EosDX 1st Data Conference

STUYVESANT HIGH SCHOOL

Analysis of Mouse Brain Structure through Fourier Transformation of XRD Patterns

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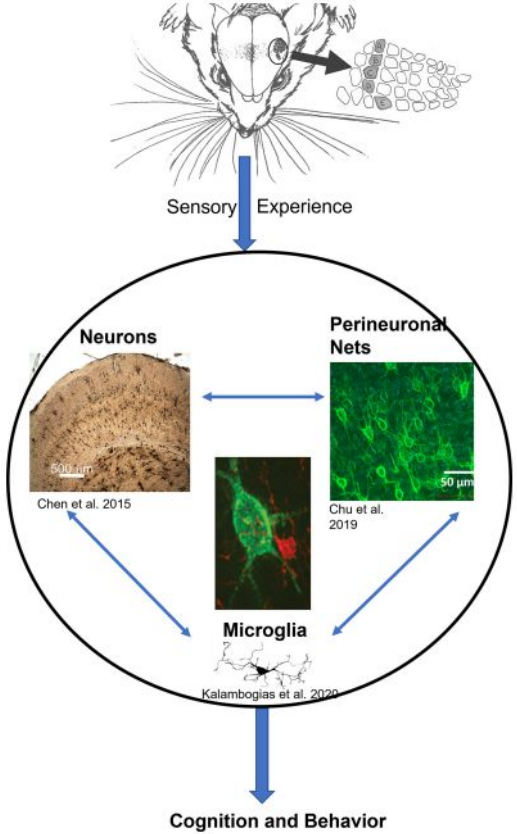
Mouse whiskers



- When mouse whiskers are removed, they are deprived of key sensory information
- When this is done early on in their lives, it causes a change in brain structure on a molecular level.
- Experiments done by Brumberg demonstrate a change in behaviour as well as brain structure of mice.

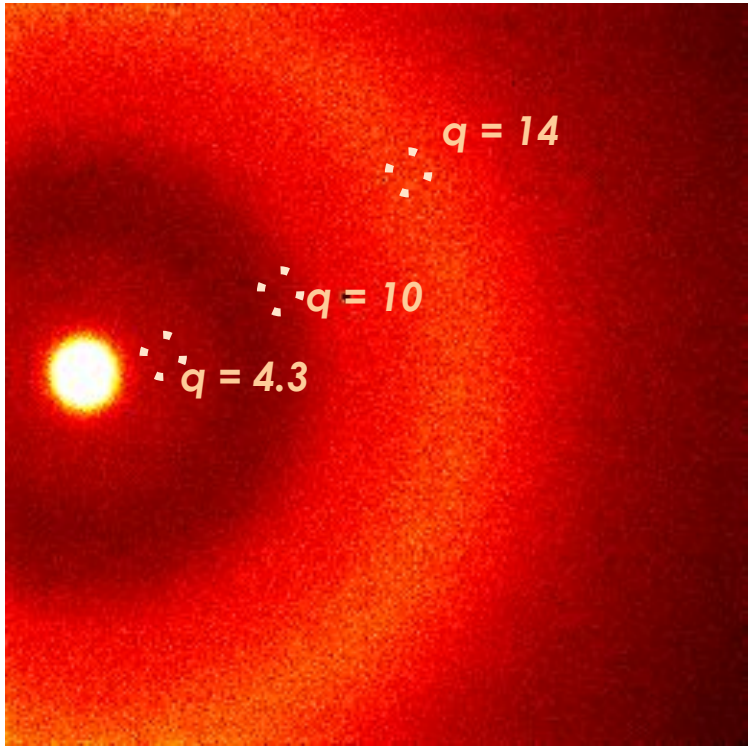
Brain samples nomenclature (28 samples)

Samples of the wild type are numbered, and samples with trimmed whiskers have the letters assigned

Wild Type:	Animal #:	Sex:	Hemisphere:	Trimmed:	Animal #:	Sex:	Hemisphere:
1	4	F	Left	A	9	F	Left
2	4	F	Right	B	9	F	Right
3	1	F	Left	C	7	F	Left
4	1	F	Right	D	7	F	Right
5	3	F	Left	E	8	F	Left
6	3	F	Right	F	8	F	Right
7	30	F	Left	G	16	M	Left
8	30	F	Right	H	16	M	Right
9	31	F	Right	I	24	M	Left
10	31	F	Left	J	24	M	Right
11	6	M	Left	K	27	M	Left
12	6	M	Right	L	27	M	Right
13	5	M	Left	M	23	M	Left
14	5	M	Right	N	23	M	Right

XRD Pattern Overview

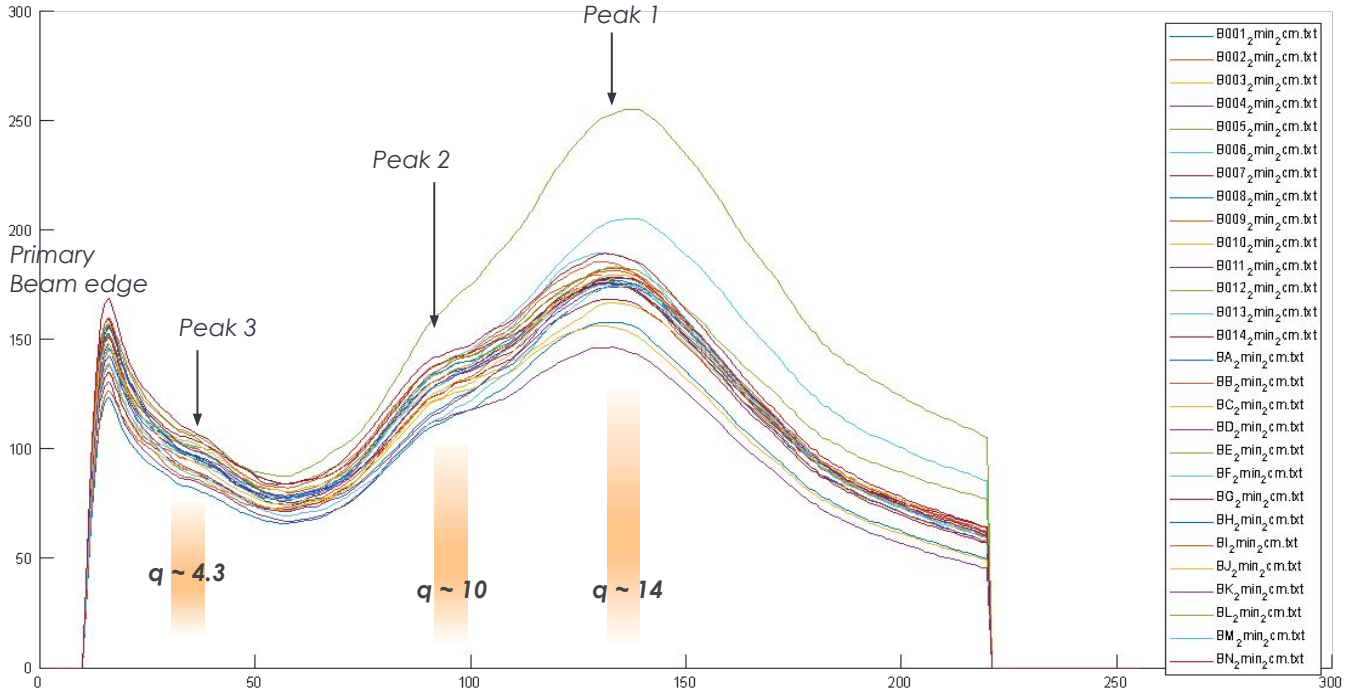
Characteristic XRD pattern



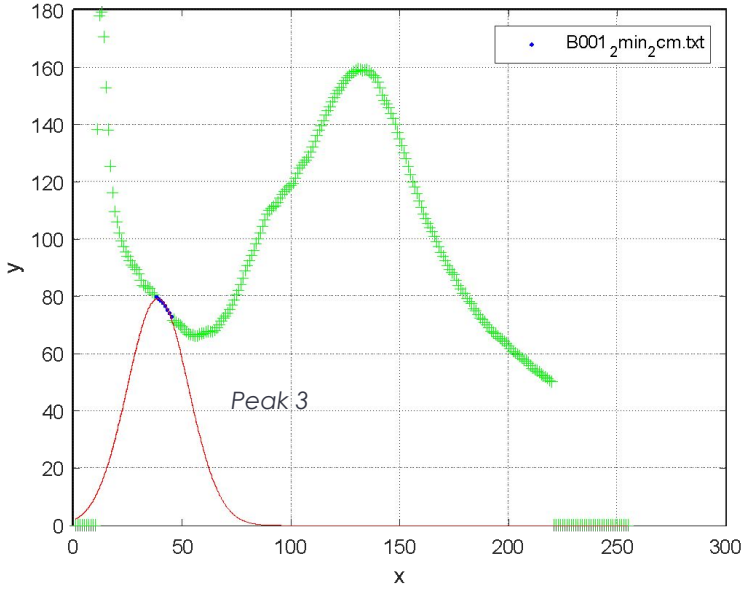
- 28 samples
- ~20 mm from sample to detector
- q – field of view range of approx 6 - 30
- All patterns are normalized by the integral of primary beam
- Concentric rings appear as peaks with associated magnitude of scattering vector:

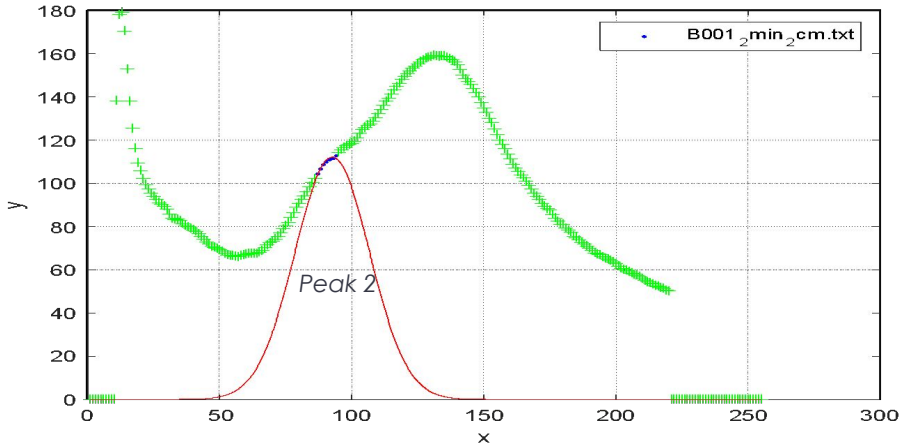
$$q = \frac{4\pi \sin\theta}{\lambda}.$$

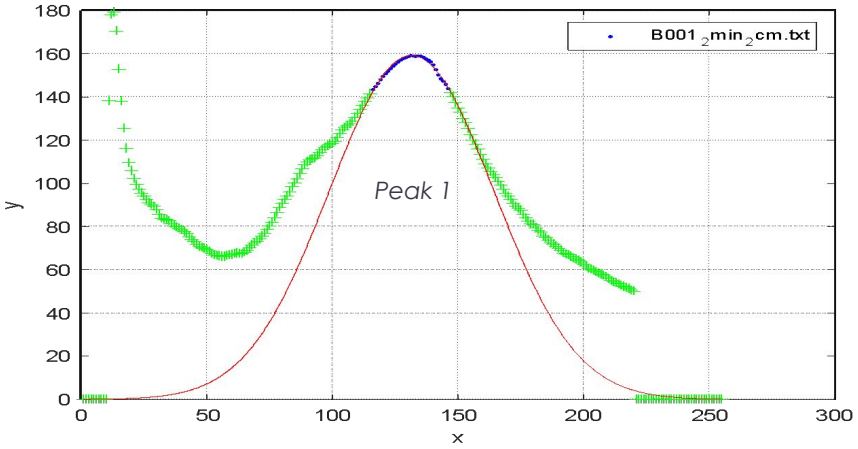
Brain samples intensity profiles (28 samples)



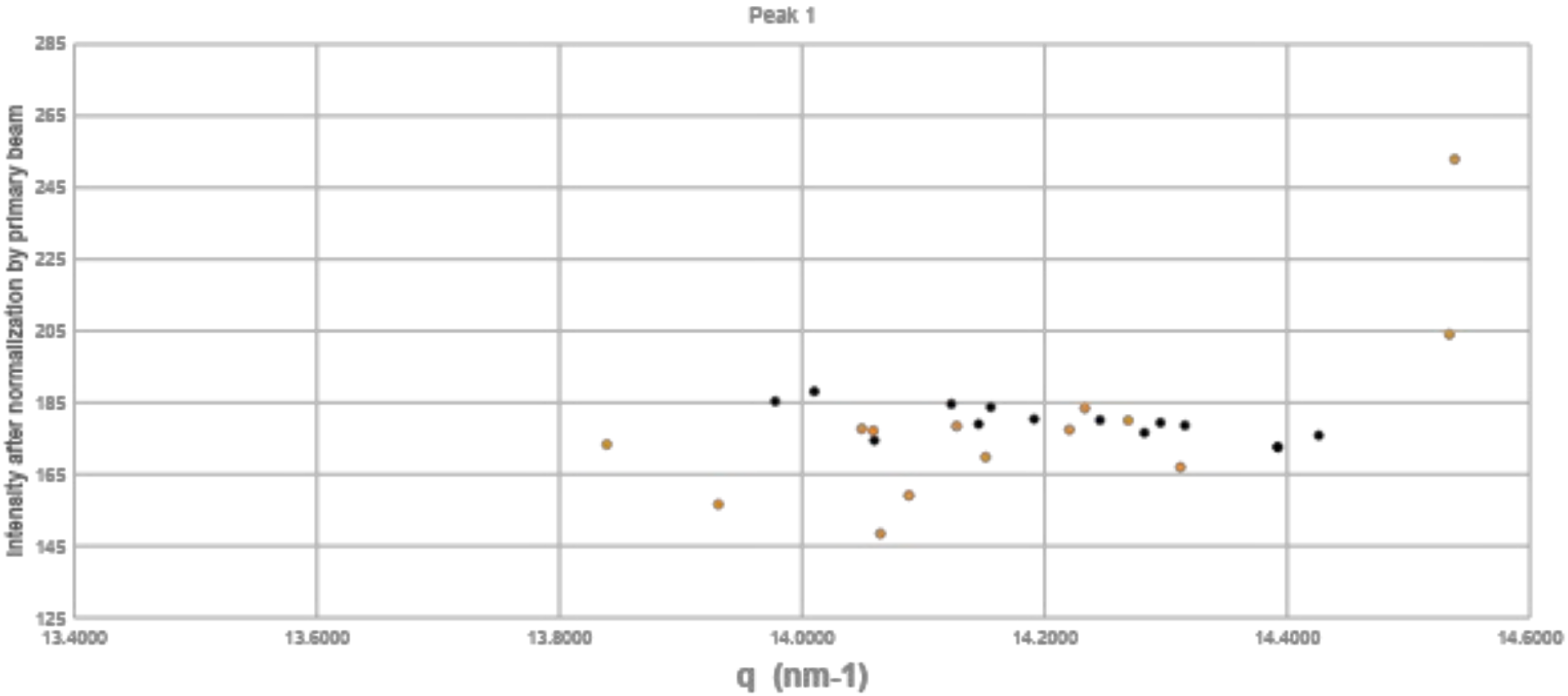
Gaussian peak analysis by Alexander Lazarev





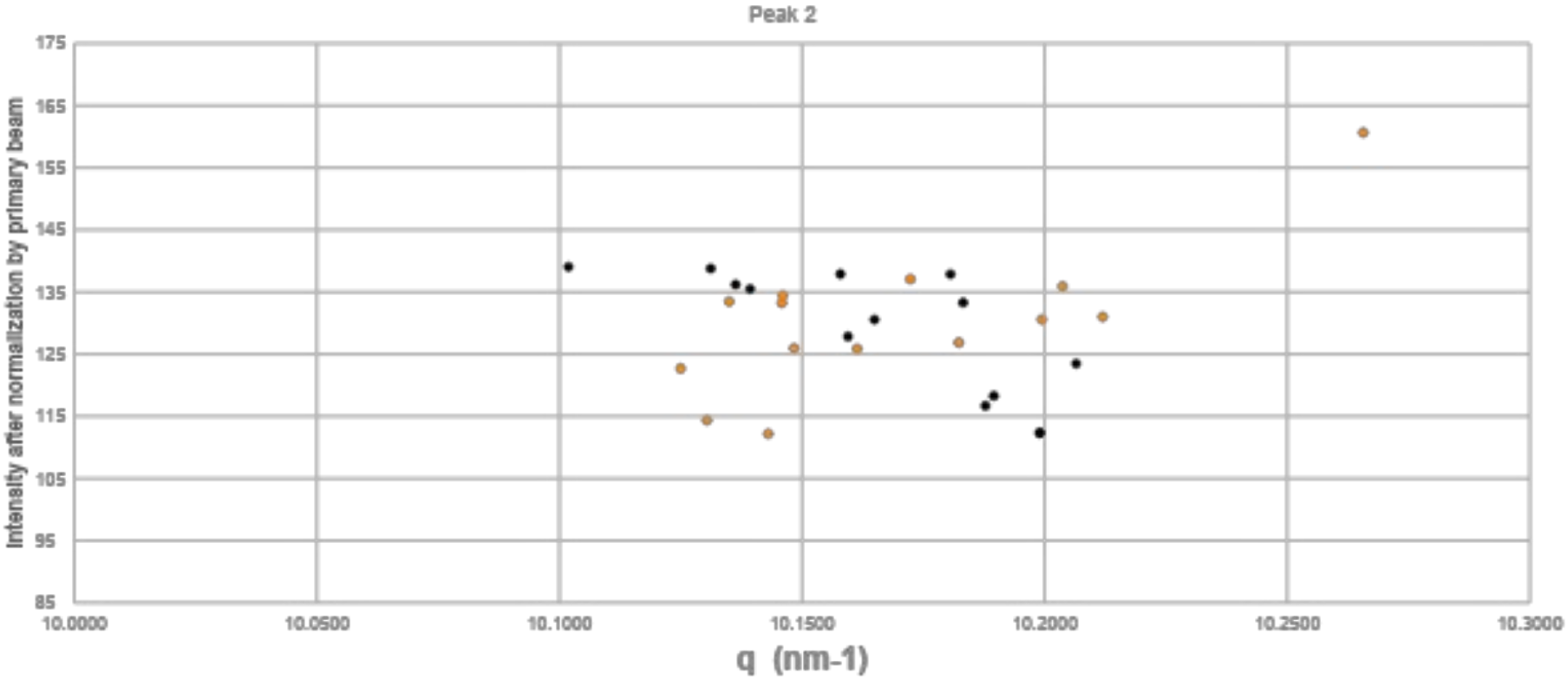


Peak 1



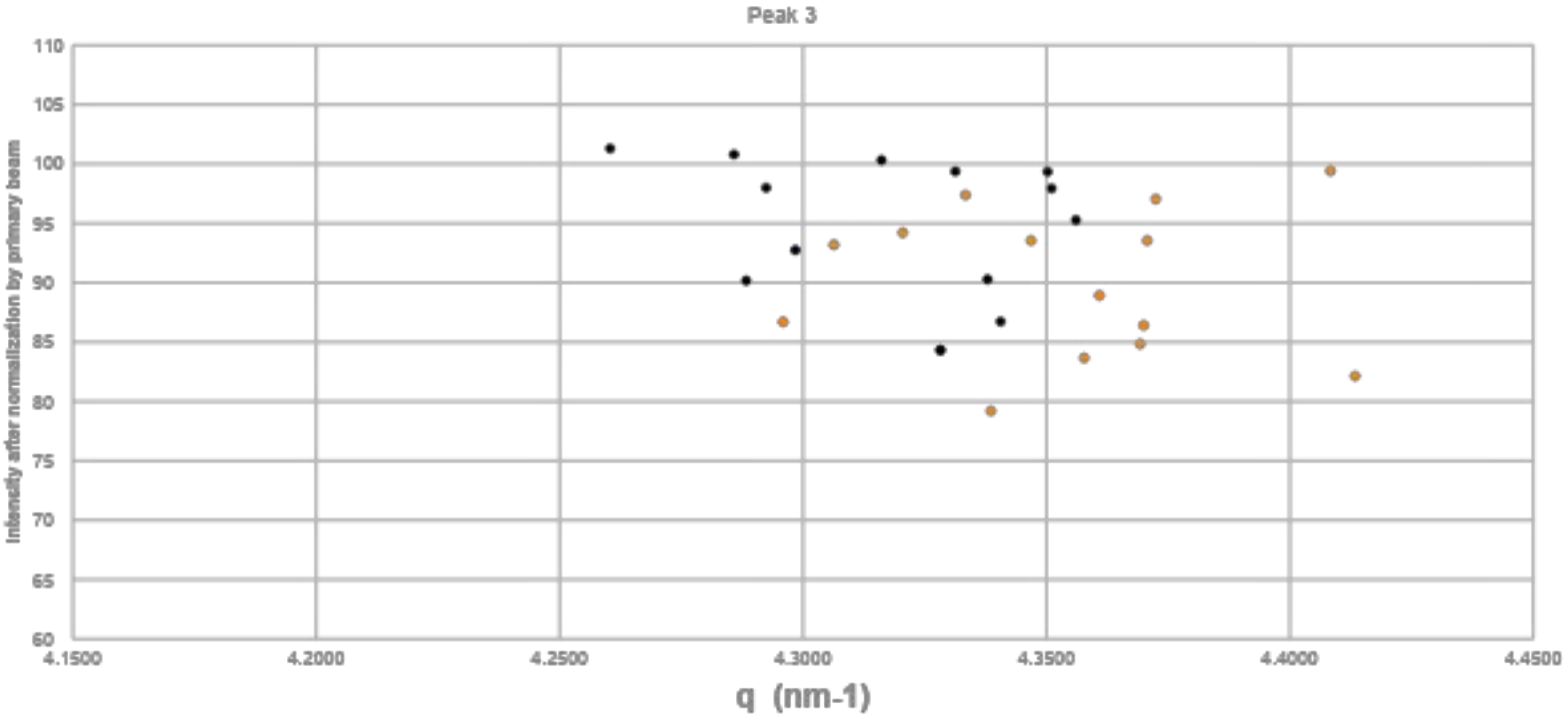
No clear separation between wild type and trimmed

Peak 2



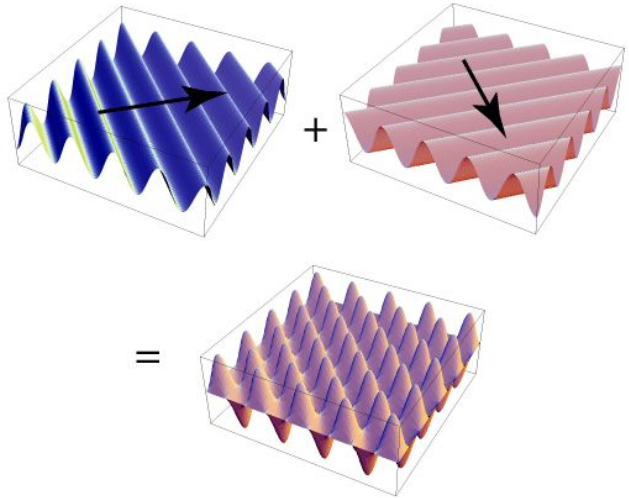
No clear separation between wild type and trimmed

Peak 3



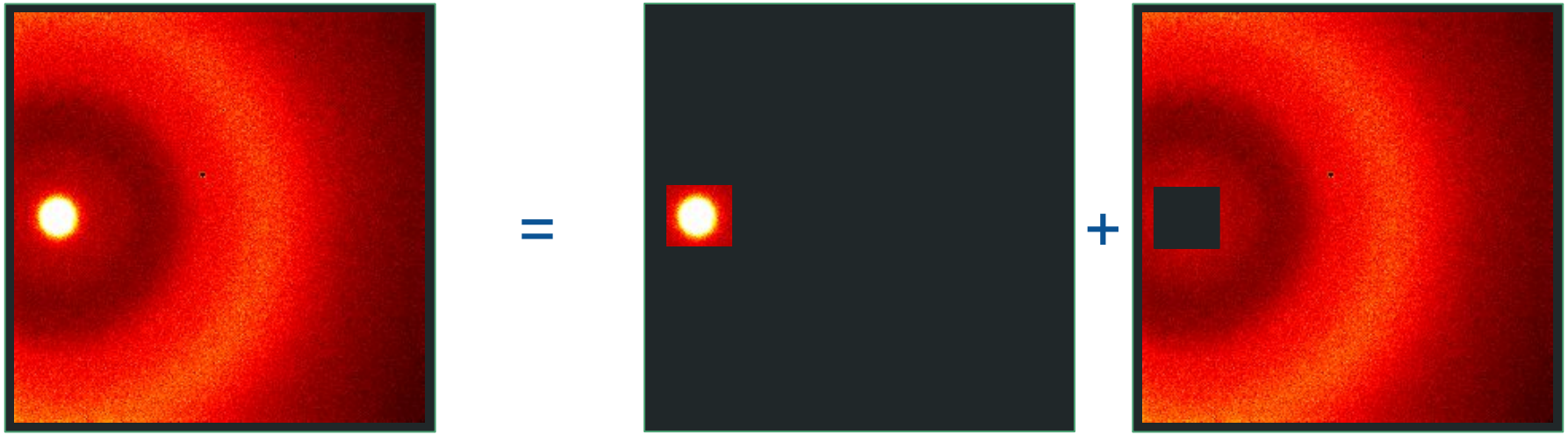
Seems to be some separation between wild type and trimmed

2D Fourier analysis



- Product of two Fourier analysis on x and y direction, allowing for a 2D representation of the XRD image

$$f(x,y) = F_0 + F_{1,0}\sin\left(k_x x + \phi_{x1}\right) + F_{0,1}\sin\left(k_y y + \phi_{y1}\right) + F_{1,1}\sin\left(k_x x + \phi_{x1}\right)\sin\left(k_y y + \phi_{y1}\right)$$
$$+ F_{2,0}\sin\left(2k_x x + \phi_{x1}\right) + F_{0,2}\sin\left(2k_y y + \phi_{y1}\right) + F_{2,1}\sin\left(2k_x x + \phi_{x1}\right)\sin\left(k_y y + \phi_{y1}\right) + \ldots$$



A B C

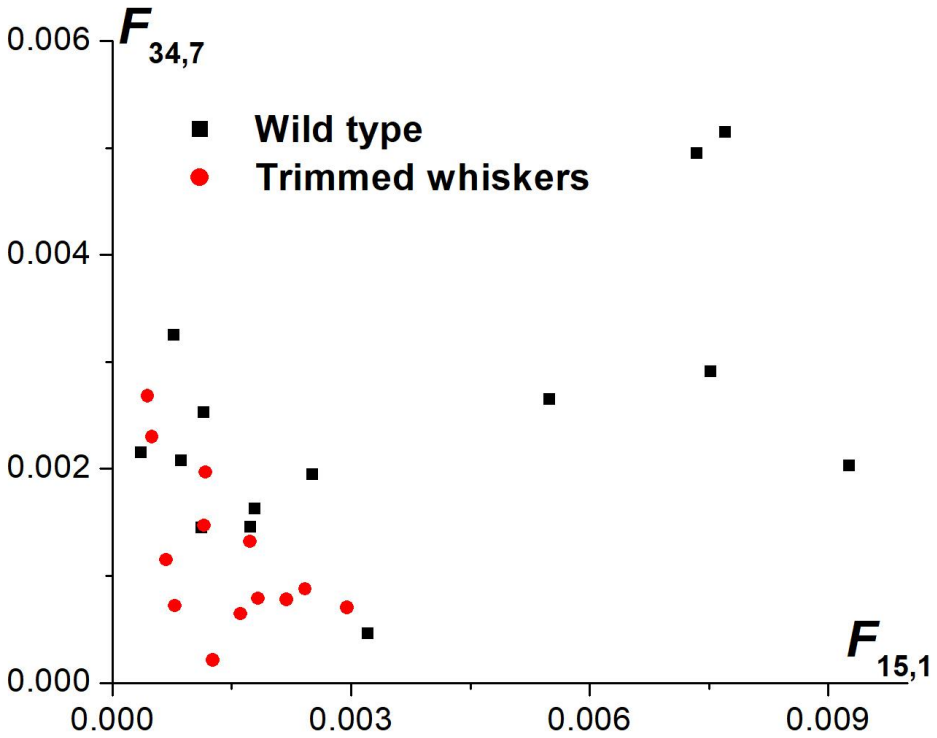
$$F(A) = F(B) + F(C)$$

$$F(C) = F(A) - F(B)$$

Procedure

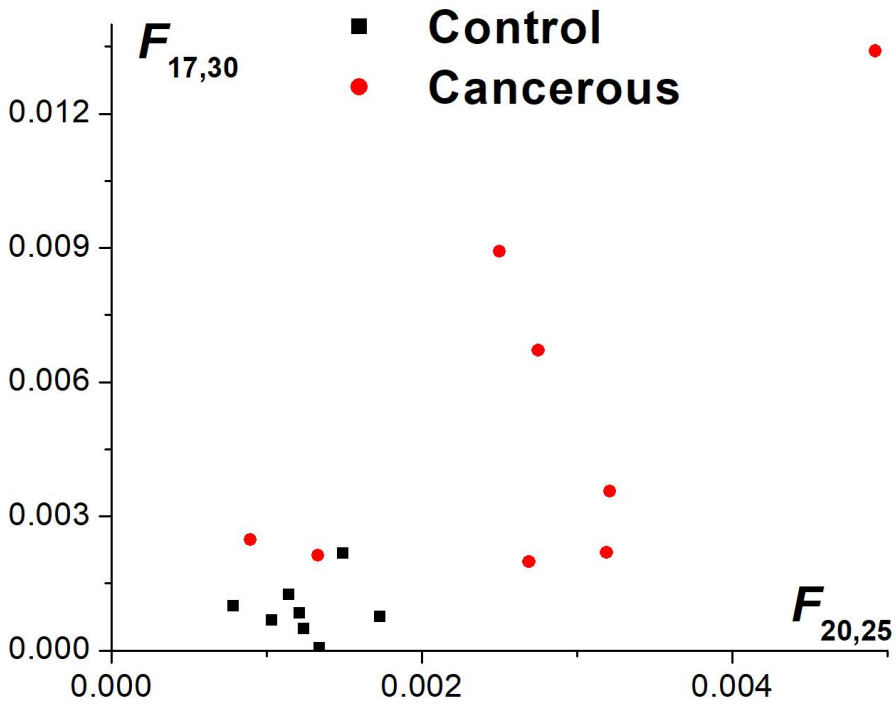
1. Separate 256x256 XRD image array into A and B
2. Fourier transformation of both
3. Subtract and absolute value for C because coefficients are complex numbers, creating a 256x256 Fourier transformation of the concentric rings
4. Normalization of each Fourier-transformed array: all values divided by (0, 0)
5. Average all 14 arrays for wild type and trimmed whiskers
6. Subtract wild type and trimmed whiskers
7. Manually find large/significant components which separate the two types of samples
8. Find and graph respective values from the normalised arrays

Results



- There is a better separation of mouse brain on a molecular level that indicate developmental changes in mice if their whiskers are removed
- Deprivation of key sensory information led to a lack of brain structural development
- The larger values indicate structure, which the trimmed samples seem to lack

Results



- Limited samples of Horizon data, provided by Jonathan
- This indicates some separation of control and cancerous elements

Improvements

- The separation between the unscattered part of the XRD and the concentric rings is harsh and there are better alternative ways of doing it gradually
- Also, significant fourier components were selected and tried manually
- This can be resolved with principal component analysis in the future, which will use not just two peaked components, but also their superposition, allowing for fourier components to be selected in a way that ensure clear clusterization.

Conclusion

- I performed Fourier component analysis on mouse brain XRD, and showed the separation, indicating change in brain structure on a molecular level.
- Fourier transformation have an advantage in precision over gaussian peak analysis, however it lacks the direct connection between key components and physical brain structure.
- Looking at a small set of Horizon samples, there is also a clear separation that can be further improved through the use of artificial intelligence methods.