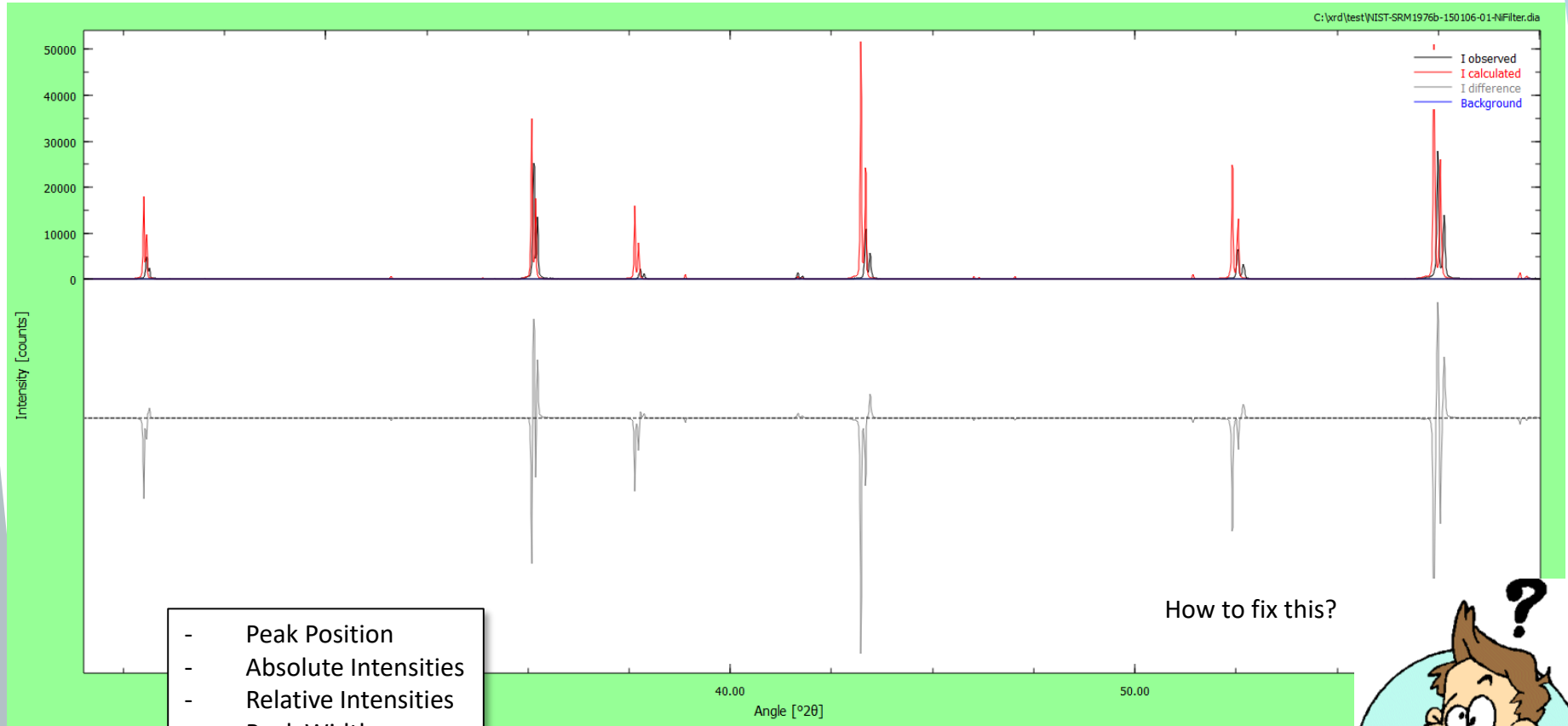
- Step 1: Phase identification
- Step 2: Obtain crystal structure models for all phases
- Step 3: Rietveld refinement:
  - Calculate XRD pattern from model structure
  - Minimize differences between calculated and measured pattern
- Accurate mathematical description of peak profile required:
  - Classical Rietveld approach: Fit a peak shape function (PV or similar) to reference pattern
  - Fundamental Parameters Approach: Calculate peak profile from device configuration



## Relation between Pattern Features and Structural Features



# Refinement Strategies

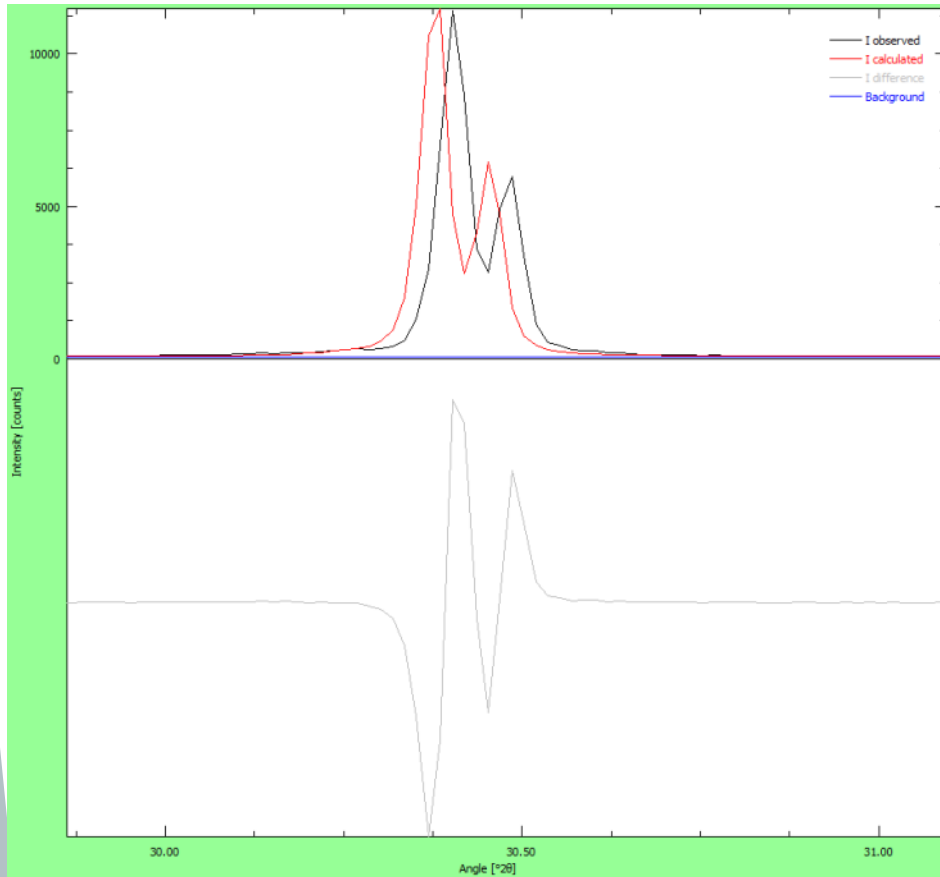


- Peak Position
- Absolute Intensities
- Relative Intensities
- Peak Width

How to fix this?



# Refinement Strategies



Wrong peak positions

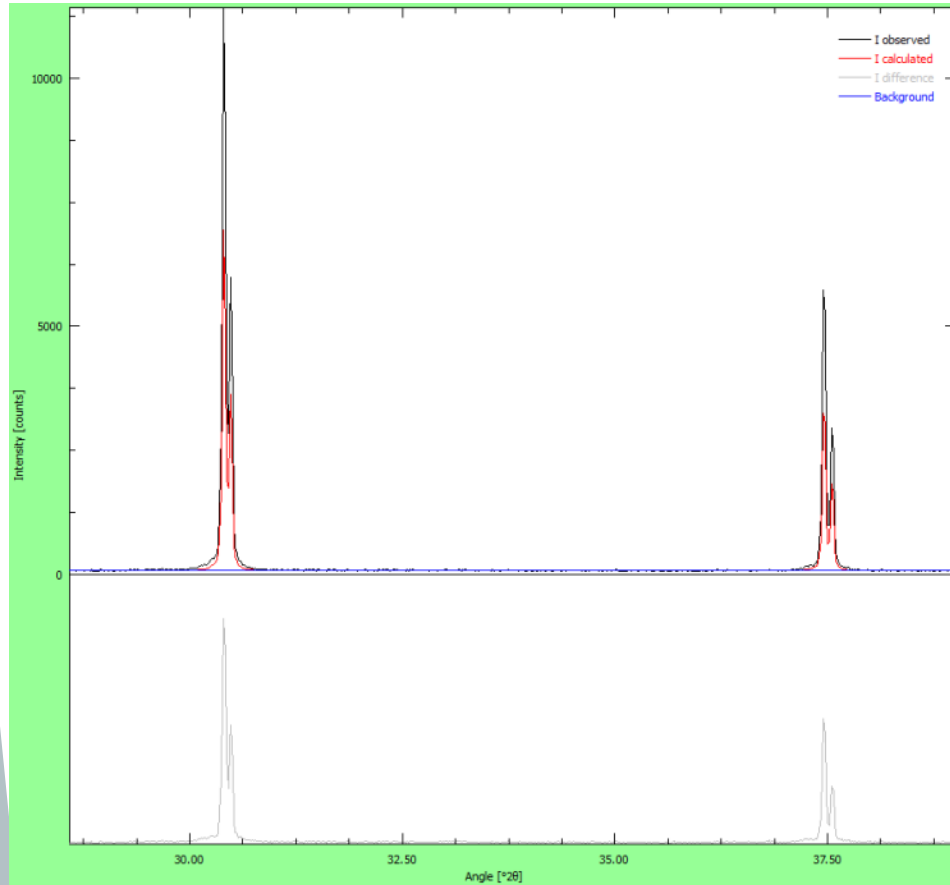
Cause:

- ▶ Cell parameters
- ▶ Sample height displacement
- ▶ Instrument misalignment

Solution:

Refine cell parameters  
(and sample height displacement)

# Refinement Strategies



Wrong absolute intensities

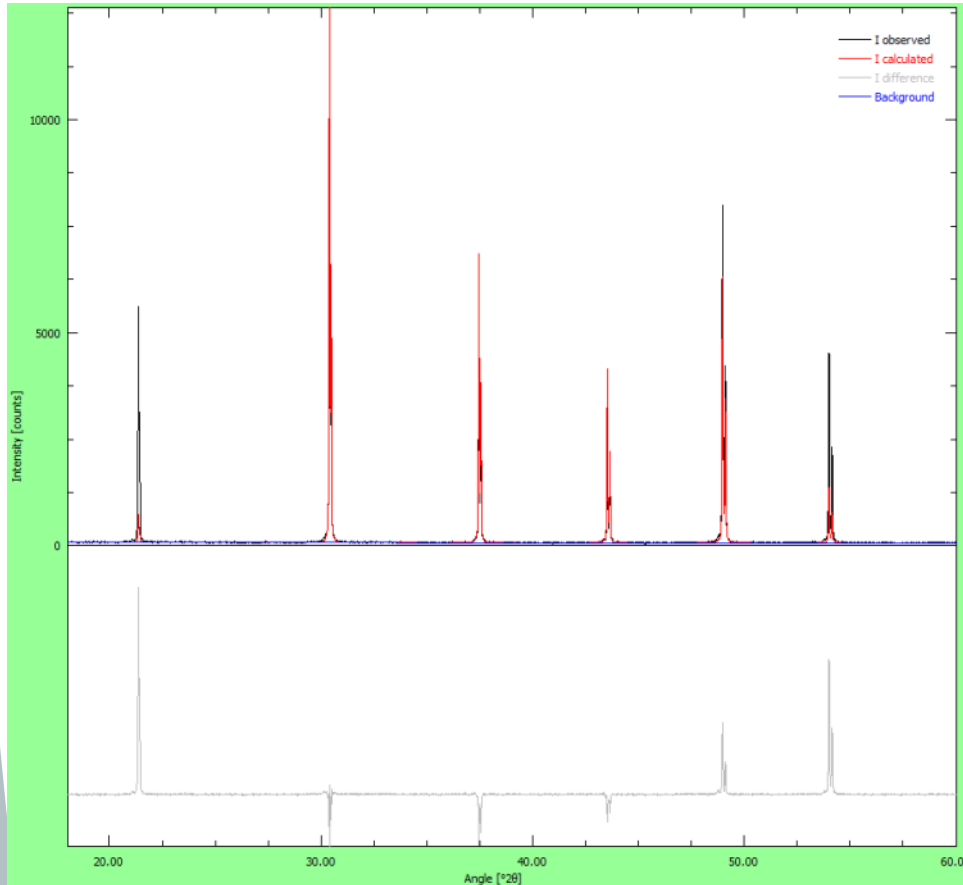
Cause:

- ▶ Weight fraction (scaling)

Solution:

Refine phase scale factor

# Refinement Strategies



## Wrong relative intensities

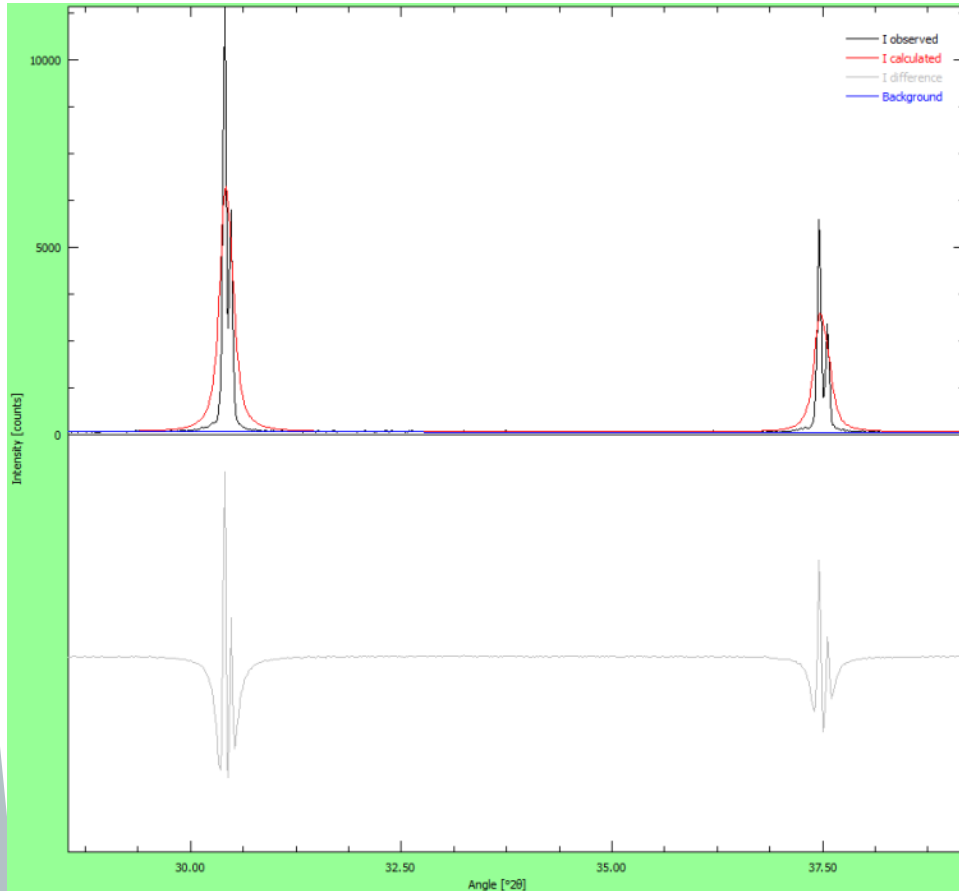
### Cause:

- Texture / Preferred orientation
- Graininess
- Atomic species / substitutions
- Atomic coordinates / site occupancies / thermal displacement

### Solution:

1. Check sample quality
2. Refine texture
3. Full structure refinement (atomic parameters)

# Refinement Strategies



Wrong peak width

Cause:

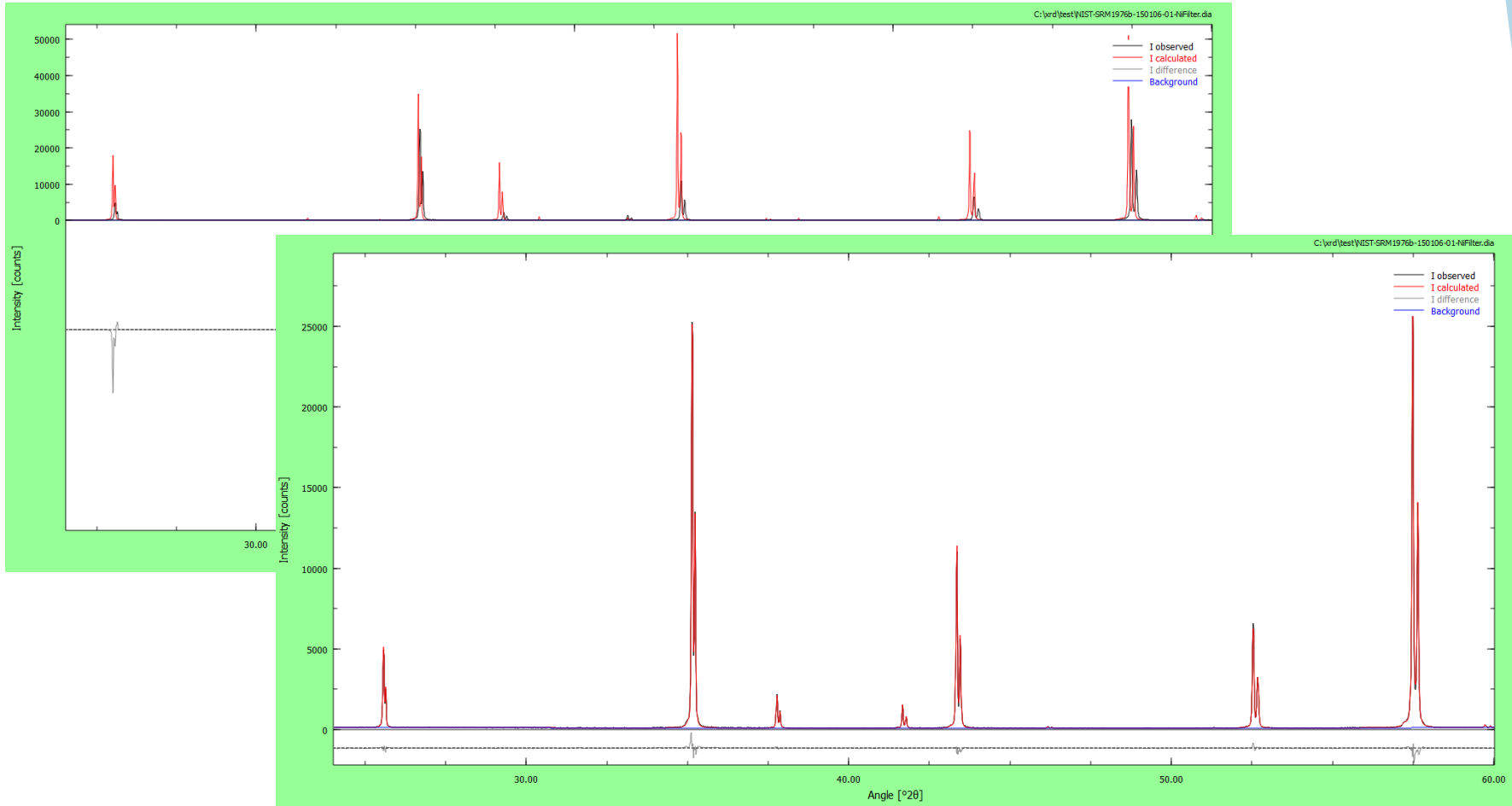
- ▶ Crystallite size
- ▶ Micro-strain
- ▶ Surface roughness
- ▶ Sample transparency

Solution:

Refine crystallite size  
and / or micro-strain



# Refinement Strategies



# Refinement Strategies

Phase composition: 100% Al<sub>2</sub>O<sub>3</sub> Corundum

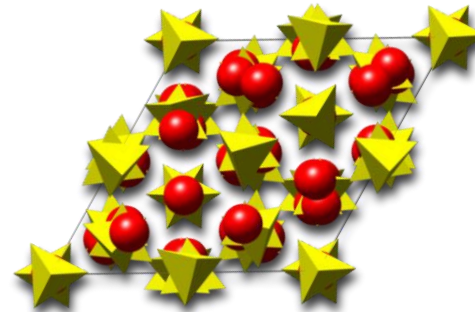
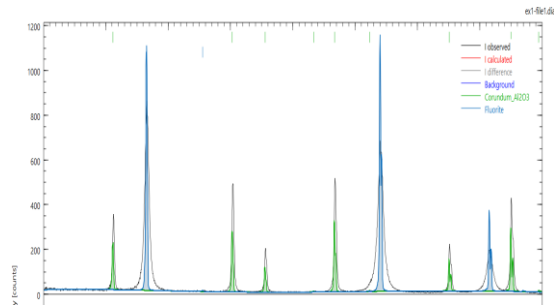
Starting Model

| Parameter             | Value               |
|-----------------------|---------------------|
| Unit cell <i>a</i>    | 0.4775 nm           |
| Unit cell <i>c</i>    | 1.2993 nm           |
| Crystallite Size      | Inf.                |
| Atomic Coordinates Al | 0.0 / 0.0 / 0.3522  |
| Atomic Coordinates O  | 0.3062 / 0.0 / 0.25 |

Refined

| Parameter             | Value                        |
|-----------------------|------------------------------|
| Unit cell <i>a</i>    | 0.4760127 +-<br>0.0000028 nm |
| Unit cell <i>c</i>    | 1.2995974 +-<br>0.0000077 nm |
| Crystallite Size      | 1267 +- 138 nm               |
| Atomic Coordinates Al | 0.0 / 0.0 / 0.3522           |
| Atomic Coordinates O  | 0.3062 / 0.0 / 0.25          |

# Summary: Refinement Strategies



| Observation in diffraction pattern | Origin in crystal structure model   |
|------------------------------------|---|
| Wrong peak positions               | Unit cell dimensions<br>Sample height displacement  |
| Wrong absolute intensities         | Weight fraction (scaling)   |
| Wrong relative intensities         | Preferred orientation<br>Atomic species / substitutions / vacancies<br>Atomic coordinates / displacement parameters |
| Wrong peak width                   | Crystallite size<br>Micro-strain  |