

**Neutron Scattering for Condensed Matter Studies**  
**Professor Saibal Basu**  
**Department of Physics**  
**Homi Bhabha National Institute**  
**Week 6: Lecture 15 C**

Keywords: Rietveld Refinement, FULLPROF, Experimental data, Model data

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Rietveld *Refinement* of structure

We need to start with a crystallographic structure for both the structure and the magnetic part

The program is heavily used both in x-rays and neutrons with parameters specific for each.

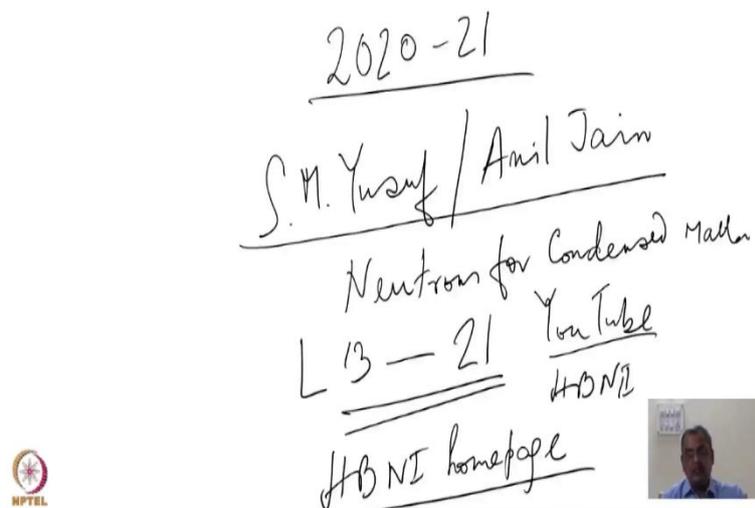
FULLPROF package

The slide features a light blue background with black text. The word 'Refinement' is in red italics. In the bottom right corner, there is a small inset video frame showing a man speaking. The NPTEL logo is visible in the bottom left corner.

Rietveld Refinement technique is the most widely used technique for magnetic structure refinement. The word refinement means this is not an ab initio solution for crystallographic and magnetic structure, rather you start with a given structure, magnetic and crystallographic, and then you keep refining it.

We need to start with a crystallography structure for both the structure and magnetic part. So, there is a starting point and then we refine that structure. That means, while we are running this fitting program, we must understand that we are undertaking optimization of the given structure. This program is available online and as I told you anybody interested to learn the technique can look into the lectures given in another course [details given].

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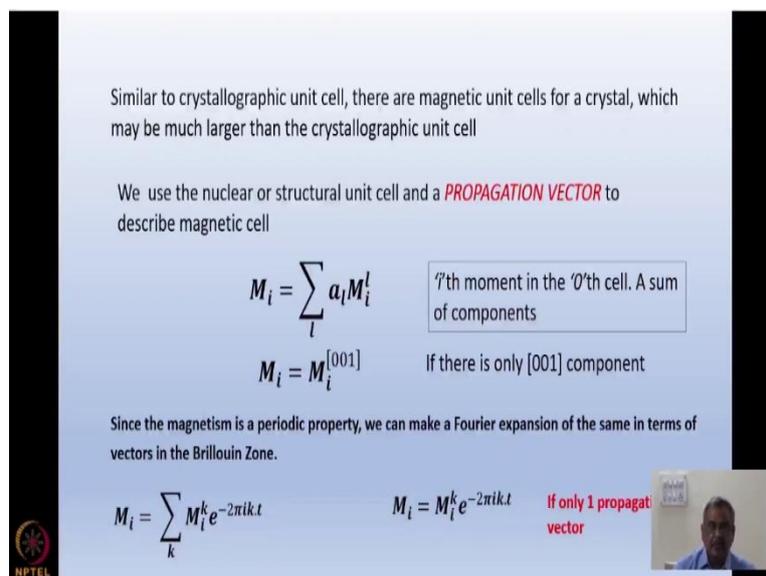


2020-21  
S. M. Yusuf / Anil Jain  
Neutron for Condensed Matter  
L 3 - 21 YouTube  
HONR  
HBNI homepage



This is used for both x-rays and neutrons all over the world and tutorials are also available online.

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Similar to crystallographic unit cell, there are magnetic unit cells for a crystal, which may be much larger than the crystallographic unit cell

We use the nuclear or structural unit cell and a **PROPAGATION VECTOR** to describe magnetic cell

$$M_i = \sum_l a_l M_i^l$$

"l"th moment in the "l"th cell. A sum of components

$$M_i = M_i^{[001]}$$

If there is only [001] component

Since the magnetism is a periodic property, we can make a Fourier expansion of the same in terms of vectors in the Brillouin Zone.

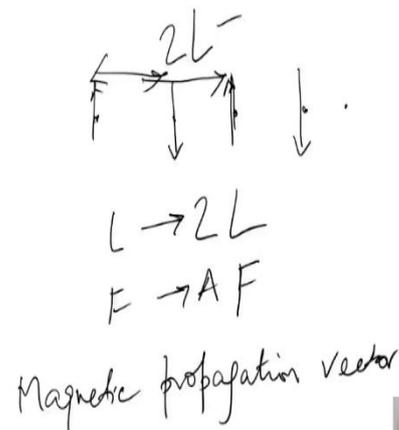
$$M_i = \sum_k M_i^k e^{-2\pi i k \cdot r}$$
$$M_i = M_i^k e^{-2\pi i k \cdot r}$$

If only 1 propagation vector



In crystallography by unit cell we understand that it is a repetitive cell that through translation gives me the entire crystal. But the magnetic unit cell can be different from the crystallographic unit cell. For example, if I consider an anti-ferromagnetic sample, then you can see that with the simplest example, a crystallographic linear chain.

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In case of ferromagnetic material, the repeat distance is  $L$ . Now if it is antiferromagnetic, then nearest neighbor will be antiferromagnetic and the repeat distance has gone to  $2L$ , that means the unit cell has doubled when it is going from ferro to anti-ferro. This is a one of the simplest possible examples that I can give. There are other kind of unit cells which are commensurate or incommensurate with respect to the crystallographic cell. I will come to it. There is something called a magnetic propagation vector. If from one crystallographic structural unit cell to the next the magnetism changes slightly, the magnetic unit cell may have thousands of atoms in them and may have a much larger length scale compared to the crystallographic unit cell.

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Similar to crystallographic unit cell, there are magnetic unit cells for a crystal, which may be much larger than the crystallographic unit cell

We use the nuclear or structural unit cell and a **PROPAGATION VECTOR** to describe magnetic cell

$$M_i = \sum_l a_l M_i^l$$

l<sup>th</sup> moment in the '0<sup>th</sup> cell. A sum of components

$$M_i = M_i^{[001]}$$

If there is only [001] component

Since the magnetism is a periodic property, we can make a Fourier expansion of the same in terms of vectors in the Brillouin Zone.

$$M_i = \sum_k M_i^k e^{-2\pi i k \cdot r}$$

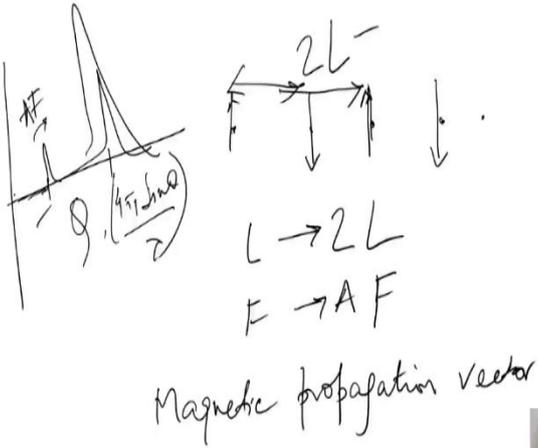
$$M_i = M_i^k e^{-2\pi i k \cdot r}$$

If only 1 propagation vector




In that case for the fitting of the data we will use the crystallography unit cell and a propagation vector which will use the properties of the crystallographic unit cell and tell me at what distance my magnetic cell is repeating.

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Magnetic propagation vector




As I showed you in the linear chain, when I go from ferromagnet to anti-ferromagnet, the repeat distance goes from  $L$  to  $2L$  and actually if you go from ferromagnet to anti-ferromagnet and look at the Bragg intensity vs.  $Q$  or  $\frac{4\pi \sin \theta}{\lambda}$  plot, you will find that the ferromagnetic peak matches with the crystallographic peak then, at smaller angles, the antiferromagnetic peak will be approximately at half of that angle. So, you do see a new peak appearing when an

antiferromagnetic order takes place. This is because if repeat distance goes from  $L$  to  $2L$  then the reciprocal lattice vector has gone to  $1/2$

(Refer Slide Time: 5:06)

Similar to crystallographic unit cell, there are magnetic unit cells for a crystal, which may be much larger than the crystallographic unit cell

We use the nuclear or structural unit cell and a **PROPAGATION VECTOR** to describe magnetic cell

$$M_i = \sum_l a_l M_i^l$$

$l^{\text{th}}$  moment in the  $l^{\text{th}}$  cell. A sum of components

$$M_i = M_i^{[001]}$$

If there is only [001] component

Since the magnetism is a periodic property, we can make a Fourier expansion of the same in terms of vectors in the Brillouin Zone.

$$M_i = \sum_k M_i^k e^{-2\pi i k \cdot r_i}$$

$$M_i = M_i^k e^{-2\pi i k \cdot r_i}$$

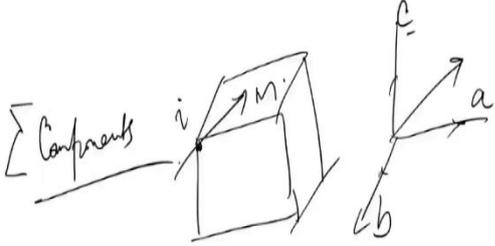
If only 1 propagation vector




That means I have to find out the magnetic propagation vector for the additional peaks. Here, I have considered a zeroth cell as one of the crystallographic or structural cells, and then the magnetic moment in this cell at any site  $i$  can have components in various directions. Now, I have to write down the magnetic moment at a site.

(Refer Slide Time: 5:39)

$\sum$  Components





Let me just geometrically show. Suppose this is my unit cell, this is the  $i^{\text{th}}$  point in my unit cell and this moment is  $M$ . Now if I consider crystallographic axes  $a$ ,  $b$  and  $c$ , then this  $M$  will have

components along  $a$ ,  $b$ ,  $c$  and basically that means that it is the vector sum of the components in three directions.

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Similar to crystallographic unit cell, there are magnetic unit cells for a crystal, which may be much larger than the crystallographic unit cell

We use the nuclear or structural unit cell and a **PROPAGATION VECTOR** to describe magnetic cell

$$M_i = \sum_l a_l M_i^l$$

l<sup>th</sup> moment in the '0<sup>th</sup> cell. A sum of components

$$M_i = M_i^{[001]}$$

If there is only [001] component

Since the magnetism is a periodic property, we can make a Fourier expansion of the same in terms of vectors in the Brillouin Zone.

$$M_i = \sum_k M_i^k e^{-2\pi i k \cdot r}$$

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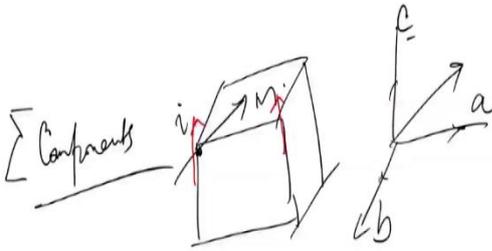
If only 1 propagat vector




Here, this  $l$  which is nothing but direction cosine and then ' $M$ ' is the vector sum of the components.  $l$  can be [0 0 1], [1 0 0], [0 1 0]. Sum of three components in  $a$ ,  $b$ ,  $c$  directions give you the magnet vector at a certain lattice site. Now, if there is only [0 0 1] component of magnetic moment, say in ' $c$ ' direction, then I can write it as  $M_i$  is nothing but  $M_i^{[001]}$ .

(Refer Slide Time: 7:00)

$\sum$  Components





That means in this diagram, moments are in the [0 0 1] direction.

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Similar to crystallographic unit cell, there are magnetic unit cells for a crystal, which may be much larger than the crystallographic unit cell

We use the nuclear or structural unit cell and a **PROPAGATION VECTOR** to describe magnetic cell

$$M_i = \sum_l a_l M_i^l$$

l'th moment in the 0'th cell. A sum of components

$$M_i = M_i^{[001]}$$

If there is only [001] component

Since the magnetism is a periodic property, we can make a Fourier expansion of the same in terms of vectors in the Brillouin Zone.

$$M_i = \sum_k M_i^k e^{-2\pi i k \cdot r}$$

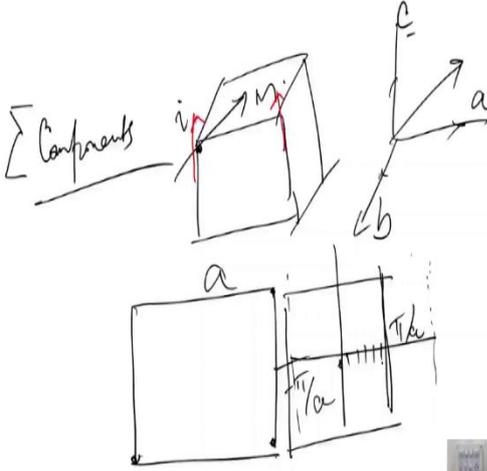
$$M_i = M_i^k e^{-2\pi i k \cdot r}$$

If only 1 propagat vector




Then I can write magnetic moment as  $M_i = M_i^{[001]}$ . Since this magnetism is a periodic property, either it is repeating every unit cell, two-unit cells or may be thousand unit cells. From mathematics we know that for any periodic function we can do a Fourier expansion in terms of vectors in the Brillouin Zone. What is a Brillouin Zone?

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Let me just explain to you. If these are the nearest neighbors at a distance  $a$ , then in the  $k$  space, I can draw a line to the nearest neighbor in the reciprocal space at  $2\pi/a$  and then draw perpendicular vector to that, and that is my first Brillouin Zone and this has boundaries at  $\pi/a$  and  $-\pi/a$ , if I take the origin here. This is known as a Brillouin Zone in reciprocal lattice space. So now, in this Brillouin Zone there are various values of allowed  $k$  vectors in a crystal lattice.

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Similar to crystallographic unit cell, there are magnetic unit cells for a crystal, which may be much larger than the crystallographic unit cell

We use the nuclear or structural unit cell and a **PROPAGATION VECTOR** to describe magnetic cell

$$M_i = \sum_t a_t M_i^t$$

't' th moment in the 't' th cell. A sum of components

$$M_i = M_i^{[001]}$$

If there is only [001] component

Since the magnetism is a periodic property, we can make a Fourier expansion of the same in terms of vectors in the Brillouin Zone.

$$M_i = \sum_k M_i^k e^{-2\pi i k \cdot t}$$

$$M_i = M_i^k e^{-2\pi i k \cdot t}$$

If only 1 propagation vector

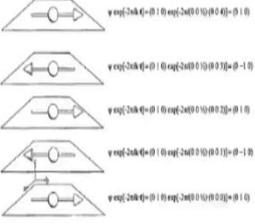



And I can write down the magnetic vector at a site in terms of its Fourier components  $M_i^k e^{-2\pi i k \cdot t}$ , where  $k$  is that propagation vector and  $t$  is the translation. If there is only one propagation vector for the system then I can write it as  $M_i = M_i^k e^{-2\pi i k \cdot t}$ , the summation will have a single component.

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**Example**

NEUTRONS ET MAGNÉTISME P19-



Antiferromagnetic order in 'c' direction [001]. Magnetic Unit cell double. Each plane is translation 't' [001]. One propagation vector  $[0 \ 0 \ \frac{1}{2}]$

Moment in 'b' direction [010].

$$M_i = M_i^k e^{-2\pi i k \cdot t}$$

$$= [010] e^{-2\pi i [0+0+\frac{1}{2}]}$$

$$= [0 \ -1 \ 0]$$

Magnetic structures and their determination using group theory  
A. Wills

J. Phys. IV France 11 (2001)  
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Let me just explain it with an example. I just take an anti-ferromagnetic order in one direction. This is a plane. And the direction of the magnetic moment switches between plus and minus from one plane to another as you go in 'c' direction.

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$$t = [001].$$
$$M = [010]$$

---

$$[00\frac{1}{2}]$$
$$M = [010] \exp(-2\pi i k \cdot t)$$
$$[00\frac{1}{2}] \quad t [001]$$
$$\exp(-2\pi i \cdot \frac{1}{2}) = \exp(-\pi i)$$



I am going in  $c$  direction, so, translation  $t$  is in  $c$  direction given by  $[001]$ . And moment is along the  $b$  direction as I showed in the drawing. So, I can write in some units this moment is  $[010]$ . Here, the moment is  $[010]$  and translation is  $[001]$ . Now, let us see, in this case when it is an anti-ferromagnetic alignment, if I take a propagation vector of  $00\frac{1}{2}$  then what happens after one translation? After one translation,

$$M = [010]e^{-2\pi i k \cdot t}$$

With  $k = [00\frac{1}{2}]$  and  $t = [001]$ , exponential term becomes  $e^{-\pi i}$ .

(Refer Slide Time: 11:47)

**Example**

NEUTRONS ET MAGNÉTISME P9-

Antiferromagnetic order in 'c' direction [001]. Magnetic Unit cell double. Each plane is translation 't' [001]. One propagation vector [0 0 1/2]

Moment in 'b' direction [010].

$$M_i = M_i^t e^{-2\pi i k t}$$

$$= [010] e^{-2\pi i (0+0+\frac{1}{2})}$$

$$= [0 -1 0]$$

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$$M^t = [010] e^{-i\pi}$$

$$= [010] [\cos \pi - i \sin \pi]$$

$$= [0 -1, 0]$$

Here  $M$  becomes,

$$M = [010] e^{-\pi i}$$

$$M = [010] [\cos \pi - i \sin \pi]$$

$$M = [0 -1 0]$$

So, after translation of  $t$ , my magnetic moment has become [0 -1 0] from [0 1 0].

(Refer Slide Time: 12:42)

**Example**

NEUTRONS ET MAGNÉTISME P19

$\psi \exp(2\pi i k \cdot r) = \exp(2\pi i (0 \ 0 \ 1/2) \cdot (0 \ 0 \ z)) = \exp(i\pi z)$   
 $\psi \exp(2\pi i k \cdot r) = \exp(2\pi i (0 \ 0 \ 1/2) \cdot (0 \ 0 \ z)) = \exp(-i\pi z)$   
 $\psi \exp(2\pi i k \cdot r) = \exp(2\pi i (0 \ 0 \ 1/2) \cdot (0 \ 0 \ z)) = \exp(i\pi z)$   
 $\psi \exp(2\pi i k \cdot r) = \exp(2\pi i (0 \ 0 \ 1/2) \cdot (0 \ 0 \ z)) = \exp(-i\pi z)$   
 $\psi \exp(2\pi i k \cdot r) = \exp(2\pi i (0 \ 0 \ 1/2) \cdot (0 \ 0 \ z)) = \exp(i\pi z)$

Magnetic structures and their determination using group theory  
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Antiferromagnetic order in 'c' direction [001]. Magnetic Unit cell double. Each plane is translation 't' [001]. One propagation vector [0 0 1/2]

Moment in 'b' direction [010].

$$M_i = M_i^k e^{-2\pi i k \cdot r}$$

$$= [010] e^{-2\pi i (0 + 0 + \frac{1}{2})z}$$

$$= [0 \ -1 \ 0]$$

That is exactly what I have shown in the diagram in an anti-ferromagnetic order. So, given this magnetic propagation vector there is only one propagation vector here which is  $k = [0 \ 0 \ 1/2]$ . For this I could straight away guess, because it is very clear  $L$  became  $2L$ , so  $k$  becomes  $1/2$ .

Instead of 't' which is 1 unit translation, it is  $2t$  now, my  $k$  is  $1/2$ . Very easy to guess in this case, I have taken it from this reference [given in transparency]. While you are fitting a magnetic sample data, we need to start with a guess of the propagation vector. I would say physically reasonable guess, which comes from knowledge in magnetic structures.

(Refer Slide Time: 13:34)

a) ferromagnetic    b) antiferromagnetic    c) ferrimagnetic  
 d) triangular    e) square    f) diamond  
 g) sine or cosine    h) circular helix    i) elliptical helix

Like, I showed you here, various kinds of alignments. For example, this is a ferromagnetic sample. Here the propagation vector will be  $[0 \ 0 \ 1]$ . In the previous diagram what I showed

was for an anti-ferromagnet it is [0 0 1/2]. This is a ferrimagnet. Then with every 't', I also have to add an  $\alpha t t$  to account for the length change of the magnetic moment. That means the length of the vectors are also changing. Not just that they are changing in site they are also changing in size. Similarly another one is a triangular kind of lattice, it is a canted lattice. This is an umbrella kind of lattice where all of these vectors we have to represent in terms of  $a, b, c$  and then the propagation vector in terms of reciprocal lattice in the Brillouin Zone I can choose a set of  $k$  vectors which can give the values correctly.

I show a sin or cosine kind of variation here. Because this is a ferrimagnet, the length of the moment is changing. Similarly, these are circular helix, where as we go ahead in one direction, for simplicity in [0 0 1] direction, the magnetic moment gets rotating, and finally, comes back to its original direction after a certain number of lattice points and  $2\pi$  divided by that will be the propagation vector for the magnetic moment,.. Then these are elliptic propagation. So, here the moment, is not only rotating, the size is also changing. There are various possible structures in magnetic crystallography that we can consider and that is the part of the game of solving a magnetic structure.

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Rietveld Refinement

It is a least square fitting technique where a calculated diffraction pattern is compared with the experimentally observed powder neutron diffraction pattern. The calculated pattern is modified (or *refined*) by changing the assumed magnetic and nuclear structure, till an *acceptable* fit is obtained with the experimental data

$$E = \sum_i w_i [y_i^{obs} - y_i^{calc}]^2$$

The intensity of the diffraction data at every angle is a convolution of several parameters

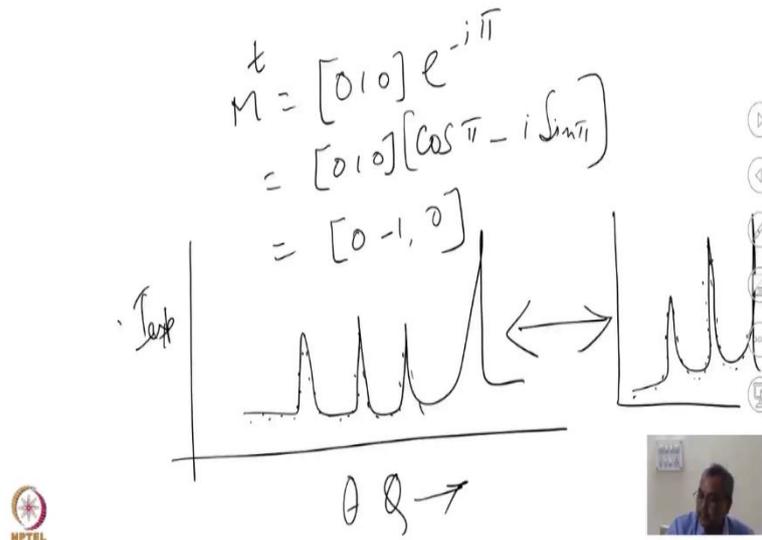
$PSF(\theta) = R(\theta) \otimes \lambda(\theta) \otimes S(\theta) + b(\theta)$

The peak shape function PSF is a convolution of  $R(\theta)$  (Wavelength distribution  $\lambda(\theta)$ ) and sample function  $S(\theta)$  at every angle plus a background  $b(\theta)$ .

NPTEL

About Rietveld refinement what I want to say is that, it is a least square fitting technique; that means you start with an assumed diffraction pattern in hand.

(Refer Slide Time: 15:55)



You have got an experimental diffraction pattern which you have measured at a certain temperature (intensity vs ' $\theta$ ' or ' $Q$ '). And on the other hand, you have got a calculated pattern and I have to compare these two. That means at every point where I have measured the data I also have a model data. I have considered a model and I have generated this and I am comparing these two patterns.

(Refer Slide Time: 16:51)

$$M = \sum_i W_i \left[ y_{\text{exp}}^i - y_{\text{model}}^i \right]^2$$

I have got  $y_{\text{exp}}$  and I have got  $y_{\text{model}}$ , and I have to minimize the values  $[y_{\text{exp}} - y_{\text{model}}]$  of them. There are many points, so you need to sum over those points  $i$ ,  $\sum_i [y_{\text{exp}}^i - y_{\text{model}}^i]^2$ . If I want, depending on physical reasoning, I can put a weight factor over here  $\sum_i W_i [y_{\text{exp}}^i - y_{\text{model}}^i]^2$ . So, I have to calculate this difference  $[\chi^2]$  and fundamentally this is the numerical comparison between data that I am using for my fitting.

(Refer Slide Time: 17:32)

Rietveld Refinement

It is a least square fitting technique where a calculated diffraction pattern is compared with the experimentally observed powder neutron diffraction pattern. The calculated pattern is modified (or *refined*) by changing the assumed magnetic and nuclear structure, till an *acceptable* fit is obtained with the experimental data

$$E = \sum_i w_i [y_i^{obs} - y_i^{calc}]^2$$

The intensity of the diffraction data at every angle is a convolution of several parameters

$$PSF(\theta) = R(\theta) \otimes \lambda(\theta) \otimes S(\theta) + b(\theta)$$

The peak shape function PSF is a convolution of  $R(\theta)$  Wavelength distribution  $\lambda(\theta)$  and sample function  $S(\theta)$  at every angle plus a background  $b(\theta)$ .



As I said,  $E = \sum_i W_i [y_{exp}^i - y_{model}^i]^2$  it is a weighted sum of the difference between the observed or experimental and the calculated(model) value. The intensity of diffraction at every angle, again is a convolution of several parameters and is given by,

$$PSF(\theta) = R(\theta)\lambda(\theta)S(\theta) + b(\theta)$$

$R(\theta)$  is resolution,  $\lambda(\theta)$  wavelength dispersion,  $S(\theta)$  sample related part and  $b(\theta)$  is the background at the specific angle.

(Refer Slide Time: 18:10)

$$M = \sum_i W_i \left[ Y_{\text{exp}}^i - Y_{\text{model}}^i \right]^2$$

$$C(x) = \int Y_1(x-x') Y_2(x') dx$$

I must mention that convolution of two functions  $Y_1$  and  $Y_2$  at a point  $x$  is given by,

$$C(x) = \int Y_1(x - x') Y_2(x') dx$$

Experimentally suppose, I have got a peak like this. Now if my instrumental resolution is a Gaussian like this, then each and every point will tend to spread out based on that Gaussian and then I will have a broader peak, whereas this is the theoretical peak and this is the convoluted peak.

(Refer Slide Time: 19:10)

Rietveld Refinement

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$$E = \sum_i w_i [y_i^{obs} - y_i^{calc}]^2$$

The intensity of the diffraction data at every angle is a convolution of several parameters

$PSF(\theta) = R(\theta) \otimes \lambda(\theta) \otimes S(\theta) + b(\theta)$

The peak shape function PSF is a convolution of  $R(\theta)$  Wavelength distribution  $\lambda(\theta)$  and sample function  $S(\theta)$  at every angle plus a background  $b(\theta)$ .

So, apart from these two over there when I wrote I have got resolution function, I have got a wavelength dispersion, because the wavelength of neutrons that I use is not unique. I use a

band of neutrons because I need intensity. If I try to make it monoenergetic then I will have very few neutrons. So, I have got a band off.

Then there is a sample; there can be a preferred orientation in the sample, there can be strain in the sample, if I know them, they also will cause broadening. There is a background, because anywhere I do the experiment there will be background neutrons and at every angle it will have a value.

The calculated value has to be convoluted with all these and then only I can compare the calculated value convoluted with all these with the experimental value. With this I come the end of this lecture. I have given a very general expression for the Rietveld refinement. But now I will tell you specifically what are the inputs in the next lecture,.

There are several tutorials available online which will give you the references and I will also mention, what are the important parameters, that need to be given in Rietveld refinement program. Let me emphasize once again that this is actually making a given model more and more commensurate with the experimentally observed pattern which is known as Rietveld refinement.

It was developed by Hugo Rietveld. The program name is FullProf and it is a very, very important program suit, which is used heavily for the magnetism. This is possibly the most important package in use today for crystallographic/magnetic structure determination. I will come back to Rietveld refinement in the next lecture. I will briefly mention some examples and then we will go ahead.