

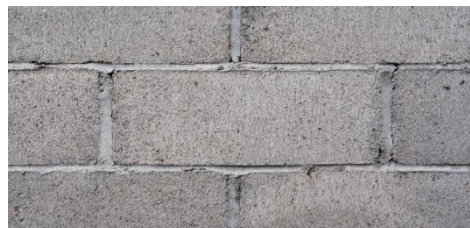
# QPA of crystalline and amorphous phase abundance with XRPD techniques: bases and methods

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- *Introduction to X-Ray Powder Diffractometry*, Jenkins & Snyder, . Publisher, Wiley 1996.
- *Quantitative X-Ray Diffractometry*, Zevin & Kimmel, Springer-Verlag, New York, 1996.
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## Articles & Reviews

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- D.L. Bish & S.A. Howard, *Quantitative phase analysis using the Rietveld method*, J. Appl. Cryst. 1988. **21**, 86-91.
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## QPA of amorphous phases, a small selection:

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- X. Chen, S. Bates & K.R. Morris, *Quantifying amorphous content of lactose using parallel beam X-ray powder diffraction and whole pattern fitting*, J. Pharm. Biomed Anal. 26 (2001) 63-72.
- S. Thakral, M.W. Terban, N. K. Thakral & R. Suryanarayanan, *Recent advances in the characterization of amorphous pharmaceuticals by X-ray diffractometry*, Adv. Drug Deliv. Rev. (2015), <http://dx.doi.org/10.1016/j.addr.2015.12.013>

# Outlook

- I. Defining the QPA problem
- II. Mathematical background
- III. Diffraction methods as a DIRECT method for QPA
- IV. Single-peak (or single-line) QPA methods
- V. Whole patterns QPA methods → Rietveld and Rietveld-like methods
- VI. Quantification methods for amorphous phases

## I. Defining the QPA problem

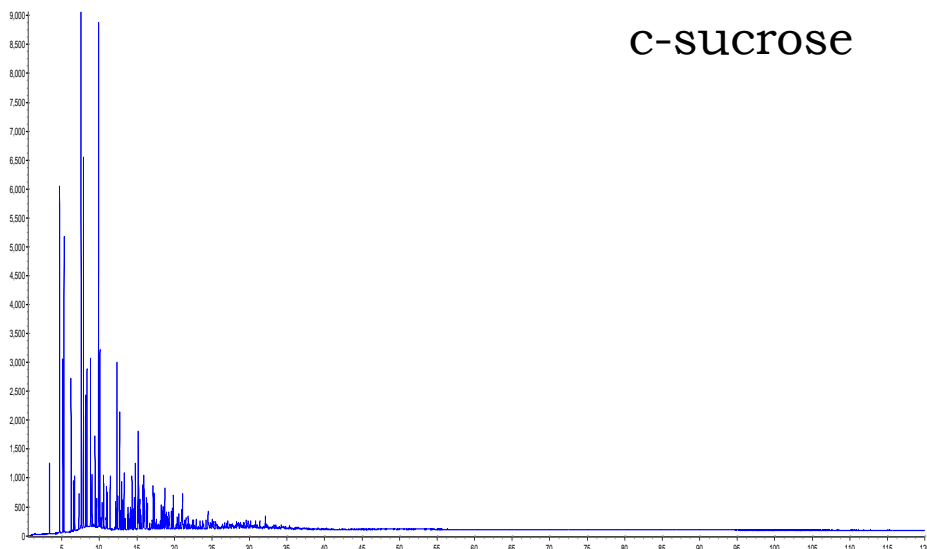
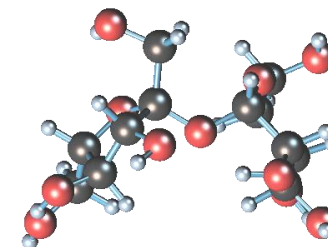
# Qualitative *versus* Quantitative phase analysis

Principal use of powder diffraction technique is the identification of crystalline or disordered structures (or phases)

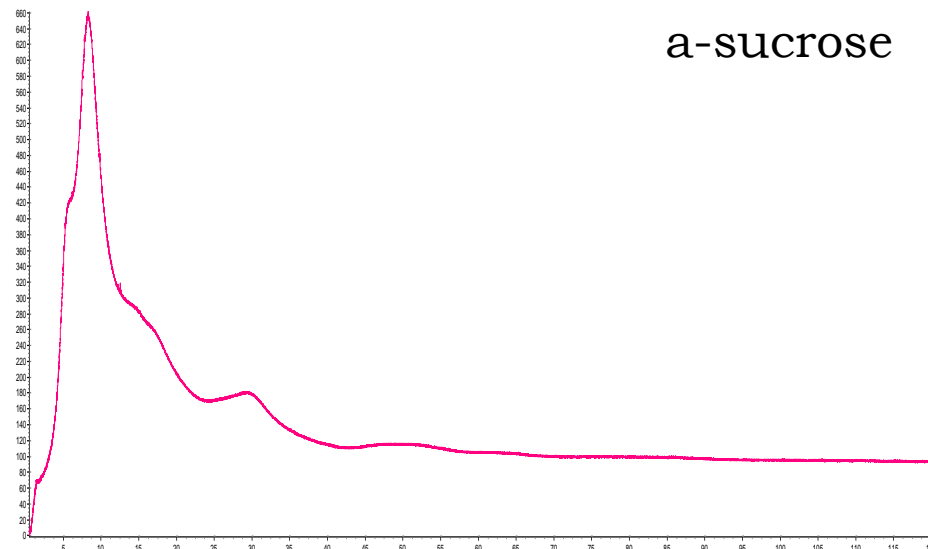
## Why?

A powder pattern is DIRECTLY produced by the structure of the component phases and can, therefore, fingerprint them

Sucrose:  $C_{12}H_{22}O_{11}$

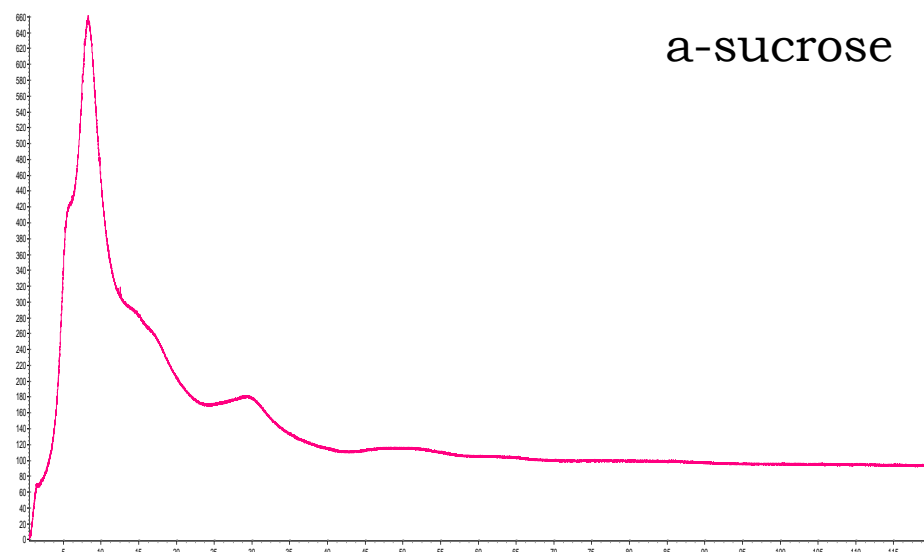
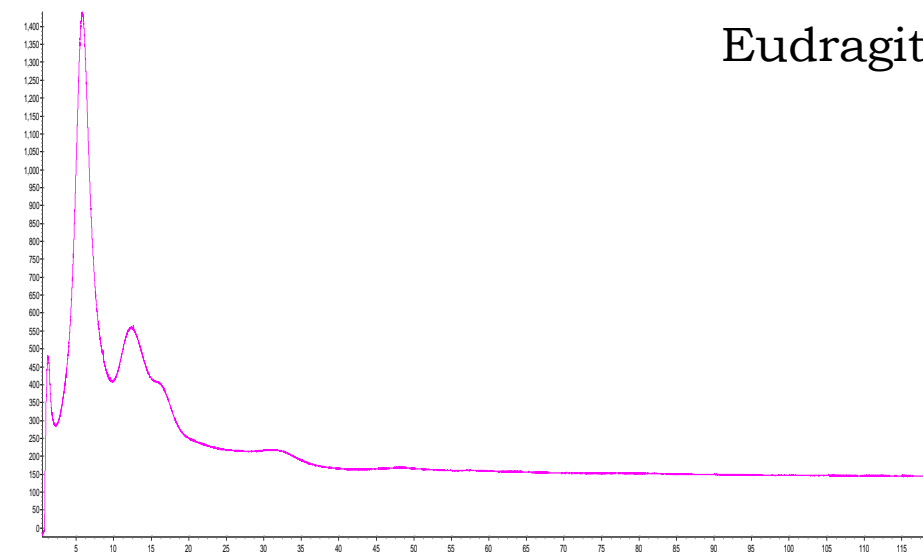
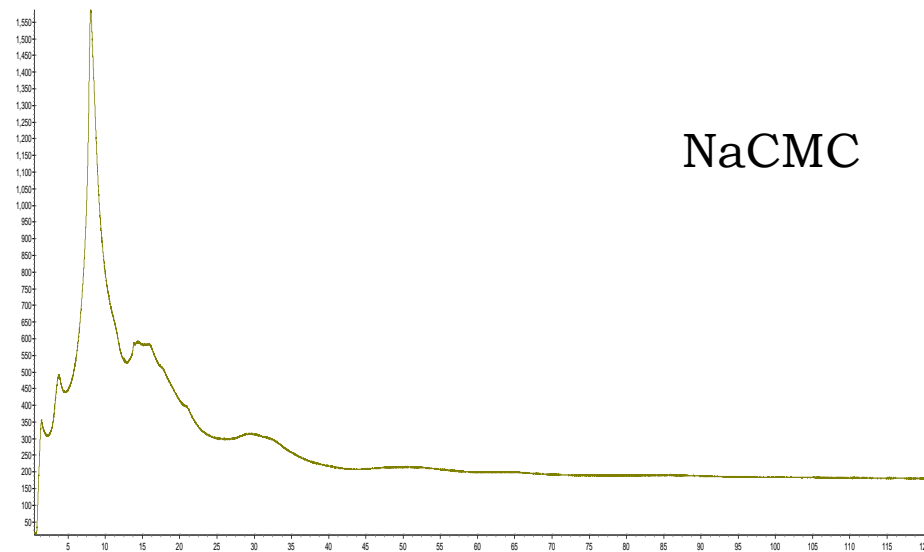
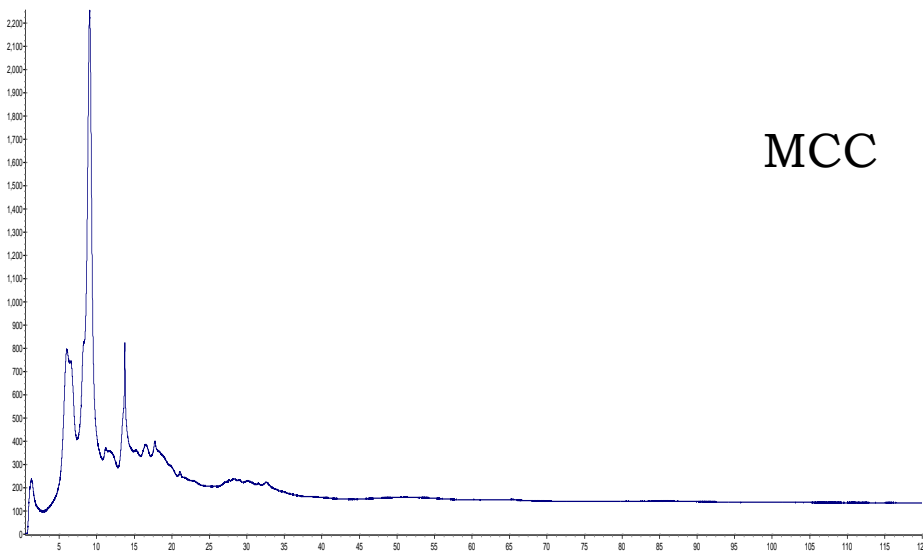


β-sucrose

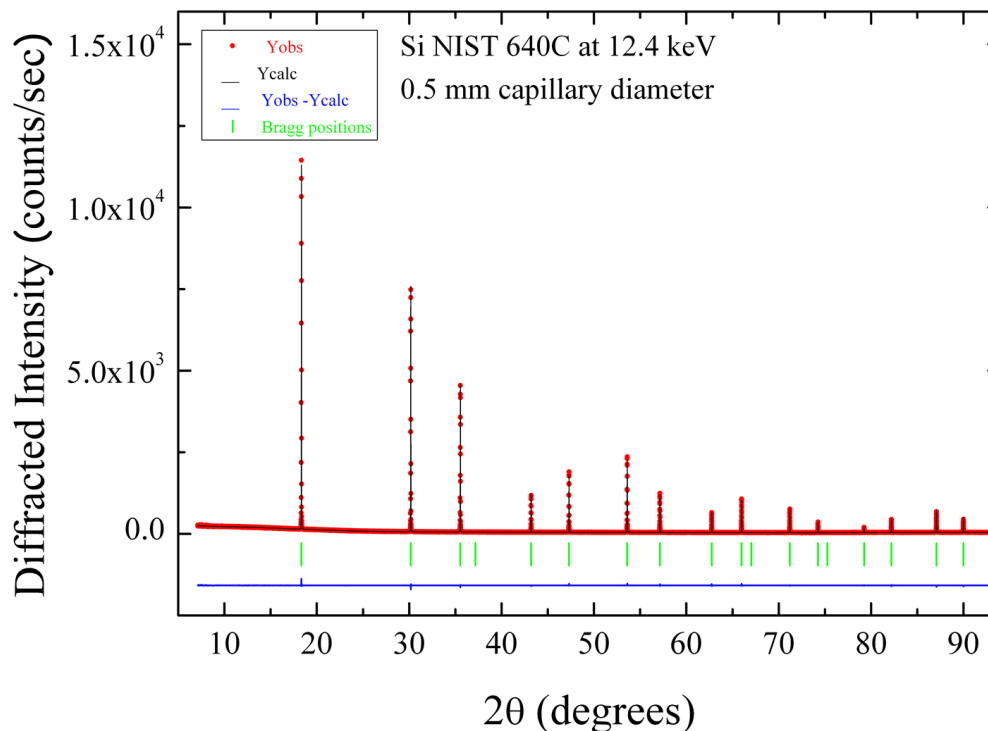


α-sucrose

# I. Defining the QPA problem



## What do we learn from a powder pattern of a crystalline structure?



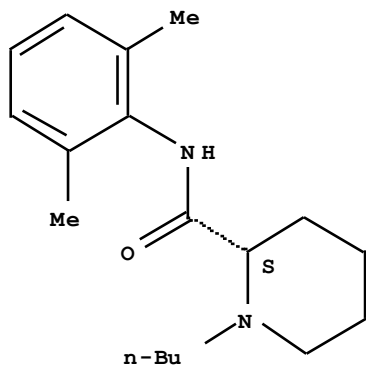
- Position of the diffracted peaks → size and dimension of the unit cell
- Intensity ratios of the diffracted peaks → type and location of atoms in the unit cell
- Full Width at Half Maximum (FWHM) of the diffracted peaks → intrinsic properties of the materials (i.e. microstructural analysis)



## Polymorphism of drugs

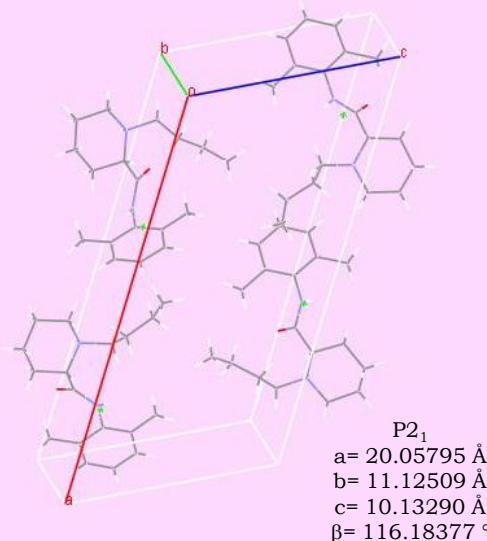
Polymorphism is the ability of substances with **identical chemical composition** to crystallize in solid state phases according to different arrangements or conformations of the basic molecule(s) in the crystal lattice

Example of  
Bupivacaine Hydrochloride

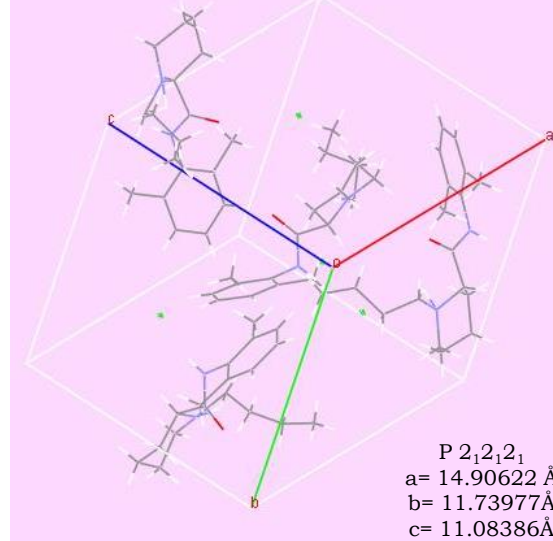


● HCl

**Form B at 112 °C, monoclinic**



**Form D at 20 °C, orthorhombic**



*Gozzo, Masciocchi, Griesser, Niederwanger, 2010*

Forms B and D share the same chemical composition, but have different solid forms

→ They are different polymorphs!

# Quantitative Phase Analysis (QPA)

QPA refers to the ability of quantitatively state the abundance of the different phases that constitute a mixture.

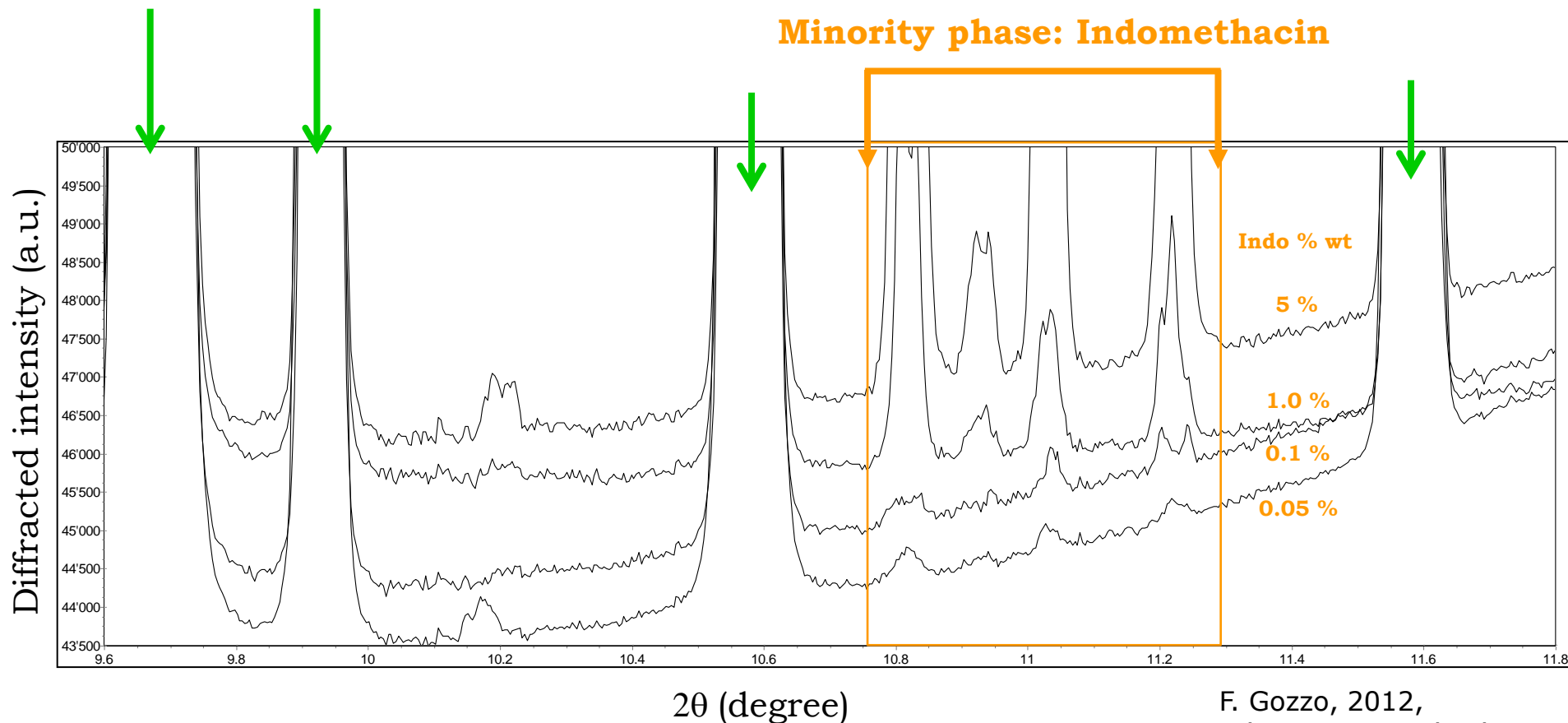
## Why is this relevant?

- ❑ **Polymorphic purity**: detect and quantify unwanted polymorphic forms in both drug substance and drug product
  - Level of Detection (LoD)
  - Level of Quantitation (LoQ)
- ❑ Assess the **polymorphic composition** in drug substance and product
- ❑ In formulated materials, the **API/excipients relative proportion** is important and needs to be kept under control
- ❑ **Degree of Crystallinity** in amorphous/crystalline mixtures

# QPA of a binary API physical mixtures with fast SR-XRPD

Majority phase (intensity up to 1.5 M counts): Haloperidol

Minority phase: Indomethacin



F. Gozzo, 2012,  
private communication

## QPA analytical methods

Several are the analytical methods used to obtain quantitative phase related information:

- Based on chemical composition (so-called *normative calculation*)
- Based on properties specific to the phases of interest (e.g. magnetism, selective dissolution, density)
- Spectroscopic methods (e.g. Raman and Infrared spectroscopy, Mass spectroscopy, Nuclear Magnetic Resonance spectroscopy)
- Thermal Methods (e.g. Differential Scanning Calorimetry, ThermoGravimetric Analysis)
- Diffraction Methods → XRPD

**Direct method**

Information is directly produced by the crystal structure of the component phases in the mixture


## QPA analytical methods

Several are the analytical methods used to obtain quantitative phase related information:

- Based on chemical composition (so-called *normative calculation*)
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- Spectroscopic methods (e.g. Raman and Infrared spectroscopy, Mass spectroscopy, Nuclear Magnetic Resonance spectroscopy)
- Thermal Methods (e.g. Differential Scanning Calorimetry, ThermoGravimetric Analysis)
- Scattering Methods → XRPD

**Direct method**

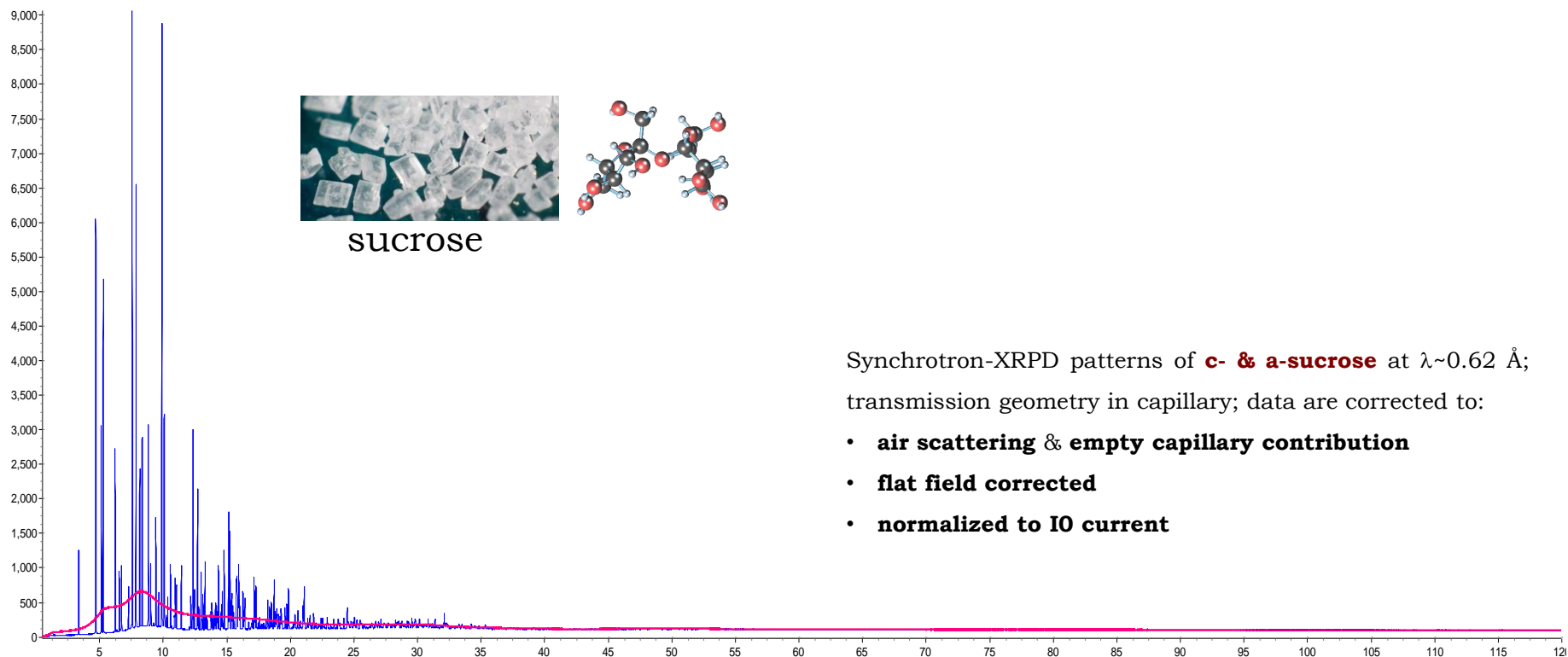
Information is directly produced by the structure of the component phases in the mixture

QPA  determining the contribution (typically in % weight) of each component phase in a mixture

Do the phases in the mixture need to be crystalline to perform their quantitative phase analysis?

Vainshtein's law:

*within identical regions of reciprocal space, the scattered intensities from a material are independent of its state of order*

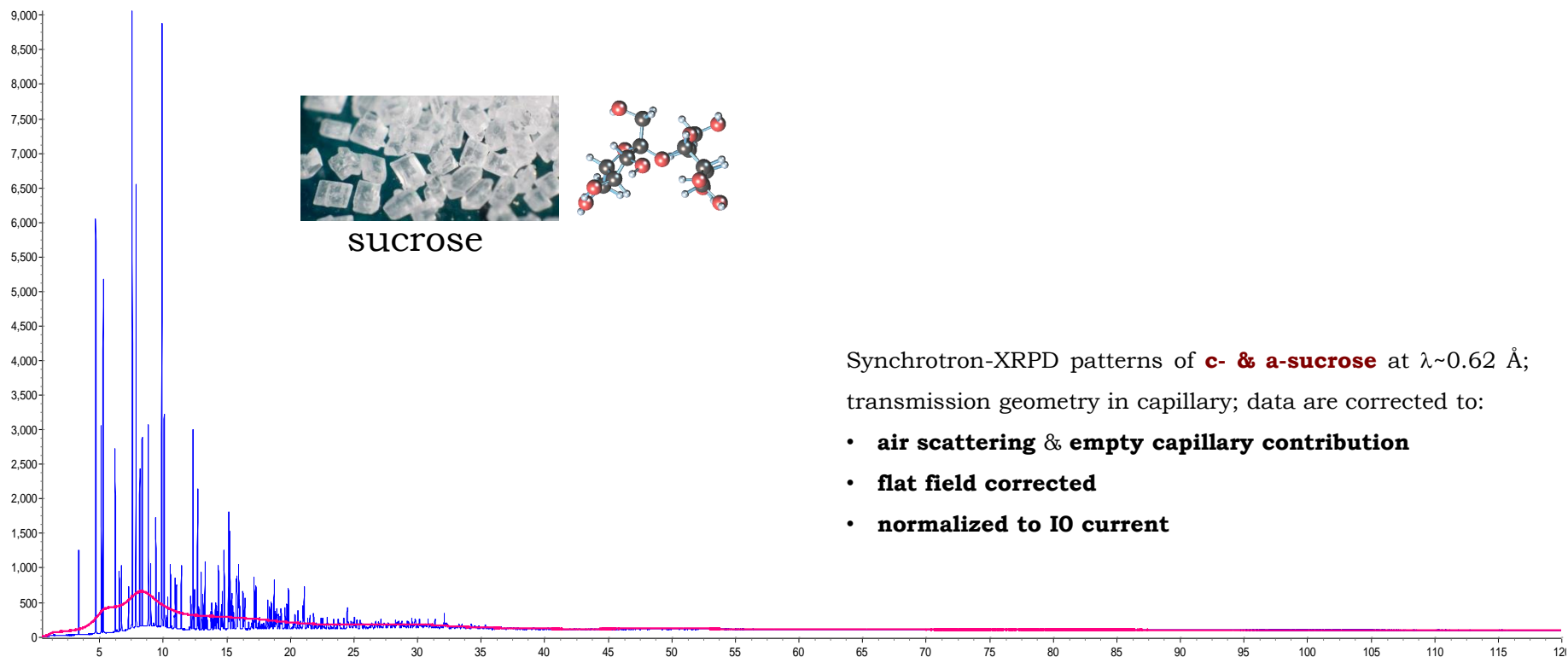


Synchrotron-XRPD patterns of **c- & a-sucrose** at  $\lambda \sim 0.62 \text{ \AA}$ ; transmission geometry in capillary; data are corrected to:

- **air scattering & empty capillary contribution**
- **flat field corrected**
- **normalized to IO current**



Quantification methods developed for crystalline phases can, therefore, often be also used for the indirect or direct quantification of amorphous phases



Synchrotron-XRPD patterns of **c- & a-sucrose** at  $\lambda \sim 0.62 \text{ \AA}$ ; transmission geometry in capillary; data are corrected to:

- **air scattering & empty capillary contribution**
- **flat field corrected**
- **normalized to I0 current**

## DIFFRACTION-BASED QPA METHODS

### Single-peak methods:

- Intensity ratio  $I_{\text{unknown}}/I_{\text{standard}}$  of one or more reflections
- No need of structural information but prone to systematic errors (e.g. caused by preferential orientation and peak overlapping)
- Need *ad-hoc* mixtures for calibration curves

### Rietveld-based methods:

- Use of full diffraction patterns
- Minimization of systematic errors (e.g. due to peak overlap)
- Preferential Orientation (PO) can be modeled
- Accuracy close to X-Ray fluorescence elemental analysis, with the advantage of being sensitive to structural differences → direct QPA of polymorphs

## DIFFRACTION-BASED QPA METHODS

### Single-peak methods:

(adapted from Cullity, *Elements of X-Ray Diffraction*)

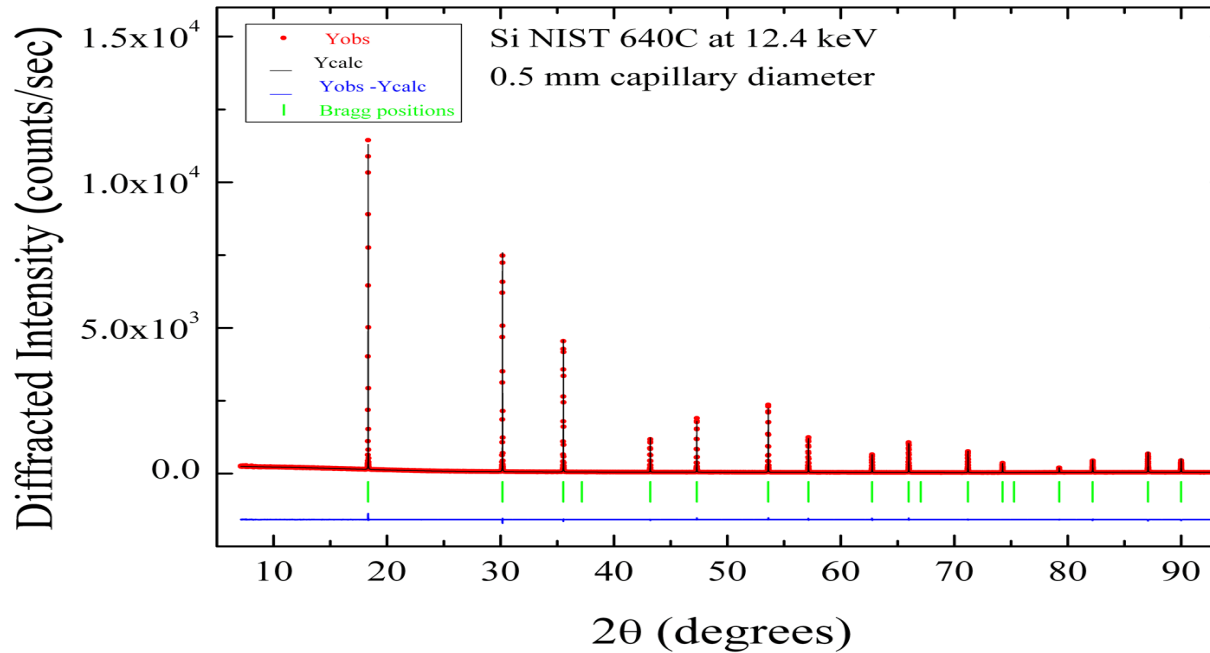
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### Rietveld-based methods:

(adapted from Madsen & Scarlett in *Powder Diffraction-Theory and Practice*)

- Use of full diffraction patterns
- Minimization of systematic errors (e.g. due to peak overlap)
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# QPA with diffraction methods: math background



The diffracted intensity distribution is defined by:

**Structural factors**

→ crystal structure

**Specimen factors**

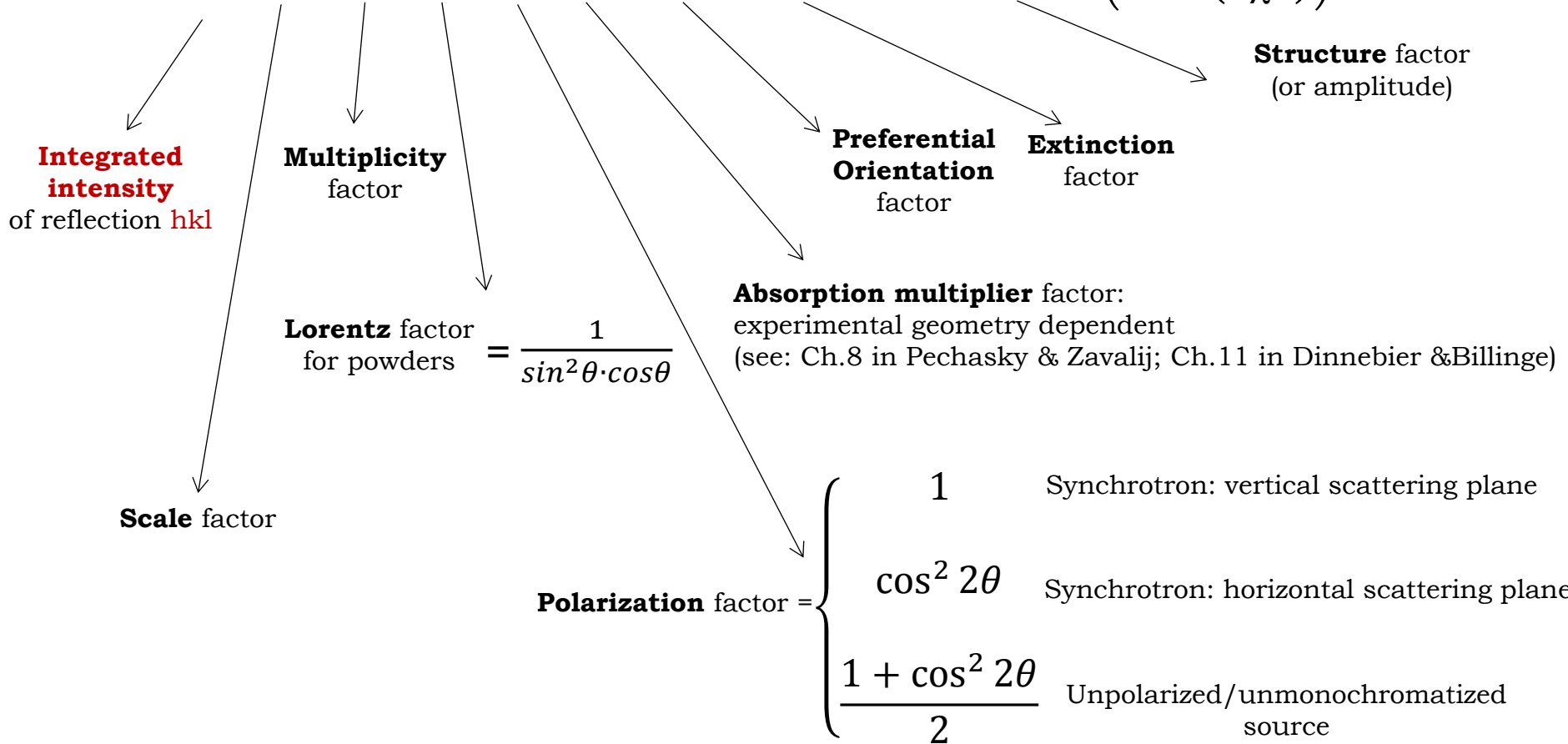
→ preferential orientation, grain size, shape and distribution, microstructure

**Instrumental factors**

→ properties of radiation, optics geometry, properties of detectors, slits and/or monochromator

For a powder diffraction pattern of a **pure crystalline phase** we can write:

$$I_{hkl} = K \cdot M_{hkl} \cdot L_{\theta} \cdot P_{\theta} \cdot A_{\theta} \cdot PO_{hkl} \cdot E_{hkl} \cdot |F_{(hkl)}|^2 \cdot \exp\left(-2B \left(\frac{\sin \theta}{\lambda}\right)\right)$$



For a powder diffraction pattern of a **pure crystalline phase** we can write:

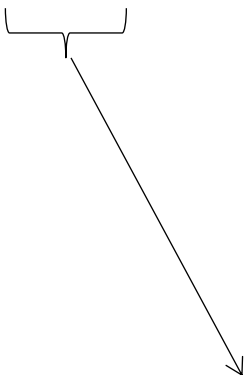
$$I_{hkl} = K \cdot M_{hkl} \cdot L_{\theta} \cdot P_{\theta} \cdot A_{\theta} \cdot PO_{hkl} \cdot E_{hkl} \cdot |F_{(hkl)}|^2 \cdot \exp\left(-2B \left(\frac{\sin \theta}{\lambda}\right)\right)$$

**Lorentz** factor  
for powders =  $\frac{1}{\sin^2 \theta \cdot \cos \theta}$

**Polarization** factor =  $\begin{cases} 1 & \text{Synchrotron: vertical scattering plane} \\ \cos^2 2\theta & \text{Synchrotron: horizontal scattering plane} \\ \frac{1 + \cos^2 2\theta}{2} & \text{Unpolarized/unmonochromatized source} \end{cases}$

For a powder diffraction pattern of a **pure crystalline phase** we can write:

$$I_{hkl} = K \cdot M_{hkl} \cdot \underbrace{L_{\theta} \cdot P_{\theta} \cdot A_{\theta}} \cdot PO_{hkl} \cdot E_{hkl} \cdot |F_{(hkl)}|^2 \cdot \exp\left(-2B \left(\frac{\sin \theta}{\lambda}\right)\right)$$



**Lorentz-Polarization factor** for powders =  $\frac{1 + \cos^2 2\theta \cos^2 2\theta_M}{\sin^2 \theta \cdot \cos \theta}$

**Lab XRPD:**

$2\theta_M$  is the Bragg angle of the reflection from a monochromator,  $2\theta_M = 0$  for unpolarized unmonochromatized source,  $2\theta_M \neq 0$  (e.g.  $26.5^\circ$  graphite mono +  $\text{CuK}\alpha$  radiation)

**Synchrotron XRPD:**

$2\theta_M$  is the angle between the scattering direction (where we place our detector!) and the direction of acceleration of the electron (e.g. the direction of the electric field of the synchrotron e.m. radiation). In the vertical plane this is always  $90^\circ$ .

For a powder diffraction pattern of a **pure crystalline phase** we can write:

$$I_{hkl} = K \cdot M_{hkl} \cdot L_{\theta} \cdot P_{\theta} \cdot A_{\theta} \cdot PO_{hkl} \cdot E_{hkl} \cdot |F_{(hkl)}|^2 \cdot \exp\left(-2B \left(\frac{\sin \theta}{\lambda}\right)\right)$$



negligible

Under the hypothesis of **A**, **PO** and **E negligible**, transmission (Debye-Scherrer) geometry, synchrotron radiation with vertical diffraction plane (as at the SLS-MS-PD), with powders loaded in capillaries and a 1D display detector (e.g. Mythen II):

$$I_{hkl} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V^2} \cdot |F_{(hkl)}|^2 \cdot \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp\left(-2B \left(\frac{\sin \theta}{\lambda}\right)\right) \cdot \left[ \frac{1}{\mu} \right]$$

$I_0$	incident beam intensity	$\mu = \rho \mu^*$	linear absorption (attenuation) coefficient of the pure phase
$\lambda$	photon beam wavelength		
$\sigma$	cross sectional area of incident beam	with $\rho$ and $\mu^*$	density of the pure phase and its mass absorption coefficient
$e$	charge of the electron		
$m_e$	mass of the electron		
$c$	speed of light	$\exp(-2B \left(\frac{\sin \theta}{\lambda}\right))$	thermal factor, B is the mean Atomic Displacement Parameter (ADP)
$V$	unit cell volume		



For a powder diffraction pattern of a **mixture** (e.g. binary  $\alpha+\beta$  mixture), for a hkl intensity line of phase  $\alpha$ , we can write:

$$I_{(hkl)\alpha} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V_\alpha^2} \cdot |F_{hkl}|_\alpha^2 \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp \left( -2B_\alpha \left( \frac{\sin \theta}{\lambda} \right) \right) \cdot \left[ \frac{c_\alpha}{\mu_m} \right]$$

$I_0$	incident beam intensity	$c_\alpha$	volume fraction of phase $\alpha$
$\lambda$	photon beam wavelength	$\mu_m = \rho_m \cdot \mu_m^*$	linear absorption (attenuation) coefficient of the entire mixture
$\sigma$	cross sectional area of incident beam		
$e$	charge of the electron		
$m_e$	mass of the electron	with $\rho_m$ and $\mu_m^*$	density of the entire mixture and its mass coefficient
$c$	speed of light		
$r$	distance scattering electron-detector	$\exp(-2B \left( \frac{\sin \theta}{\lambda} \right))$	thermal factor, with B mean Atomic Displacement Parameter (ADP)
$V_\alpha$	unit cell volume of phase $\alpha$		

And similarly, for a h'k'l' line of phase  $\beta$ , we can write:

$$I_{(h'k'l')\beta} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V_\beta^2} \cdot |F_{(h'k'l')}|_\beta^2 \cdot \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp \left( -2B_\beta \left( \frac{\sin \theta}{\lambda} \right) \right) \cdot \left[ \frac{c_\beta}{\mu_m} \right]$$

For a powder diffraction pattern of a **mixture** (e.g. binary  $\alpha+\beta$  mixture), for a hkl intensity line of phase  $\alpha$ , we can write:

$$I_{(hkl)\alpha} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V_\alpha^2} \cdot |F_{hkl}|_\alpha^2 \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp \left( -2B_\alpha \left( \frac{\sin \theta}{\lambda} \right) \right) \cdot \left[ \frac{c_\alpha}{\mu_m} \right]$$

All factors are constant and independent of the concentration of the  $\alpha$  phase with the exception of  $c_\alpha$  and  $\mu_m$



$$I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot c_\alpha}{\mu_m} \quad \text{and equivalently:} \quad I_{(hkl)\beta} = \frac{K_{1,\beta} \cdot c_\beta}{\mu_m}$$

The simplified expression:  $I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot c_{\alpha}}{\mu_m}$  can also be written in terms of weight

fractions  $w_{\alpha}$  (and  $w_{\beta}$ ):  $I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot w_{\alpha} \cdot \rho_m}{\mu_m \cdot \rho_{\alpha}} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \frac{\mu_m}{\rho_m}} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \mu_m^*}$  with  $\rho_{\alpha}$  the density

of phase  $\alpha$  and  $\mu_m^*$  the mass absorption coefficient ( $= \frac{\mu_m}{\rho_m}$ ) of the entire mixture.

DEMO:

Assuming a unit volume of mixture ( $V_m=1$ ):  $\rho_m$ =density of mixture=weight of mixture  $\rightarrow w_{\alpha}\rho_m$  and  $w_{\beta}\rho_m$  represent the weights of the  $\alpha$  and  $\beta$  contents in our binary mixture with  $w_{\alpha}$  and  $w_{\beta}$  the weight fractions  $\rightarrow \rho_{\alpha} = \frac{w_{\alpha}\rho_m}{c_{\alpha}} \rightarrow c_{\alpha} = \frac{w_{\alpha}\rho_m}{\rho_{\alpha}}$  and equivalently  $c_{\beta} = \frac{w_{\beta}\rho_m}{\rho_{\beta}} \rightarrow \frac{c_{\alpha}}{\mu_m} =$

$\frac{w_{\alpha}\rho_m}{\rho_{\alpha}\mu_m} = \frac{w_{\alpha}}{\rho_{\alpha}} \cdot \frac{1}{\mu_m^*}$  with  $\mu_m$  linear absorption (or attenuation) coefficient and  $\mu_m^*$  mass absorption coefficient.

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fractions  $w_{\alpha}$  (and  $w_{\beta}$ ):  $I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot w_{\alpha} \cdot \rho_m}{\mu_m \cdot \rho_{\alpha}} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \frac{\mu_m}{\rho_m}} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \mu_m^*}$  with  $\rho_{\alpha}$  the density

of phase  $\alpha$  and  $\mu_m^*$  the mass absorption coefficient ( $= \frac{\mu_m}{\rho_m}$ ).

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$\frac{w_{\alpha}\rho_m}{\rho_{\alpha}\mu_m} = \frac{w_{\alpha}}{\rho_{\alpha}} \cdot \frac{1}{\mu_m^*}$  with  $\mu_m$  linear absorption (or attenuation) coefficient and  $\mu_m^*$  mass absorption coefficient.

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fractions  $w_{\alpha}$  (and  $w_{\beta}$ ):  $I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot w_{\alpha} \cdot \rho_m}{\mu_m \cdot \rho_{\alpha}} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \frac{\mu_m}{\rho_m}} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \mu_m^*}$  with  $\rho_{\alpha}$  the density

of phase  $\alpha$  and  $\mu_m^*$  the mass absorption coefficient ( $= \frac{\mu_m}{\rho_m}$ ).

If we can access a powder sample of pure phase  $\alpha$ :  $I_{(hkl)\alpha,pure} = \frac{K_{1,\alpha}}{\rho_{\alpha} \mu_{\alpha}^*} = \frac{K_{1,\alpha}}{\mu_{\alpha}}$

and we can write:  $\frac{I_{(hkl)\alpha}}{I_{(hkl)\alpha,pure}} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \frac{\mu_m}{\rho_m}} \cdot \frac{\mu_{\alpha}}{K_{1,\alpha}} = \frac{w_{\alpha} (\mu_{\alpha} / \rho_{\alpha})}{(\mu_m / \rho_m)} = \frac{w_{\alpha} (\mu_{\alpha} / \rho_{\alpha})}{w_{\alpha} (\mu_{\alpha} / \rho_{\alpha} - \mu_{\beta} / \rho_{\beta}) + \mu_{\beta} / \rho_{\beta}}$

[demo p.389-390 Cullity]

$$\frac{I_{(hkl)\alpha}}{I_{(hkl)\alpha,pure}} = \frac{w_{\alpha}(\mu_{\alpha}/\rho_{\alpha})}{w_{\alpha}(\mu_{\alpha}/\rho_{\alpha}) + \mu_{\beta}/\rho_{\beta}}$$

QPA of a binary mixture can, therefore be performed provided that we can access:

- the mass absorption coefficients of the two phases (if not, a calibration curve can be prepared using mixtures of known composition)
- one pure phase (or a mixture with a known amount of that phase)
- No need of structural information,  $K_{1,\alpha}$  cancels out

What can we observe?

$$\frac{I_{(hkl)\alpha}}{I_{(hkl)\alpha,pure}} = \frac{w_{\alpha}(\mu_{\alpha}/\rho_{\alpha})}{w_{\alpha}(\mu_{\alpha}/\rho_{\alpha}) + w_{\beta}(\mu_{\beta}/\rho_{\beta})}$$

- The intensity of a particular diffraction line depends on the mass absorption coefficient of the other phase
- For binary mixtures of phases with the same mass absorption coefficient:

$$\frac{I_{(hkl)\alpha}}{I_{(hkl)\alpha,pure}} = w_{\alpha}$$

The binary mixture case that we have worked out together is an example of the so-called **single-line** or **single-peak methods of QPA**, for which *the measurement of the weight fraction of phase in a mixture depends on the measurement of the ratio of the intensity of a diffraction line from that phase to the intensity of some standard reference line!*

In the case discussed, the reference standard is the pure phase  $\alpha$ !

DIRECT COMPARISON METHOD

INTERNAL STANDARD METHOD



## DIRECT COMPARISON METHOD

Let us again consider a  $\alpha+\beta$  binary mixture:

$$I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot c_{\alpha}}{\mu_m} = \frac{K_{1,\alpha} \cdot w_{\alpha}}{\rho_{\alpha} \mu_m^*} \qquad I_{(h'k'l')\beta} = \frac{K_{1,\beta} \cdot c_{\beta}}{\mu_m} = \frac{K_{1,\beta} \cdot w_{\beta}}{\rho_{\beta} \mu_m^*}$$

Let us separate in  $K_{1,\alpha}$  the phase-dependent from the phase-independent part:

$K_{1,\alpha} = K_2 \cdot R_{\alpha}$        $K_2$  is a constant independent of the kind and amount of diffracting substance;  $R$  depends on  $\theta$ ,  $hkl$ , kind of substance

$$I_{(hkl)\alpha} = \frac{K_2 \cdot R_{\alpha} \cdot c_{\alpha}}{\mu_m} \qquad \longrightarrow \qquad \frac{I_{(hkl)\alpha}}{I_{(h'k'l')\beta}} = \frac{R_{\alpha} \cdot c_{\alpha}}{R_{\beta} \cdot c_{\beta}} \qquad \longrightarrow \qquad \frac{c_{\alpha}}{c_{\beta}} = \frac{I_{(hkl)\alpha}}{I_{(h'k'l')\beta}} \cdot \frac{R_{\beta}}{R_{\alpha}}$$

$$I_{(h'k'l')\beta} = \frac{K_2 \cdot R_{\beta} \cdot c_{\beta}}{\mu_m}$$

Details here:  $K_2 = \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4}$  and  $R_{\alpha} = \left[ \frac{M_{hkl}}{V_{\alpha}^2} \cdot |F_{(hkl)}|_{\alpha}^2 \cdot \left( \frac{1 + \cos^2 2\theta}{2} \right) \right] \cdot \exp \left( -2B_{\alpha} \left( \frac{\sin \theta}{\lambda} \right) \right)$

## DIRECT COMPARISON METHOD

Let us again consider a  $\alpha+\beta$  binary mixture:

$$I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot c_\alpha}{\mu_m} = \frac{K_{1,\alpha} \cdot w_\alpha}{\rho_\alpha \mu_m^*} \qquad I_{(h'k'l')\beta} = \frac{K_{1,\beta} \cdot c_\beta}{\mu_m} = \frac{K_{1,\beta} \cdot w_\beta}{\rho_\beta \mu_m^*}$$

Let us separate in  $K_{1,\alpha}$  the phase-dependent from the phase-independent part:

$K_{1,\alpha} = K_2 \cdot R_\alpha$        $K_2$  is a constant independent of the kind and amount of diffracting substance;  $R$  depends on  $\theta$ ,  $hkl$ , kind of substance

$$I_{(hkl)\alpha} = \frac{K_2 \cdot R_\alpha \cdot c_\alpha}{\mu_m} \qquad \longrightarrow \qquad \frac{I_{(hkl)\alpha}}{I_{(h'k'l')\beta}} = \frac{R_\alpha \cdot c_\alpha}{R_\beta \cdot c_\beta} \qquad \longrightarrow \qquad \frac{w_\alpha}{w_\beta} = \frac{I_{(hkl)\alpha}}{I_{(h'k'l')\beta}} \cdot \frac{\rho_\alpha \cdot R_\beta}{\rho_\beta \cdot R_\alpha}$$

$$I_{(h'k'l')\beta} = \frac{K_2 \cdot R_\beta \cdot c_\beta}{\mu_m}$$

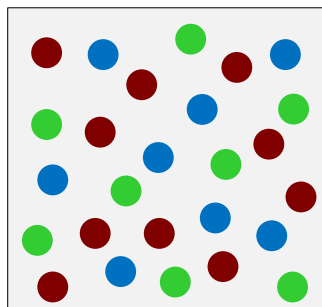
Details here:  $K_2 = \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4}$     and     $R_\alpha = \left[ \frac{M_{hkl}}{V_\alpha^2} \cdot |F_{(hkl)}|_\alpha^2 \cdot \left( \frac{1 + \cos^2 2\theta}{2} \right) \right] \cdot \exp \left( -2B_\alpha \left( \frac{\sin \theta}{\lambda} \right) \right)$

## INTERNAL STANDARD METHOD

A diffraction line from the phase that we need to quantify in a given mixture (e.g.  $I_{hkl,\alpha}$ ) is compared with a line from a standard (e.g.  $I_{h'k'l',Std}$ ) mixed with our original mixture in known proportion → the **ISM method is only applicable to powders!**

Let us consider a mixture M of n phases  $\alpha, \beta, \gamma \dots$

Mixture M  
(e.g. 3 phases)

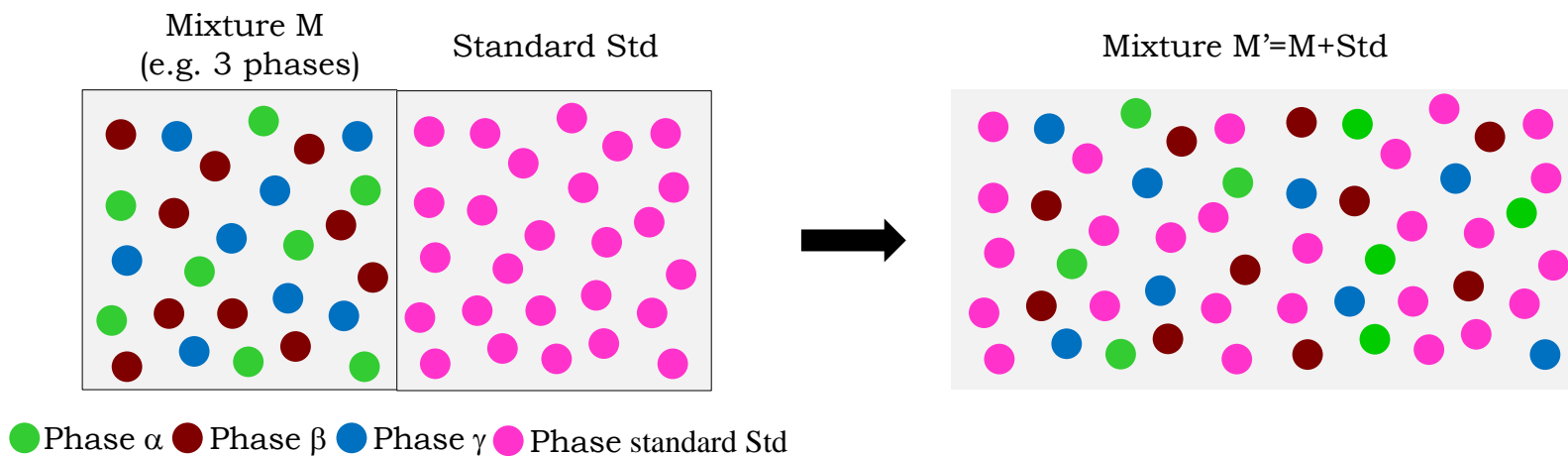


● Phase  $\alpha$  ● Phase  $\beta$  ● Phase  $\gamma$

We need to quantify the **amount of phase  $\alpha$**  in a series of mixtures of type M in which the relative proportion of the other phases  $\beta, \gamma \dots$  might change from mixture to mixture.

## INTERNAL STANDARD METHOD: how does it work?

- i. We mix a known amount of original mixture **M** with a known amount of a known standard **Std** and form a new mixture **M'=M+Std** (e.g. 50% M + 50% Std)



- ii. Let  $c_\alpha$  and  $c'_\alpha$  the volume fractions of phase  $\alpha$  in M and M' (both unknown!) and  $c_{Std}$  the volume fraction of the standard Std (that we know!)

## INTERNAL STANDARD METHOD: how does it work?

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- ii. Let  $\mathbf{c}_\alpha$  and  $\mathbf{c}'_\alpha$  the volume fractions of phase  $\alpha$  in M and M' (both unknown!) and  $\mathbf{c}_{Std}$  the volume fraction of the standard Std (that we know!)
- iii. From a powder diffraction pattern recorded on the new mixture M', we obtain:

$$I_{(hkl)\alpha} = I_\alpha = \frac{K_{1,\alpha} \cdot c_\alpha'}{\mu_m} \quad \text{and similarly:} \quad I_{(h'k'l')Std} = I_{Std} = \frac{K_{1,Std} \cdot c_{Std}}{\mu_m}$$

Note that  $\mu_m$  **cancels out!**

$$\longrightarrow \frac{I_\alpha}{I_{Std}} = \frac{K_{1,\alpha} \cdot c_\alpha'}{K_{1,Std} \cdot c_{Std}}$$

It physically means that the variation of absorption due to the variation of the relative amounts of the other phases present in the original mixture ( $\beta$ ,  $\gamma$ , ...) does not affect the  $\mathbf{I}_\alpha/\mathbf{I}_{Std}$  ratio since such variations equivalently affects  $\mathbf{I}_\alpha$  and  $\mathbf{I}_{Std}$ !

## INTERNAL STANDARD METHOD: how does it work?

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- iii. From a powder diffraction pattern recorded on the new mixture M', we obtain:

$$\frac{I_\alpha}{I_{Std}} = \frac{K_{1,\alpha} \cdot c'_\alpha}{K_{1,Std} \cdot c_{Std}} \longrightarrow \text{with } \frac{c'_\alpha}{c_{Std}} = \frac{w'_\alpha \cdot \rho_{Std}}{\rho_\alpha \cdot w_{Std}} \longrightarrow \frac{I_\alpha}{I_{Std}} = \frac{K_{1,\alpha}}{K_{1,Std}} \cdot \frac{w'_\alpha \cdot \rho_{Std}}{\rho_\alpha \cdot w_{Std}}$$

If  $w_{Std}$  is kept constant in all mixtures of type M', then  $\frac{K_{1,\alpha}}{K_{1,Std}} \cdot \frac{\rho_{Std}}{\rho_\alpha \cdot w_{Std}} \stackrel{\text{def}}{=} K_3$

$$\longrightarrow \frac{I_\alpha}{I_{Std}} = K_3 \cdot w'_\alpha \longrightarrow \frac{I_\alpha}{I_{Std}} = K_4 \cdot w_\alpha \quad \text{being: } w'_\alpha = w_\alpha (1 - w_{Std})$$

## INTERNAL STANDARD METHOD: how does it work?

- i. We mix a known amount of original mixture **M** with a known amount of a known standard **Std** and form a new mixture **M'=M+Std** (e.g. 50% M + 50% Std)
- ii. Let  $c_\alpha$  and  $c'_\alpha$  the volume fractions of phase  $\alpha$  in M and M' (both unknown!) and  $c_{Std}$  the volume fraction of the standard Std (that we know!)
- iii. From a powder diffraction pattern recorded on the new mixture M', we obtain:

$$\frac{I_\alpha}{I_{Std}} = K_4 \cdot w_\alpha$$

Slope of the  
straight line

- The intensity ratio  $\frac{I_\alpha}{I_{Std}}$  is therefore a **linear function** of the weight fraction  $w_\alpha$  of phase  $\alpha$ .
- A calibration curve can be prepared from XRPD measurements on a set of *ad-hoc* synthetic samples containing **known** concentrations of phase  $\alpha$  and a **constant** concentration  $w_{Std}$  of a suitable standard
- The concentration of  $\alpha$  in an unknown mixture is obtained by measuring the ratio  $\frac{I_\alpha}{I_{Std}}$  in a mixture of type M' (so-called **spiked** sample) containing the unknown original mixture and the standard in the same proportion as used to build up the calibration curve.

# Generalization of the Internal Standard Method →

## → The Reference Intensity Ratio (RIR)

$$\frac{I_{\alpha}}{I_{Std}} = K_4 \cdot w_{\alpha}$$

The calibration constant  $K_4$  depends on:  $\alpha$ ,  $Std, (hkl)_{\alpha}$ ,  $(h'k'l')_{Std}$  and  $w_{Std}$

(remember:  $I_{\alpha} = I_{(hkl)\alpha}$  and  $I_{Std} = I_{(h'k'l')S}$ )

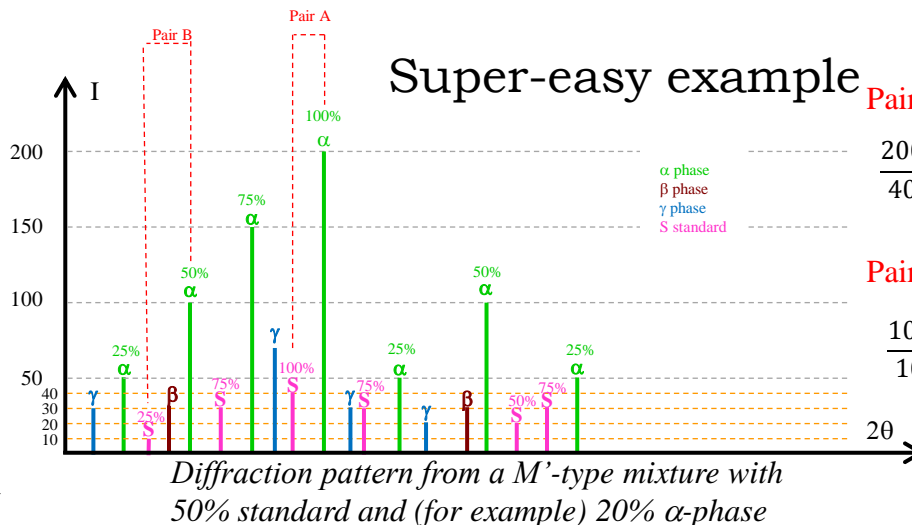
For a more reliable quantification, the use of several analyte-line/internal standard-line pair is preferable → each pair requires a calibration constant!

The use of **relative intensities  $I^{rel}$**  and so-called **Relative Intensity Ratio (RIR)** allows us to use multiple analyte/standard reflection pairs without the need of multiple reference standards:

Hubbard & Snyder, (1988)  
Powder Diffraction 3, 74-78.

$$\frac{I_{i\alpha}}{I_{jS}} \cdot \frac{I_{jS}^{rel}}{I_{i\alpha}^{rel}} \cdot \frac{w_S}{w_{\alpha}} = K = RIR_{\alpha,S}$$

i denotes one hkl reflection of  $\alpha$  phase  
j denotes one h'k'l' reflection of the internal standard





## The Reference Intensity Ratio (RIR)

$$K = RIR_{\alpha,S} = \frac{I_{i\alpha}}{I_{jS}} \cdot \frac{I_{jS}^{rel}}{I_{i\alpha}^{rel}} \cdot \frac{w_S}{w_\alpha}$$

Universal calibration constant relating the scattering power of phase  $\alpha$  to that of the standard Std

→ So-called **Reference Intensity Ratio** or **RIR**

**Standard Std → NIST Corundum → RIR=I/I<sub>C</sub>**

**The Powder Diffraction File (PDF) contains I/I<sub>C</sub> ratios for more than 2500 phases!**

**Quantitative Phase Analysis with I/I<sub>C</sub> (RIR or Chung Method)**

$$w_\alpha = \frac{I_{i\alpha}}{I_{jC}} \cdot \frac{I_{jC}^{rel}}{I_{i\alpha}^{rel}} \cdot \frac{w_S}{RIR_{\alpha,C}} = \frac{I_{i\alpha}}{I_{jC}} \cdot \frac{I_{jC}^{rel}}{I_{i\alpha}^{rel}} \cdot \frac{w_S}{(I/I_C)_\alpha}$$

With the addition of a known %wt of corundum, no calibration curves needed!

Or **standardless QPA**, if all phases in the mixture are crystalline, identified, and the RIR values known for each of them!

# DIFFRACTION-BASED QPA METHODS

## Single-peak methods:

(adapted from Cullity, *Elements of X-Ray Diffraction*)

- Intensity ratio  $I_{\text{unknown}}/I_{\text{standard}}$  of one or more reflections
- No need of structural information but prone to systematic errors (e.g. caused by preferential orientation and peak overlapping)
- Need *ad-hoc* mixtures for calibration curves

## Rietveld-based methods:

(adapted from Madsen & Scarlett in *Powder Diffraction-Theory and Practice*)

- Use of full diffraction patterns
- Minimization of systematic errors (e.g. due to peak overlap)
- Preferential Orientation (PO) can be modeled
- Accuracy close to X-Ray fluorescence elemental analysis, with the advantage of being sensitive to structural differences → direct QPA of polymorphs

## Rietveld QPA METHOD

*“The Rietveld method uses a model to calculate a diffraction pattern which is then compared with observed data. The difference between the two patterns is then reduced through least square minimization. **The refinable parameters used in the models provide the analyst with information regarding** the crystal structure of the component phases, the crystalline size and strain and, importantly, **their relative proportions**. The **Rietveld scale factor S**, which is a multiplier for each component’s contribution to the pattern, is related to the relative abundance of that phase and can be used in the quantification of phases.”*

(textual citation from **Quantitative Phase Analysis using the Rietveld Method**, Madsen, Scarlett, Riley & Raven, Ch.10 in *Modern Diffraction Methods*, Mittemeijer & Welzel Edts, 2013)

## Rietveld QPA METHOD

$$I_{(hkl)\alpha} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V_\alpha^2} \cdot |F_{hkl}|_\alpha^2 \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp \left( -2B_\alpha \left( \frac{\sin \theta}{\lambda} \right) \right) \cdot \left[ \frac{c_\alpha}{\mu_m} \right]$$

D-S geometry with capillary, assuming absorption, PO and extinction negligible

## Rietveld QPA METHOD

$$I_{(hkl)\alpha} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V_\alpha^2} \cdot |F_{hkl}|_\alpha^2 \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp \left( -2B_\alpha \left( \frac{\sin \theta}{\lambda} \right) \right) \cdot \left[ \frac{w_\alpha}{\rho_\alpha \mu_m^*} \right]$$

D-S geometry with capillary, assuming absorption, PO and extinction negligible

$$I_{(hkl)\alpha} = \frac{K_{1,\alpha} \cdot w_\alpha}{\rho_\alpha \cdot \mu_m^*} \longrightarrow w_\alpha = \frac{I_\alpha \cdot \rho_\alpha \cdot \mu_m^*}{K_{1,\alpha}} = \frac{S_\alpha \cdot (ZMV)_\alpha \cdot \mu_m^*}{K}$$

☺  $K_{1,\alpha} \propto \frac{1}{V_\alpha^2}$

☺  $I_\alpha \propto S_\alpha$  R. J. Hill, Powder Diffr. 1991, **6**, 74-77

☺  $\rho_\alpha = 1.6604 \cdot \frac{ZM_\alpha}{V_\alpha}$  Z=number of formula units  
M=molecular mass of the formula unit

## Rietveld QPA METHOD

$$I_{(hkl)\alpha} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V_\alpha^2} \cdot |F_{hkl}|_\alpha^2 \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp \left( -2B_\alpha \left( \frac{\sin \theta}{\lambda} \right) \right) \cdot \left[ \frac{w_\alpha}{\rho_\alpha \mu_m^*} \right]$$

D-S geometry with capillary, assuming absorption, PO and extinction negligible

$$w_\alpha = \frac{S_\alpha \cdot (ZMV)_\alpha \cdot \mu_m^*}{K}$$



IMPORTANT RELATION

In 1988, O'Connor & Raven demonstrated that the scaling factor K is independent of individual phases and overall sample-related parameters (Powder Diffr. **3**, 2-6) .



This implies that K only needs to be estimated once for a given instrumental configuration and using an appropriate standard

→ **EXTERNAL STANDARD METHOD** for absolute QPA analysis

**Warning:** the term “*instrumental configuration*” really refers to all experimental details →  
→ in DS geometry with powders in capillaries it would imply also the same powder packing!

## Rietveld QPA METHOD

$$I_{(hkl)\alpha} = \left[ \frac{I_0 \lambda^3}{32 \pi r} \cdot \frac{\sigma e^4}{m_e^2 c^4} \right] \cdot \left[ \frac{M_{hkl}}{V_\alpha^2} \cdot |F_{hkl}|_\alpha^2 \left( \frac{1}{\sin^2 \theta \cdot \cos \theta} \right) \right] \cdot \exp \left( -2B_\alpha \left( \frac{\sin \theta}{\lambda} \right) \right) \cdot \left[ \frac{w_\alpha}{\rho_\alpha \mu_m^*} \right]$$

D-S geometry with capillary, assuming absorption, PO and extinction negligible

$$w_\alpha = \frac{S_\alpha \cdot (ZMV)_\alpha \cdot \mu_m^*}{K}$$



IMPORTANT RELATION

$(ZMV)_\alpha$  is the so-called **calibration constant** for phase  $\alpha$  that can be calculated from the structural model (either from crystallographic database or the refinement of the pure  $\alpha$  phase)

Absolute QPA analysis can, then, be obtained provided we correctly estimate **K** and  $\mu_m^*$  for all our mixtures and calibration standards (the latter for K determination)

## Rietveld QPA METHOD: Q&A

$$w_{\alpha} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha} \cdot \mu_m^*}{K}$$



Q<sub>1</sub>: Can we still perform **absolute QPA** analyses without estimating **K** and  $\mu_m^*$ ?

A<sub>1</sub>: Yes, we can, if we “spike” our unknown mixture with a known amount  $w_S$  of an appropriate reference standard Std of well known crystallographic structure (**INTERNAL STANDARD METHOD**)

$$w'_{\alpha} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha} \cdot \mu_m^*}{K}$$

$$w'_{\alpha} = w_{Std} \cdot \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_{Std} \cdot (ZMV)_{Std}}$$



For  $\alpha$  and Std

$$w_{Std} = \frac{S_{Std} \cdot (ZMV)_{Std} \cdot \mu_m^*}{K}$$

$$w'_{\alpha} = w_{\alpha}(1 - w_{Std})$$

**Remark:** note that there is no need of a calibration curve as for the Internal Standard Method as implemented in the single-line diffraction method in virtue of performing here a Rietveld refinement!



## Rietveld QPA METHOD: Q&A

$$w_{\alpha} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha} \cdot \mu_m^*}{K} \quad \star$$

$$w'_{\alpha} = w_{Std} \cdot \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_{Std} \cdot (ZMV)_{Std}} \quad \star \star$$

$$w'_{\alpha} = w_{\alpha} (1 - w_{Std})$$

Q<sub>2</sub>: What if we **do NOT** dispose of the whole composition of the unknown mixture?

A<sub>2</sub>: We have 2 possibilities:

- if we can reasonably estimate K and  $\mu_m^*$ , we apply  $\star$ , that is the External Standard Method.
- we spike the sample with a known amount of a known standard and apply the  $\star \star$  (Internal Standard Method)

## Rietveld QPA METHOD: Q&A

$$w_{\alpha} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha} \cdot \mu_m^*}{K} \quad \star$$

$$w'_{\alpha} = w_{Std} \cdot \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_{Std} \cdot (ZMV)_{Std}} \quad \star \star$$

$$w'_{\alpha} = w_{\alpha} (1 - w_{Std})$$

Q<sub>2</sub>: What if we dispose of the whole composition of the unknown mixture?

A<sub>2</sub>: For a mixture of n crystalline phases  $\alpha, \beta, \gamma, \delta \dots$  we can write:

$$w_{\alpha} + w_{\beta} + w_{\gamma} + \dots = \sum_{i=1}^n w_i = 1$$



$$w_{\alpha} = \frac{w_{\alpha}}{\sum_{i=1}^n w_i} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{\sum_{i=1}^n S_i \cdot (ZMV)_i}$$

and equivalent expressions for  $w_{\beta}, w_{\gamma} \dots$

**Hill & Howard** (JAC (1987). 20, 467-474 ) modification of the Rietveld QPA method, known as the *ZMV approach* inspired by the *Matrix Flushing Method* of **Chung** (JAC, 1974, 7, 519-525 and 526-531)

## Rietveld QPA METHOD: Q&A

$$w_{\alpha} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha} \cdot \mu_m^*}{K} \quad \star$$

External Standard Method

$$w'_{\alpha} = w_{Std} \cdot \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_{Std} \cdot (ZMV)_{Std}} \quad \star \star$$

$$w'_{\alpha} = w_{\alpha} (1 - w_{Std})$$

Internal Standard Method

$$w_{\alpha} + w_{\beta} + w_{\gamma} + \dots = \sum_{i=1}^n w_i = 1$$

$$w_{\alpha} = \frac{w_{\alpha}}{\sum_{i=1}^n w_i} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{\sum_{i=1}^n S_i \cdot (ZMV)_i}$$

Hill & Howard (ZMV) Approach



- Warning:** the (ZMV) approach assumes that:
- All phases in the mixtures are crystalline!
  - We have identified them all!



If our mixture has **unknown crystalline phases** or **amorphous components**, a QPA analysis via (ZMV) approach inevitably **overestimates** the  $w_i$  weight fractions

## Rietveld QPA METHOD: Q&A

$$w_{\alpha} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha} \cdot \mu_m^*}{K} \quad \star$$

External Standard Method

$$w'_{\alpha} = w_S \cdot \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_S \cdot (ZMV)_S} \quad \star \star$$

$$w'_{\alpha} = w_{\alpha}(1 - w_S)$$

Internal Standard Method

$$w_{\alpha} + w_{\beta} + w_{\gamma} + \dots = \sum_{i=1}^n w_i = 1$$

$$w_{\alpha} = \frac{w_{\alpha}}{\sum_{i=1}^n w_i} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{\sum_{i=1}^n S_i \cdot (ZMV)_i}$$



**What do we do in such cases?**

Hill & Howard (ZMV)  
Approach

We apply the Internal Standard Method:

- We add a known amount of an appropriate standard Std
- We write  $\star \star$  for all identified crystalline phases  $i$  and for Std
- For each phase  $i$  we can write:  $Corrected(W_i) = W_{i,Rietveld} \frac{W_{Std,true}}{W_{Std,Rietveld}}$
- $W_{unknown} = 1.0 - \sum_{k=1}^n Corrected(W_k)$

What if a **structural model is NOT available** or if it does not work well with our experimental data?

## ➤ Partial Or No Known Crystal Structure (**PONKCS**) Method

Madsen & Scarlett, Powder Diffr. 21(4), 2006, 278-284;  
Madsen, Scarlett & Kern, Z. Kristallogr. 226 (2011) 944-955

→ implemented in Topas

- If *partial structure available* (i.e. unit cell and SG) → real structure factors substituted with empirical values derived from a Pawley or LeBail refinement performed on pure phases → **an hkl\_Is phase in Topas**
- If *partial structure NOT available* → real structure factor substituted by fictitious phases consisting each of a series of related peaks with **FIXED** relative intensities and **GROUP-SCALED** as a single entity during the QPA analysis → **a x0\_Is phase or peak-phase in Topas**
- Compute empirical **ZM** or **ZMV calibration constants** from the refinement of ad-hoc mixtures of pure phases with a known amount of a known standard (e.g. via spiking) → so-called **PONKCS phases**.

$$w_{\alpha} + w_{\beta} + w_{\gamma} + \dots = \sum_{i=1}^n w_i = 1$$

$$w_{\alpha} = \frac{w_{\alpha}}{\sum_{i=1}^n w_i} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{\sum_{i=1}^n S_i \cdot (ZMV)_i}$$



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- Compute empirical **ZM** or **ZMV calibration constants** from the refinement of ad-hoc mixtures of pure phases with a known amount of a known standard (e.g. via spiking) → so-called **PONKCS phases**.

$$w_{\alpha} + w_{Std} = \sum_{i=1}^2 w_i = 1$$

For the PONKCS binary mixtures (phase  $\alpha$  + Std);  
for every a phase we want a PONKCS phase of!

$$w_{\alpha} = \frac{w_{\alpha}}{w_{\alpha} + w_{Std}} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_{\alpha} \cdot (ZMV)_{\alpha} + S_{Std} \cdot (ZMV)_{Std}}$$

... and the same written  
for the Std



## ➤ Partial Or No Known Crystal Structure (**PONKCS**) Method

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$$w_{\alpha} + w_{std} = \sum_{i=1}^2 w_i = 1$$

★★★ For phase  $\alpha$

$$w_{\alpha} = \frac{w_{\alpha}}{w_{\alpha} + w_{std}} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_{\alpha} \cdot (ZMV)_{\alpha} + S_{std} \cdot (ZMV)_{std}}$$

★★★ For standard Std

$$w_{std} = \frac{w_{std}}{w_{\alpha} + w_{std}} = \frac{S_{std} \cdot (ZMV)_{std}}{S_{\alpha} \cdot (ZMV)_{\alpha} + S_{std} \cdot (ZMV)_{std}}$$



## ➤ Partial Or No Known Crystal Structure (**PONKCS**) Method

Madsen & Scarlett, Powder Diffr. 21(4), 2006, 278-284;  
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→ implemented in Topas

- If *partial structure available* (i.e. unit cell and SG) → real structure factors substituted with empirical values derived from a Pawley or LeBail refinement performed on pure phases → **an hkl\_Is phase in Topas**
- If *partial structure NOT available* → real structure factor substituted by fictitious phases consisting each of a series of related peaks with **FIXED** relative intensities and **GROUP-SCALED** as a single entity during the QPA analysis → **a x0\_Is phase or peak-phase in Topas**
- Compute empirical **ZM or ZMV calibration constants** from the refinement of ad-hoc mixtures of pure phases with a known amount of a known standard (e.g. via spiking) → so-called **PONKCS phases**.

$$w_{\alpha} + w_{std} = \sum_{i=1}^2 w_i = 1$$

From the ratio:

$$\frac{w_{\alpha}}{w_{std}} = \frac{S_{\alpha} \cdot (ZMV)_{\alpha}}{S_{std} \cdot (ZMV)_{std}} \rightarrow$$

$$\rightarrow (ZM)_{\alpha} = \frac{w_{\alpha}}{w_{std}} \cdot \frac{S_{std} \cdot (ZM)_{std} \cdot V_{std}}{S_{\alpha} \cdot (ZM)_{\alpha} \cdot V_{\alpha}}$$

## ➤ Partial Or No Known Crystal Structure (**PONKCS**) Method

Madsen & Scarlett, Powder Diffr. 21(4), 2006, 278-284;  
Madsen, Scarlett & Kern, Z. Kristallogr.226 (2011) 944-955

→ implemented in Topas

- If *partial structure available* (i.e. unit cell and SG) → real structure factors substituted with empirical values derived from a Pawley or LeBail refinement performed on pure phases → **an hkl\_Is phase in Topas**
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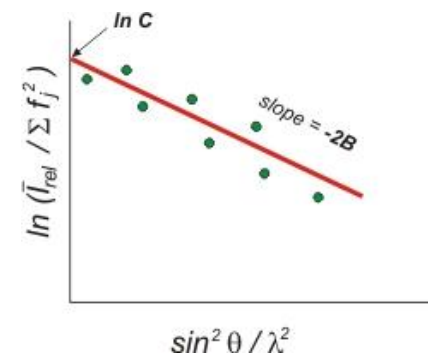
### Requirements:

- Pure phases (or pure phases with known impurities) must be available
- *Ad-hoc* mixtures of pure phases with an appropriate standard in known %wt must be available to build the so-called PONKCS phase

### Benefits:

- No need of a valid structural model
- PONKCS phases can be “re-used” provided the QPA analyses are conducted at the same photon energy! → Careful with SR-XRPD data!
- PONKCS works for **crystalline** as well as **amorphous phases**

## Whole-patterns QPA Methods



### ➤ QUANTO+

Giannini, Guagliardi & Mililli, JAC (2002). 35, 481-490

- If *partial structure available* (i.e. unit cell and SG) → for each phase in the mixture a reflection intensity file is built via whole pattern decomposition (e.g. Le Bail refinement) performed on pure phases
- This «external» file is used instead of the calculated structural factors from the model ( $|F_c|^2$ ) for the absolute scaling of the diffracted intensity via a Wilson plot

#### Requirements:

- Pure phases must be available
- Partial structure (unit cell and SG) must be known
- Crystalline phases

#### Benefits:

- No need to have a valid structural model
- No need to prepare *ad-hoc* mixtures with an appropriate standard!

→ implemented in Quanto (CNR-IC)

## Quantification of amorphous (X-ray amorphous) phases based on X-ray scattering methods

- ❑ Conventional XRD methods
- ❑ Total scattering techniques
- ❑ Principal Component Analyses

## Quantification of amorphous (X-ray amorphous) phases based on X-ray scattering methods

### ❑ Conventional XRD methods

### ❑ Total scattering techniques

Both Bragg peaks and diffuse scattering is interpreted: e.g. Pair Distribution Function

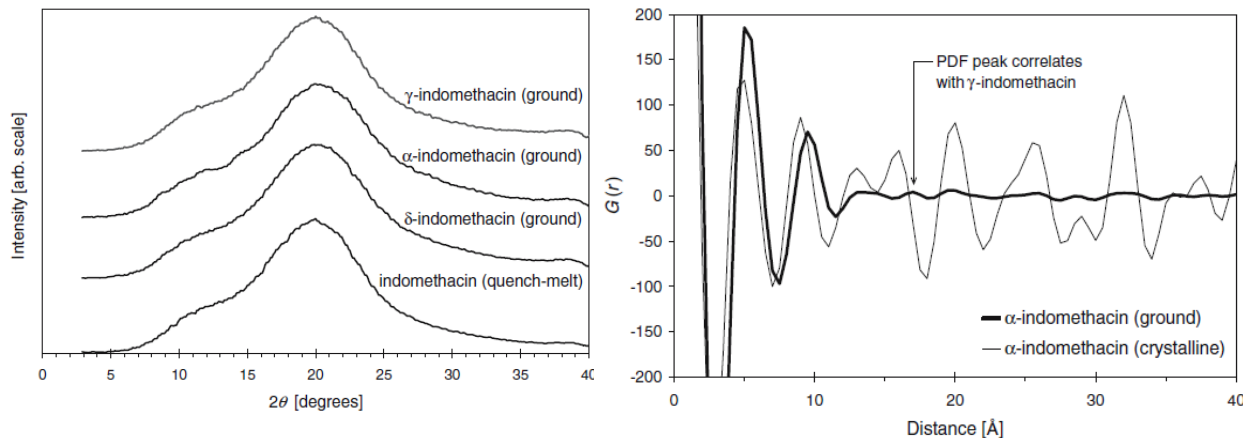
PDF (so-called  $G(r)$  function) is the probability of finding a couple of atoms separated by a distance  $r$

### ❑ Principal Component Analyses

## Quantification of amorphous (X-ray amorphous) phases based on X-ray scattering methods

❑ Conventional XRD methods

❑ Total scattering techniques → Quantification via PDF refinement of mixtures



Billinge et al, CrystEngComm 12, 1366-1368 (2010)

Trakral et al, *Recent advances in the characterization of amorphous pharmaceuticals by X-ray diffractometry*, Adv. Drug Deliv. Rev. (2015),  
<http://dx.doi.org/10.1016/j.addr.2015.12.013>

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*H. Abdi and L. J. Williams, Principal Components Analysis, 2010 John Wiley & Sons, Inc. WIREs Comp Stat 2010 2 433–459*

*→ for generalities*

*K. Chapman, S. Lapidus & P.J. Chupas, Applications of principal components analysis to Pair Distribution Function data, J. Appl. Cryst. (2015). 48, 1619-1626* *→ for applications of PCA to PDF*

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## Quantification of amorphous (X-ray amorphous) phases based on X-ray scattering methods

### ❑ Conventional XRD methods

- single peak or whole pattern methods
- Direct or Indirect methods

Implemented or implementable in virtually all XRD software

### ❑ Total scattering techniques

Both Bragg peaks and diffuse scattering is interpreted: e.g. Pair Distribution Function

PDF (so-called  $G(r)$  function) is the probability of finding a couple of atoms separated by a distance  $r$

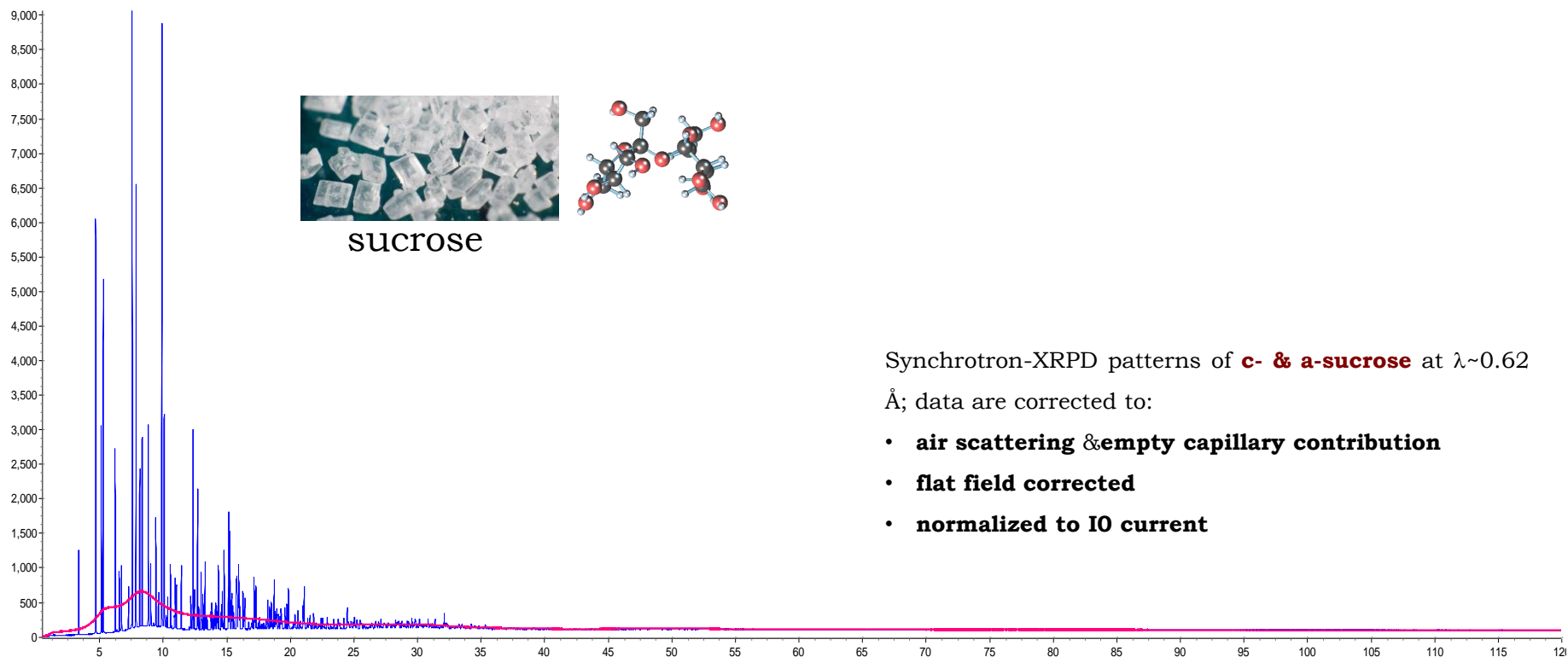
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Vainshtein's law:

*within identical regions of reciprocal space, the scattered intensities from a material are independent of its state of order*



## Quantification of amorphous (X-ray amorphous) phases based on X-ray scattering methods

- ❑ Conventional XRD methods
  - **Single peak** approach
  - **Whole pattern** approach

### **Direct** XRD methods:

the contribution of the amorphous component(s) to the pattern is used to obtain an estimate of the amorphous concentration

### **Indirect** XRD methods:

the absolute abundances of the crystalline components are used to estimate the amorphous component by difference

Review article: Madsen, Scarlett & Kern, *Description and survey of methodologies for the determination of amorphous content via X-Ray powder diffraction*, Z. Kristallogr. 226 (2011) 944-955

## Direct XRD methods:

- ❑ Single peak & Linear Calibration Method (LCM)
- ❑ PONKCS (**P**artial **O**r **N**o **K**nown **C**ystal **S**tructure) Method → the same we have seen for crystalline phases!
- ❑ DoC (Degree of Crystallinity) Method
- ❑ Full Structure Method

## Direct XRD methods:

- ❑ Single peak & Linear Calibration Method (LCM)
  - Calibration suite of samples needed
  - Amorphous contribution needs to be distinguishable from background
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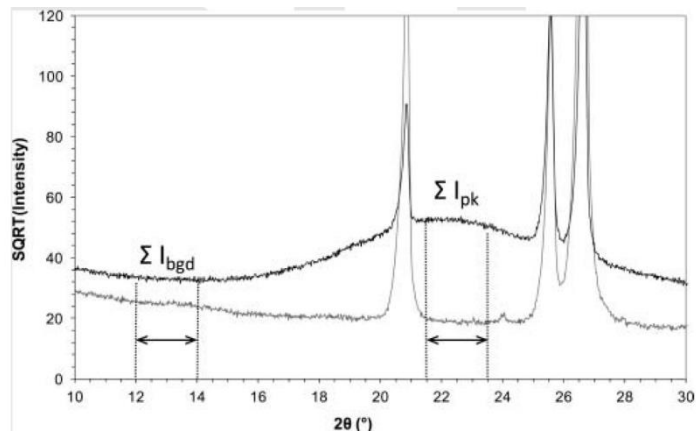


Fig.1 from Madsen, Scarlett & Kern,  
*Z. Krist.* 226 (2011) 944-955

← In this example, the authors had available one sample “free” of amorphous phase and used its diffraction pattern to estimate the background under the amorphous broad peak, but bkg determination is in principle not necessary!

$$W_a = A * I_a + B \quad \text{Linear calibration curve}$$



Refined scale factor for the LCM

## Direct XRD methods:

### ❑ Single peak & Linear Calibration Method (LCM)

- Calibration suite of samples needed
- Amorphous contribution needs to be distinguishable from background

### ❑ PONKCS (**P**artial **O**r **N**o **K**nown **C**ystal **S**tructure) Method → the same we have seen for crystalline phases!

- Empirical determination of ZMV constant for amorphous component(s)
- Determination of PONKCS phases for each component, via incorporation of a crystalline Std in known %wt, but only ONCE! Careful: photon wavelength dependent!

### ❑ DoC (Degree of Crystallinity) Method

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## ➤ Partial Or No Known Crystal Structure (**PONKCS**) Method

Madsen & Scarlett, Powder Diffr. 21(4), 2006, 278-284;  
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**RECALL**

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### ❑ DoC (Degree of Crystallinity) Method

- Estimate of the total intensity scattered by crystalline and amorphous component(s)

$$DoC = \frac{\text{Crystalline area}}{\text{Crystalline area} + \text{Amorphous Area}} \rightarrow W_{\text{amorphous}} = 1 - DoC$$

### ❑ Full Structure Method

## Direct XRD methods:

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- Identification of a structure model that adequately models positions and relative intensities of experimental pattern of amorphous

## Direct XRD methods:

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### ❑ Full Structure Method

- Identification of a structure model that adequately models positions and relative intensities of experimental pattern of amorphous

**Indirect XRD methods:**

❑ Internal Standard Method

- Crystalline components put on an absolute scale
- Amorphous contribution calculated by difference

$$Corrected(W_i) = W_{i,Rietveld} \frac{W_{Std,true}}{W_{Std,Rietveld}} \rightarrow$$

$$W_{unknown} = 1.0 - \sum_{k=1}^n Corrected(W_k)$$



$$W_{amorphous} = 1.0 - \sum_{k=1}^n Corrected(W_k)$$

❑ External Standard Method



$$W_\alpha = \frac{S_\alpha \cdot (ZMV)_\alpha \cdot \mu_m^*}{K}$$

Mass absorption coefficient of the entire mixture

Normalization constant to put  $W_\alpha$  on an absolute scale; K dependent on the instrument configuration

Thanks for your kind attention

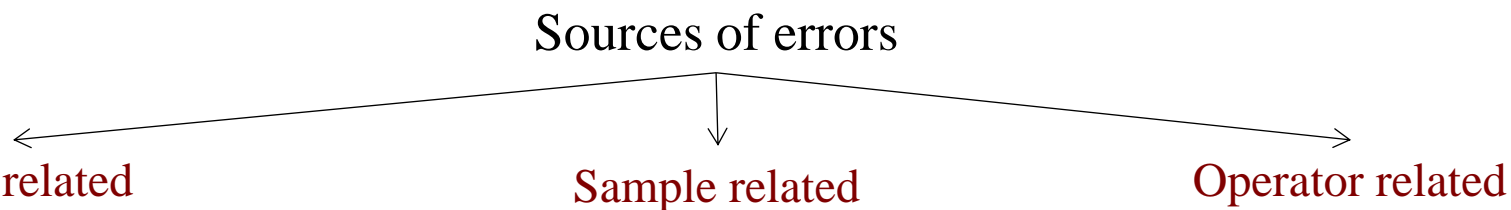
EXTRA – NOT included in the PPXRD lecture

## Factors influencing QPA

For a detailed and exhaustive discussion and references citation see:

- ❖ Madsen & Scarlett (*Ch. 11, Powder Diffraction – Theory and Practice*), **2009**
- ❖ Madsen, Scarlett, Riley & Raven (*Ch.10, Modern Diffraction Methods*), **2013**

Accurate QPA  $\longleftrightarrow$  Accurate integrated intensity  
(ca. 1-2% relative)



- **Experimental geometry:**  
BB (reflection)  $\theta$ – $2\theta$   
BB fixed- $\theta$   
DS (transmission) capillary or thin layer
- **Counting errors** (random and systematic)

- **Particle statistics**
- **Preferential Orientation**
- **Absorption and microabsorption**
- Incorrect or insufficient **crystal structure** model
- Crystallite **size** and **strain** broadening

- **Analyst choices** during QPA analysis affect the results → QPA Round Robin 1996-2002 (see Madsen & Scarlett)
- Dangerous side of **easy-to-use QPA software**
- Importance of setting up **QPA guidelines**

## Accuracy & Precision associated to QPA

What sets QPA accuracy and precision?

What does a Rietveld (or Rietveld-like) refinement return?



## Sources of errors

### Instrument related

- **Experimental geometry:**  
BB (reflection)  $\theta-2\theta$   
BB fixed- $\theta$   
DS (transmission) capillary or thin layer
- **Counting errors** (random and systematic)

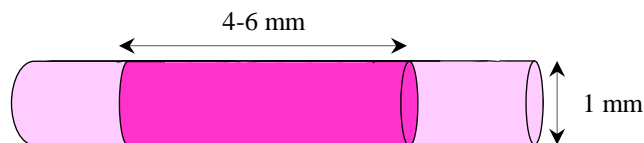
### Sample related

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### Operator related

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- Important of setting up **QPA guidelines**

The accuracy in the  $I_{hkl}$  estimate is strongly influenced by  $N_{diff}$  in a powder sample



Glass capillary

$$V \sim 3 - 5 \text{ mm}^3 \rightarrow N_{diff} \sim 3 \rightarrow \sigma_{PS} \sim 0.6$$

**Table 11.1** Relationship between crystallite diameter and the number diffracting (after Smith<sup>24</sup>).

Crystallite diameter ( $\mu\text{m}$ )	40	10	1
Crystallites ( $20 \text{ mm}^3$ )	$5.97 \times 10^5$	$3.82 \times 10^7$	$3.82 \times 10^{10}$
Number diffracting $N_{diff}$	12	760	38 000
$\sigma_{PS}$	0.289	0.036	0.005

From Madsen & Scarlett, *Powder Diffraction-Theory and Practice*, p. 309 reported from original work by D.K. Smith, *Adv. X-Ray Anal.* 1992, 35, 1-15; Elton & Salt, *Powder Diffr.*, 1996, 11, 218-229.

## Sources of errors

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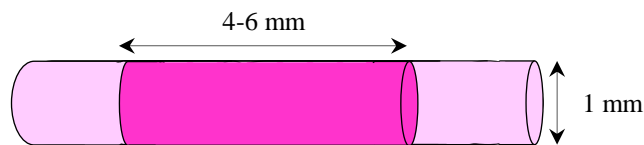
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### Remedies:

- Increase instrument beam divergence
- Sample spinning or oscillation
- Increase the powder volume analyzed or powder repacking
- Mechanical comminution (grinding, milling)

## Sources of errors

### Instrument related

- **Experimental geometry:**  
BB (reflection)  $\theta$ – $2\theta$   
BB fixed- $\theta$   
DS (transmission) capillary or thin layer
- **Counting errors** (random and systematic)

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### Operator related

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- Important of setting up **QPA guidelines**

DS geometry + capillary + 1D position sensitive detectors:

- intensity modulation due to inhomogeneous capillary packing
- inhomogeneous photon beam distribution

### Remedies:

- Partial photon beam focusing
- Analysis of a large number of powder volumes

## Sources of errors

### Instrument related

- **Experimental geometry:**  
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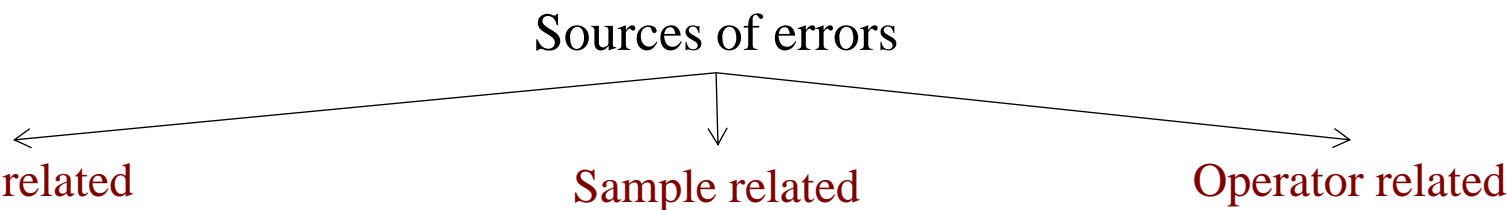
### Operator related

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- Dangerous side of **easy-to-use QPA software**
- Important of setting up **QPA guidelines**

- The need of absorption corrections should be minimized and corrections appropriate for the given experimental geometry applied
- **Microabsorption** (i.e. absorption contrast) occurs when the phases in a mixture are characterized by different mass absorption  $\mu^*$  coefficients and/or different crystallite size → the %wt of the phase with higher  $\mu^*$  and/or larger crystallite size would be underestimated

#### Remedies:

- Choose an appropriate  $\lambda$
- Reduce crystallite size



➤ **Experimental geometry:**

BB (reflection)  $\theta$ – $2\theta$

BB fixed- $\theta$

DS (transmission) capillary or thin layer

➤ **Counting errors** (random and systematic)

➤ **Particle statistics**

➤ **Preferential Orientation**

➤ **Absorption and microabsorption**

➤ **Incorrect or insufficient crystal structure model**

➤ **Crystallite size and strain broadening**

➤ **Analyst choices** during QPA analysis affect the results → QPA Round Robin 1996-2002 (see Madsen & Scarlett)

➤ Dangerous side of **easy-to-use QPA software**

➤ Important of setting up **QPA guidelines**

- Strong correlation between the **Rietveld scale factor** and the **Atomic Displacement Parameters** ( $ADP$ ,  $B_{iso}$ ,  $U_{iso}$ ).

**WARNING:** very often .cif files in the crystallographic database DO NOT report such parameters → commercial programs use in such cases default values (i.e.  $1 \text{ \AA}^2$ )

Be careful: most programs require as input  $B_{iso}$  (e.g. Topas, FullProf), often you find in literature and database  $U_{iso} \rightarrow B_{iso} = 8\pi^2 U_{iso}$