

SOLVING ATOMIC STRUCTURE USING STATISTICAL MECHANICAL SEARCHES ON
X-RAY SCATTERING DERIVED POTENTIAL ENERGY SURFACES

by

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DEDICATION

ACKNOWLEDGMENTS

ABSTRACT

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¹

INTRODUCTION

² This is the introduction to the thesis.

3

CHAPTER 1

4 ATOMIC STRUCTURE: EXTRACTION AND APPLICATION

5 1.1 ATOMISTIC GOALS

6 The only way to truly understand the fundamental souce of material and chemical
7 properties is through atomic structure. The goal of atomistic engineering is to pro-
8 duce novel structures and combinations of structures to engender new properties and
9 functions. This includes producing stronger materials, more durable catalysts, more
10 energy dense batteries, and many more engineering applicatons. The true power of
11 atomistic engineering has been shown in biochemistry and pharmicuttical design. Al-
12 though the production of drugs and biomeical treatments is usually considered to be
13 rather far from the field of catalyst design and materials science, the atomistic nature
14 of these fields can not be denied. The field of protiene structural analysis stands
15 as an example of structural science, elcuidating the three dimensional coordinates of
16 thousands of atoms. These structures are then used to describe how the molecular
17 machinery of the biological world works, enabling the development of new drugs and
18 treatments for diseases and a deeper understanding of how we evolved. The develop-
19 ment of protene inhibitor drugs, which are important to so many treatments, would
20 have not been possible without very detailed atomic structures. The asperation of
21 this work is to create this level of accuracy and utility, generating structures which
22 allow for the understanding of how materials work on a fundamental level.

23 1.2 ATOMISTIC EXPERIMENTS

24 Single Crystal Diffraction

25 Electron Microscopy

26 X-ray Total Scattering

27 1.3 ATOMISTIC SIMULATIONS

28 The goals of atomistic simulations are usually to produce atomic structures from
29 quantum mechanical first principles, as in the case of Density Functional Theory
30 (DFT), or classical approximations to quantum mechanics.

31 Density Functional Theory

32 Classical Force Field

33 Monte Carlo and Statistical Mechanics

34 Maybe put the ensemble and PES work here, since it is more general than the PDF
35 per say. Also the rational for the gradients and fast computation make much more
36 sense knowing we are going to be very sample happy and follow the gradient of the
37 PES.

38

CHAPTER 2

39

STATISTICAL MECHANICAL ENSEMBLES AND POTENTIAL ENERGY SURFACES

41 2.1 INTRODUCTION

42 The approach taken in this work for solving the atomic structures of materials is
43 one of optimization. The positional variables of the system are optimized so as to
44 minimize the value of a potential energy surface (PES). The

45 2.2 POTENTIAL ENERGY SURFACES

46 A PES simply describes the potential energy of the system as a function of all its
47 relevant coordinates in phase space, essentially providing a mapping $\mathbb{R}^n \rightarrow \mathbb{R}$. Usually
48 these coordinates are the positions of the atoms q and their conjugate momenta p .
49 Note that there could be more variables associated with the system, for instance the
50 magnetic moments of the atoms could play a role in describing the system. In this
51 magnetic system there would be positional variables for the atomwise spin vectors
52 and their "momenta". Application of the term "momenta" might seem odd here, as
53 the magnetic spin does not have a mass or a velocity. However, since the magnetic
54 "position" is defined on the PES we need to describe its conjugate variable to properly
55 formulate Hamiltonian dynamics and the kinetic portion of the PES.

56 **Experimentally Derived Potential Energy Surfaces**

57 Generally PESs are obtained from purely computational experiments including: ab-
 58 initio DFT, classical approximations via the embedded atom method, or even param-
 59 eter driven models with experimentally fitted parameters. However, one can derive
 60 a PES from an experiment which describes how well the model reproduces the ex-
 61 perimental data. In this case one needs a theoretical and computational framework
 62 mapping the atomistic variables of the simulation to the same space of the data ob-
 63 tained from the experiment. This allows the experiment to be compared directly
 64 against the predicted data via an experimentally derived PES.

65 **Potentials**

66 For an experiment which produces 1D data, like powder diffraction, EXAFS or XPS,
 67 the implemented potentials are:

$$\chi^2 = \sum_{a=a_{\min}}^{a_{\max}} (A_{\text{obs}} - \alpha A_{\text{calc}})^2 \quad (2.1)$$

$$Rw = \sqrt{\frac{\sum_{a=a_{\min}}^{a_{\max}} (A_{\text{obs}} - \alpha A_{\text{calc}})^2}{\sum_{a=a_{\min}}^{a_{\max}} A_{\text{obs}}^2}} \quad (2.2)$$

$$\chi_{\text{INVERT}}^2 = \frac{1}{N} \sum_j \sum_r [A_{\text{obs}}(r) - \alpha A_{j,\text{calc}}(r)]^2 \quad (2.3)$$

$$\alpha = \frac{\sum_{a=a_{\min}}^{a_{\max}} A_{\text{obs}} A_{\text{calc}}}{\sum_{a=a_{\min}}^{a_{\max}} A_{\text{calc}}^2} = \frac{\vec{A}_{\text{obs}} \cdot \vec{A}_{\text{calc}}}{|\vec{A}_{\text{calc}}|^2} \quad (2.4)$$

71 where A_{calc} and A_{obs} are the calculated and observed 1D experimental data and $A_{\text{calc},j}$
 72 is the calculated data for a single atom interacting with the other atoms of the system.
 73 Note that A_{calc} has a dependence on q , the positions of the system.

74 **Forces**

$$\vec{\nabla} \chi^2 = -2 \sum_{a=a_{\min}}^{a_{\max}} (\alpha \frac{\partial A_{\text{calc}}}{\partial \gamma_{i,w}} + A_{\text{calc}} \frac{\partial \alpha}{\partial \gamma_{i,w}})(A_{\text{obs}} - \alpha A_{\text{calc}}) \quad (2.5)$$

75

$$\vec{\nabla}Rw = \frac{Rw}{\chi^2} \sum_{a=a_{\min}}^{a_{\max}} (\alpha \frac{\partial A_{\text{calc}}}{\partial \gamma_{i,w}} + A_{\text{calc}} \frac{\partial \alpha}{\partial \gamma_{i,w}})(\alpha A_{\text{calc}} - (A_{\text{obs}})) \quad (2.6)$$

76

$$\frac{\partial \alpha}{\partial \gamma_{i,w}} = \frac{(\sum_{a=a_{\min}}^{a_{\max}} A_{\text{obs}} \frac{\partial A_{\text{calc}}}{\partial \gamma_{i,w}} - 2\alpha \sum_{a=a_{\min}}^{a_{\max}} A_{\text{calc}} \frac{\partial A_{\text{calc}}}{\partial \gamma_{i,w}})}{\sum_{a=a_{\min}}^{a_{\max}} A_{\text{calc}}^2} \quad (2.7)$$

77

$$\vec{\nabla}\chi^2_{\text{INVERT}} = \frac{-2}{N} \sum_{a=a_{\min}}^{a_{\max}} \sum_j (\alpha \frac{\partial A_{j,\text{calc}}}{\partial \gamma_{i,w}} + A_{j,\text{calc}} \frac{\partial \alpha}{\partial \gamma_{i,w}})(A_{\text{obs}} - \alpha A_{j,\text{calc}}) \quad (2.8)$$

78 where $\gamma_{i,w}$ is the i th arbitrary positional variable in the w th direction. The concept
 79 of an "arbitrary positional variable" might seem a bit cumbersome but it allows us
 80 to define the forces for any atomic parameter which can be represented as a vector
 81 in 3-space. This comes in handy when trying to define the forces acting on variables
 82 like anisotropic displacement parameters or atomic magnetic spins.

83 DISCUSS INVERT A BUNCH. ALSO COMPARE RW AND CHI**2, POTEN-
 84 TIALY WITH A FIGURE.

85 2.3 ENSEMBLES

86 While PESs describe which atomic configurations are the most desirable and how
 87 the atoms would like to get there, the ensemble describes how the atoms move on
 88 the PES. The abstraction of the PES from the ensemble is an important one, as it
 89 allows for the reuse and exchange of both PESs and ensembles for a wide array of
 90 problems. Statistical mechanical ensembles can be described in two ways, analytically
 91 and stochastically. For long simulation times and fine enough numerical or analytical
 92 integration these two descriptions should be identical. In either case one starts by
 93 defining the Hamiltonian \mathcal{H} as the total energy of the system. Thus, the Hamiltonian
 94 is described as the sum of the potential $U(q)$ and kinetic $K(p)$ energies, where q is
 95 the positions of the atoms and p is their momenta

$$\mathcal{H}(q, p) = U(q) + K(p) \quad (2.9)$$

96 where $K(p) = \frac{1}{2} \sum_i \frac{p_i^2}{m_i}$ and i denotes the i th particle. Analytically one generally defines
 97 a partition function, which describes the sum of probabilities over all potential atomic
 98 states.

$$\Xi = \sum_i P_i(q, p)$$

99 where P_i is the probability of the i th state and is a function of the total energy of
 100 that state. This partition function can then be used to obtain the probability of any
 101 specific state.

102 Hamiltonian Monte Carlo

In order to model dynamics we need to describe the motion of the particles in our system, thus:

$$\frac{dq_i}{dt} = \frac{\partial \mathcal{H}}{\partial p_i} = p_i \quad (2.10)$$

$$\frac{dp_i}{dt} = -\frac{\partial \mathcal{H}}{\partial q_i} = -\vec{\nabla}U \quad (2.11)$$

Using these equations we can derive the position and momentum vectors at any point in time using the leap-frog algorithm:

$$p_i(t + \delta t/2) = p_i(t) - \frac{\delta t}{2} \frac{\partial}{\partial q_i} U(q(t)) \quad (2.12)$$

$$q_i(t + \delta t) = q_i(t) + \delta t * p_i(t + \delta t/2) \quad (2.13)$$

$$p_i(t + \delta t) = p_i(t + \delta t/2) - \frac{\delta t}{2} \frac{\partial}{\partial q_i} U(q(t + \delta t)) \quad (2.14)$$

103 Note that $\frac{\partial}{\partial q_i}$ is the gradient with respect to q where i denotes the i th atom being
 104 moved. Using this notation the gradient is

$$\vec{\nabla}U = \begin{bmatrix} \frac{\partial U}{\partial q_{0,x}} & \frac{\partial U}{\partial q_{0,y}} & \frac{\partial U}{\partial q_{0,z}} \\ \vdots & \frac{\partial U}{\partial q_{i,w}} & \vdots \\ \frac{\partial U}{\partial q_{n,x}} & \frac{\partial U}{\partial q_{n,y}} & \frac{\partial U}{\partial q_{n,z}} \end{bmatrix} = \begin{bmatrix} \vec{\mathcal{F}}_0 \\ \vdots \\ \vec{\mathcal{F}}_i \\ \vdots \\ \vec{\mathcal{F}}_n \end{bmatrix} \quad (2.15)$$

105 where $\frac{\partial}{\partial q_{i,w}}$ is the derivative with respect to q where w denotes direction of the deriva-
106 tive (x , y , or z), n is the number of atoms and U is the potential which depends on
107 q , and \vec{F}_i is the "force" on the i th atom.

108 **No-U-Turn-Sampling**

109 **Grand Canonical Ensemble**

110 **Ensemble description**

111 In the Grand Canonical Ensemble (GCE) two sets of variables are allowed to change,
112 the atomic positions and the total number of atoms and their associated identities.
113 These two variables are controlled by temperature and chemical potential. The par-
114 tition function is

$$\Xi = e^{-\beta(\mathcal{H}+\mu)} \quad (2.16)$$

115 This is translated into a Monte Carlo system, producing Grand Canonical Monte
116 Carlo (GCMC).

117 **Grand Canonical Monte Carlo**

118 While the probabilities for atomic motion are the same as in the Canonical Ensemble,
119 the addition or removal of an atom have their own probabilities. For the addition of
120 an atom the probability is formally:

$$\min[1, \frac{V}{(N+1)\Lambda(T)^3} e^{-\beta\Delta U + \beta\mu}] \quad (2.17)$$

121 Similarly the removal of an atom has the probability:

$$\min[1, \frac{(N)\Lambda(T)^3}{V} e^{-\beta\Delta U - \beta\mu}] \quad (2.18)$$

122 However, both of these equations depend of the overall simulation volume and the
123 thermal wavelength, which is undesirable as these are not really properties that we

124 are of interest to these simulations. Thus, we roll them into the definition of the
125 chemical potential, essentially setting the base chemical potential to counteract these
126 effects. This makes certain that our simulation does not change if we change the
127 overall cell volume. A GCMC move consists of creating a new atomic configuration,
128 where an atom has been added or removed, and checking the above criteria. However,
129 previous results have shown that this method is computationally expensive in dense
130 liquids, and exceedingly expensive in solid materials. The long simulation times
131 are due to the random nature of the atomic additions or removals which produce:
132 over-tightly packed atoms, atoms in the middle of nowhere, or unphysical vacancies.
133 These configurations are rejected by the GCMC criteria but their probability of being
134 sampled is much higher than configurations which are lower in energy, since the
135 number of incorrect ways to add/remove atoms is much larger than the correct ways.
136 Thus we have implemented methods for biasing the atomic addition positions and
137 the atomic removals toward configurations which are more likely to be accepted.

138 GCMC biasing

139 The first method is to remove some of the excess options from the probability pool.
140 Initially the insertion positions are calculated at random using a random number gen-
141 erator and scaled to the size of the simulation cell. This produces probabilities which
142 have floating point level precision, which is effectively infinite. While this produces
143 a potentially infinite number of ways to create energetically favorable configurations,
144 the infinite ways to produce bad configurations is much larger. Thus we can limit this
145 by moving to voxels. In this case atoms are added to the center of voxels which have
146 a pre-set resolution, limiting our total number of valid addition points. While this
147 could produce some problems with ergodicity, we avoid this by allowing the atoms to
148 translate throughout the system. Each voxel has a probability of being tried:

$$P_{i,j,k} = \frac{xyz}{abc} \quad (2.19)$$

149 where x, y, z and a, b, c are the resolutions and cell side lengths in the cardinal di-
150 rections, respectively. While this does help to limit the total probability space it
151 does not tell us which voxels are likely to lead to better configurations, leading to
152 many rejected atomic additions. To combat this issue we can weigh the individual
153 voxels, giving more probability to voxels which show promise and less to those with
154 less likelihood to be accepted.

155 The approach most likely to yield success would be to measure the change in
156 potential energy associated with the addition of an atom at the center of the voxel
157 where the probability of a voxel to be tried is:

$$P_{i,j,k} = \frac{e^{\beta\Delta U_{i,j,k}}}{\sum_{i,j,k} e^{\beta\Delta U_{i,j,k}}} \quad (2.20)$$

158 where $\Delta U_{i,j,k}$ is the change in energy. However, calculating $\Delta U_{i,j,k}$ can be particu-
159 larly expensive, especially when calculating scattering from atomic positions. The
160 computational expense can be mitigated by using a cheaper potential, if only for the
161 evaluation of the voxel energy, as previously shown. Similar to previous work we can
162 use the Lennard Jones potential to approximate the addition potential.

163

CHAPTER 3

164

ATOMIC PAIR DISTRIBUTION FUNCTION:

165

THEORY AND COMPUTATION

166 3.1 THEORY

167 To properly understand the PDF and its limitations we need to derive its mathemat-
168 ics. The following derivation has been performed numerous times but most recently
169 and completely by Farrow and Billinge, it is reproduced here for clarity and com-
170 pleteness.

171 **Derivation**

172 **Analytical Gradients**

173 Many optimization algorithms and simulations methodologies, including HMC, re-
174 quire not only the potential energy of a given configuration but also the forces acting
175 on that configuration. These forces are described by the gradient of potential energy
176 of the system which in turn requires the gradient of the PDF. As previously shown the
177 PDF is the Fourier Transform of the Debye equation. Since the Fourier Transform is
178 expressed as an integral we can exchange the order of the gradient and the integral,
179 allowing us to calculate the analytical gradient of the Debye equation and FFT the
180 resulting function. The Debye equation, with a Debye-Waller vibrational correction
181 is

$$F(Q) = \frac{1}{N\langle f \rangle^2} \sum_{j \neq i} f_i^*(Q) f_j(Q) \exp(-\frac{1}{2}\sigma_{ij}^2 Q^2) \frac{\sin(Qr_{ij})}{r_{ij}} \quad (3.1)$$

182 where

$$\sigma_{ij}^2 = (\vec{u}_{ij} * \hat{d}_{ij})^2 \quad (3.2)$$

$$\vec{u}_{ij} = \vec{u}_i - \vec{u}_j \quad (3.3)$$

$$\hat{d}_{ij} = \frac{\vec{d}_{ij}}{r_{ij}} \quad (3.4)$$

$$r_{ij} = \|\vec{d}_{ij}\| \quad (3.5)$$

$$\vec{d}_{ij} = \begin{bmatrix} q_{ix} - q_{jx} \\ q_{iy} - q_{jy} \\ q_{iz} - q_{jz} \end{bmatrix} \quad (3.6)$$

183 where Q is the scatter vector, f_i is atomic scattering factor of the i th atom, and r_{ij}
 184 is the distance between atoms i and j and has q dependence. For simplicities sake
 185 we will break up $F(Q)$ so that

$$F(Q) = \alpha \sum_{j \neq i} \beta_{ij} \tau_{ij} \Omega_{ij} \quad (3.7)$$

186 where

$$\alpha = \frac{1}{N\langle f \rangle^2} \quad (3.8)$$

$$\beta_{ij} = f_i^*(Q) f_j(Q) \quad (3.9)$$

$$\tau_{ij} = \exp\left(-\frac{1}{2} \sigma_{ij}^2 Q^2\right) \quad (3.10)$$

$$\Omega_{ij} = \frac{\sin(Qr_{ij})}{r_{ij}} \quad (3.11)$$

187 The derivatives are as follows:

$$\frac{\partial}{\partial q_{i,w}} F(Q) = \alpha \sum_j \beta_{ij} \left(\frac{\partial \tau_{ij}}{\partial q_{i,w}} \Omega_{ij} + \tau_{ij} \frac{\partial \Omega_{ij}}{\partial q_{i,w}} \right) \quad (3.12)$$

188 where

$$\frac{\partial \Omega_{ij}}{\partial q_{i,w}} = \frac{Q \cos(Qr_{ij}) - \Omega_{ij}}{r_{ij}^2} (q_{i,w} - q_{j,w}) \quad (3.13)$$

$$\frac{\partial \tau_{ij}}{\partial q_{i,w}} = \frac{\sigma_{ij} Q^2 \tau_{ij}}{r_{ij}^3} ((q_{i,w} - q_{j,w}) \sigma_{ij} - (u_{i,w} - u_{j,w}) r_{ij}^2) \quad (3.14)$$

189 Since \vec{u}_{ij} is a variable as well, we need the derivative with respect to it as well.

190 Thus

$$\frac{\partial}{\partial u_{i,w}} F(Q) = \alpha \sum_j \beta_{ij} \frac{\partial \tau_{ij}}{\partial u_{i,w}} \Omega_{ij} \quad (3.15)$$

$$\frac{\partial \tau_{ij}}{\partial u_{i,w}} = -\frac{\sigma_{ij} Q^2 \tau_{ij}}{r_{ij}} (q_{i,w} - q_{j,w}) \quad (3.16)$$

191 Without ADPs

192 Without ADPs the equations simplify down to

$$F(Q) = \frac{1}{N \langle f \rangle^2} \sum_{j \neq i} f_i^*(Q) f_j(Q) \frac{\sin(Qr_{ij})}{r_{ij}} \quad (3.17)$$

193 and

$$\frac{\partial}{\partial q_{i,w}} F(Q) = \alpha \sum_j \beta_{ij} \frac{\partial \Omega_{ij}}{\partial q_{i,w}} \quad (3.18)$$

194 use of these equations, when ADPs are not appropriate (like at cryogenic tempera-
195 tures), greatly speeds up the computaiton.

196 3.2 COMPUTATION

197 Simply deriving the equations for the PDF is not enough. The many body nature of
198 the PDF equation make analytical solution of the structure from the PDF impossible.
199 Thus, the PDF must be computed from a structural candidates and compared against
200 experimental results to evaluate the reliability of the model.

201 HPC and GPUs

202 To properly solve the structure of materials the PDF will need to be computed many
203 times and checked against experimental results. This requires computation of the
204 PDF, potentialy over many atoms. Calculating these PDFs requires a fast, highly
205 parallized, computational framework.

206 **GPUs and Parallelization**

207 Computing the PDF is an embarrassingly parallel problem. The basic procedure is
208 to calculate the reduced structure factor $F(Q)$ for each atom pair and momentum
209 transfer vector, sum over all the atom pairs, and Fourier transform the structure to
210 the PDF. The first part of this procedure is perfectly parallelizable, as each atom pair is
211 separate from the others. The summation over all the atomic reduced structure factors
212 can be parallelized via distributed summing. Lastly the FFT can be parallelized using
213 existing parallel FFT algorithms.

214 GPUs are particularly well suited to the task of computing PDFs. GPU chip
215 architecture is designed to perform many tasks simultaneously by having potentially
216 thousands of cores.

217 **Map from ij space to k space**

218 The above equations, although formally correct, are very inefficient. $F(Q)$ and its
219 gradient are indexed over all the atoms twice, however there are symmetries that
220 allow us to only compute over the atom pairs essentially mapping from an $n \times n$ space,
221 ij space, to a $\frac{n(n-1)}{2}$ space, k space. For $F(Q)$ we apply the following mapping where

$$\begin{array}{ccccc} & & \psi & & \\ E & \xrightarrow{\quad} & E' & \xrightarrow{\Sigma} & Z \\ \phi \downarrow & & & \nearrow \Sigma' & \\ B & \xrightarrow{\quad} & B' & & \end{array}$$

222 E denotes the atomic coordinates in ij space, E' denotes $F(Q)$ before the summation
223 in ij space, B denotes the atomic pairs in k space, B' denotes $F(Q)$ in k space, and
224 Z denotes the final summed $F(Q)$. For the operators, ϕ denotes the mapping from
225 ij space to k space $k = j + i * \frac{i-1}{2}$, ψ and ψ' denote the $F(Q)$ operation in ij and k
226 space, respectively. Σ denotes the sum over all the atoms.

227 To properly define Σ' we must establish whether $F(Q)$ is an even function. We
 228 can accomplish this by examining each of the portions of $F(Q)$, $\alpha, \beta, \tau, \Omega$. Ω is even,
 229 since r_{ij} is the interatomic distance, which is the same despite a flip of indicies, Q
 230 does not depend on the atomic indicies, and since Qr_{ij} is even so is $\sin Qr_{ij}$. Thus,
 231 Ω is even. Providing similar analysis to τ we can see that while \vec{u}_{ij} is odd, so is
 232 the unit displacement vector between the two atoms, thus the two odds cancel out.
 233 Intuitivly this makes sense, since the $F(Q)$ equation is fundamentally interested in the
 234 interatomic distances which is even. Thus, switching atom indicies does not change
 235 $F(Q)$. Due to the even nature of the $F(Q)$ operator the Σ' operator sums over all the
 236 atom pairs, and multiplies by two to reflect the double counting of the Σ operator.

For the gradient a similar mapping is used:

$$\begin{array}{ccccc}
 & & \psi & & \\
 E & \xrightarrow{\quad} & E' & \xrightarrow{\Sigma} & Z \\
 \phi \downarrow & & & \swarrow \tilde{\phi}\Sigma & \\
 B & \xrightarrow{\quad} & B' & &
 \end{array}$$

237
 238 In this mapping, however, we use the $\tilde{\phi}\Sigma$ operator. This operator simultaniously
 239 performs a reverse mapping from k to ij space, and a summation with the correct
 240 symmetry. In this case the ψ and ψ' operators, which denote the $\vec{\nabla}F(Q)$ operator
 241 in ij and k space, are antisymmetric. Intuitivly this makes sense as an extension of
 242 Newton's Second Law, since each particle's interation is felt oppositely by its partner.

243 Periodic Boundary Conditions

244 Periodic boundary conditions can be helpful when simulating extended solids or large
 245 nanoparticles. In this case all the non-crystallinity is contained within the simulation
 246 box and the box is repeated to create the longer distance peaks observed in the PDF.
 247 To perform this we can break up the Debye equation into two main parts, the part

248 that describes the interatomic distances within the simulation box and those between
249 boxes. Neglecting the thermal motion portion:

$$F(Q) = \frac{1}{N\langle f \rangle^2} \left(\sum_{j \neq i} f_i^*(Q) f_j(Q) \frac{\sin(Qr_{ij})}{r_{ij}} + \sum_{i,j} f_i^*(Q) f_j(Q) \frac{\sin(QR_{ij})}{R_{ij}} \right) \quad (3.19)$$

250 where

$$R = |\vec{r} + \vec{u}| \quad (3.20)$$

$$\vec{u} = \gamma_1 * \vec{a} + \gamma_2 * \vec{b} + \gamma_3 * \vec{c} \quad (3.21)$$

251 **3.3 EXPERIMENT**

252 PDF experiments are generally performed at synchrotron light sources, as only these
253 sources can provide the need flux, energy, and high momentum transfer vectors needed
254 to obtain reliable PDFs.

255 **3.4 DATA PROCESSING WORKFLOW**

256 Processing the raw pixel intensities to the PDF is very important as we are extracting
257 most of our interesting information out of very high Q data. This data relies on good
258 statistics and sound background subtraction. Talk about papers from Billinge Group
259 with thin film PDF and dilute NP solutions. Diagram of the overall data processing
260 workflow. Discuss the NSLS-II data stack.

261 **MetadataStore Side Loading**

262 Design of sidewinder-spec for loading the data into metadatastore. Most of the design
263 considerations went into the loaders, which are different for each experiment.

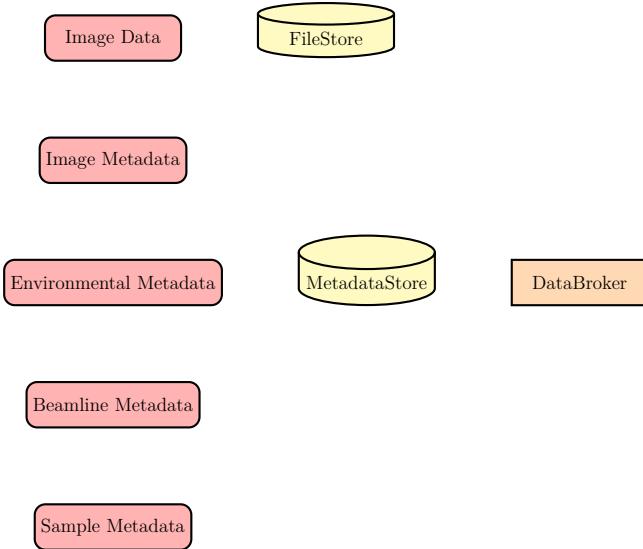


Figure 3.1: Database Loading Workflow. Data is loaded from various sources, including images and text files, into the FileStore and MetadataStore databases. Data is then retrieved from the databases using the databroker.

264 Automated Image Azimuthal Integration

265 Mux data as needed. Use pyFAI to get the radial distance array. Note that to
 266 properly mask and integrate the system we need to compute the bin edges for the
 267 pixels. The bin edges change as a function of Q , as the angle subtended by a pixel
 268 shrinks essentially giving high Q pixels more resolution.

269 Detector Q resolution

270 Automated Mask Generation

271 Introduction

272 Detector masking is an important part of any x-ray scattering workflow as dead/hot
 273 pixels, streak errors, and beamstop associated features can be averaged into the data
 274 changing the signal and its statistical significance. While some features, like the
 275 beamstop holder, can be easily observed and masked by hand other are much more
 276 difficult to observe even on large computer monitors. Additionally, while dead/hot

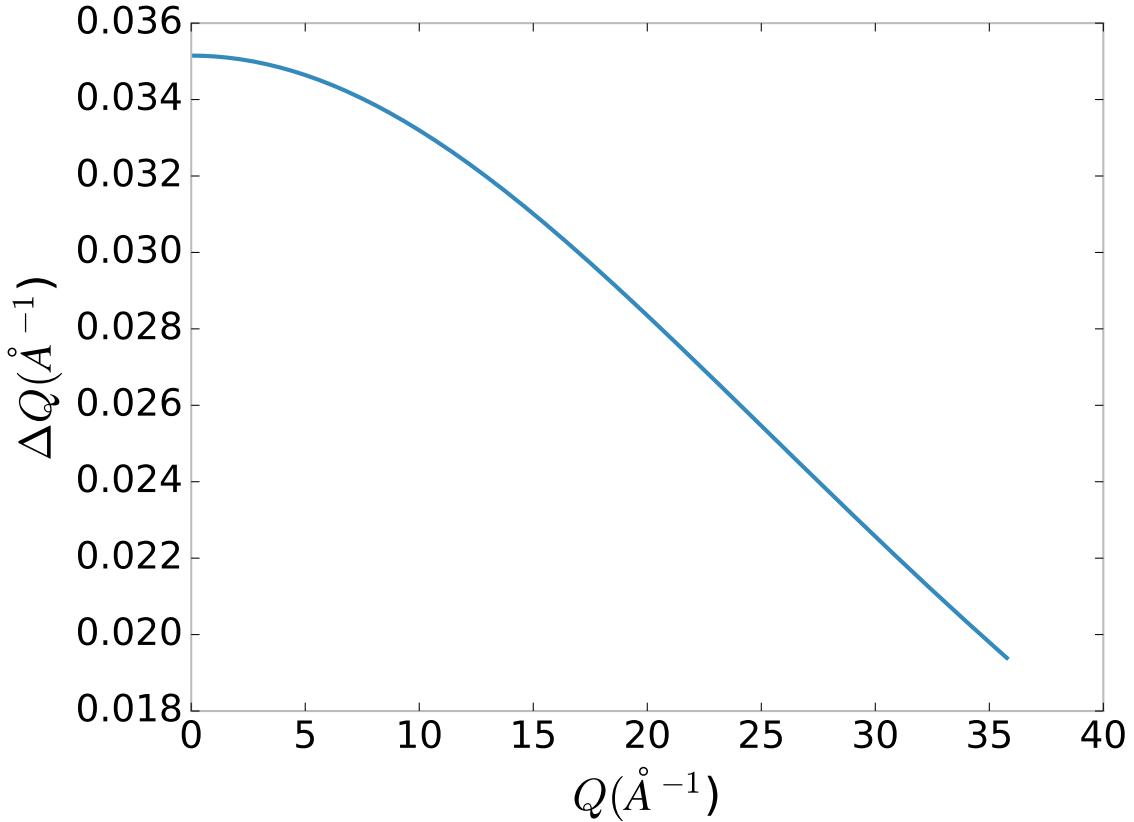


Figure 3.2: Q resolution as a function of Q .

277 pixels and streaks are usually static the hot pixels associated with textured or sin-
 278 gle crystal scattering or cosmic rays are not. Thus, coming up with an automated
 279 method for finding such erroneous pixels is important, especially as high flux diffrac-
 280 tion beamlines can generate data very quickly.

281 While this problem can be quite complex in the most general case, we can use the
 282 annular symmetry of the powder scattering pattern to our advantage, by comparing
 283 a pixel against pixels in the same ring. Since non-textured powder scattering should
 284 produce the same pixel intensity for a given ring we can mask any pixels which are α
 285 standard deviations away from the mean. This method relies on the aforementioned
 286 pixel binning algorithm, as using miss sized bins will cause some pixels which should
 287 be in separate rings to be put together, and others which should be in the same ring
 288 to be separated. In that case the masking algorithm will overestimate the number of

289 pixels to be masked due to the additional statistical variation in the sample.

290 **Algorithm Design**

291 The masking algorithm procedure takes in the image and a description of the pixel
292 positions in either distance from the point of incidence or in Q . The image is then
293 integrated twice, producing both the mean $I(Q)$ and the standard deviation of each
294 $I(Q)$ ring. The mask is created by comparing the pixel values against each ring's
295 standard deviation and threshold α . Note that the threshold can be a function of
296 distance from the point of incidence or Q .

297 **Test Cases**

298 To study the effectiveness of the masking we ran the algorithm against both simulated
299 experimental data. In the case of the simulated data four systems were created: 1)
300 dead/hot pixels with varying numbers of defective pixels, 2) beamstop holder with
301 varying beamstop holder transmittance, 3) rotated beamstop holder with varying
302 beamstop holder transmittance, and 4) beamstop holder with dead/hot pixels. The
303 base scattering was produced by

$$I = 100 \cos(50r)^2 + 150 \quad (3.22)$$

304 where r is a pixel's distance from the beam point of incidence. The positions of
305 the dead/hot pixels were chosen at random as was the dead or hot nature of the
306 defect. Dead pixels had values from 0 to 10, while hot pixels had values from 200
307 to 255. The beamstop was positioned at the vertical center of the detector with an
308 initial width of 60 pixels and final width of 120 pixels. The height of the beamstop
309 was 1024 pixels. The beamstop was calculated to attenuate the x-ray scattering
310 signal at various transmittance, as various beamstop holder materials have different
311 transmittance. Two versions of the masking algorithm were run for each test case, one

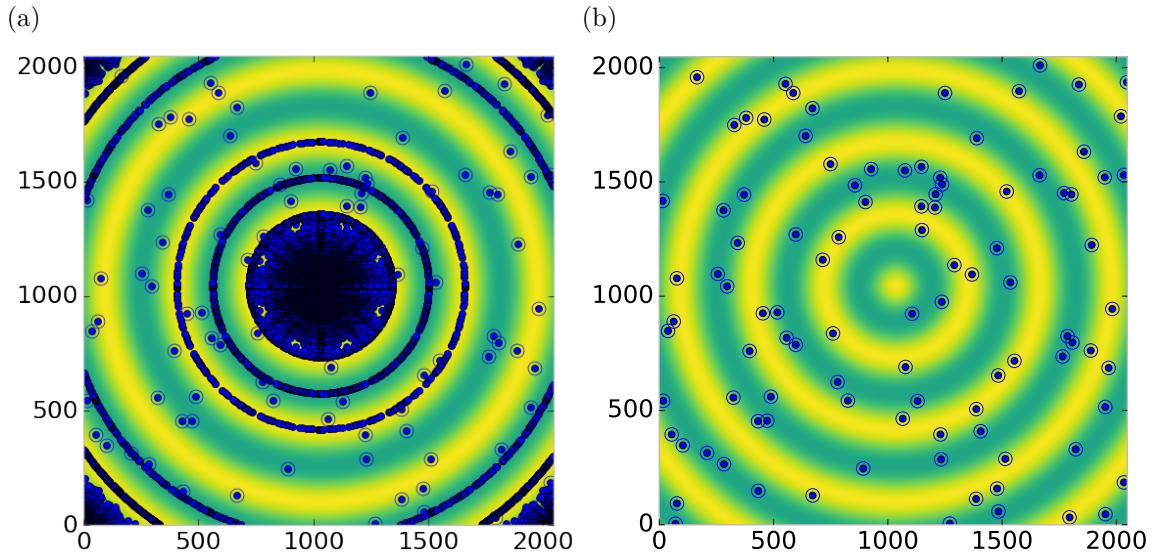


Figure 3.3: Generated dead/hot pixel masks for a detector with 100 bad pixels. a) the poorly binned mask and b) the properly binned mask

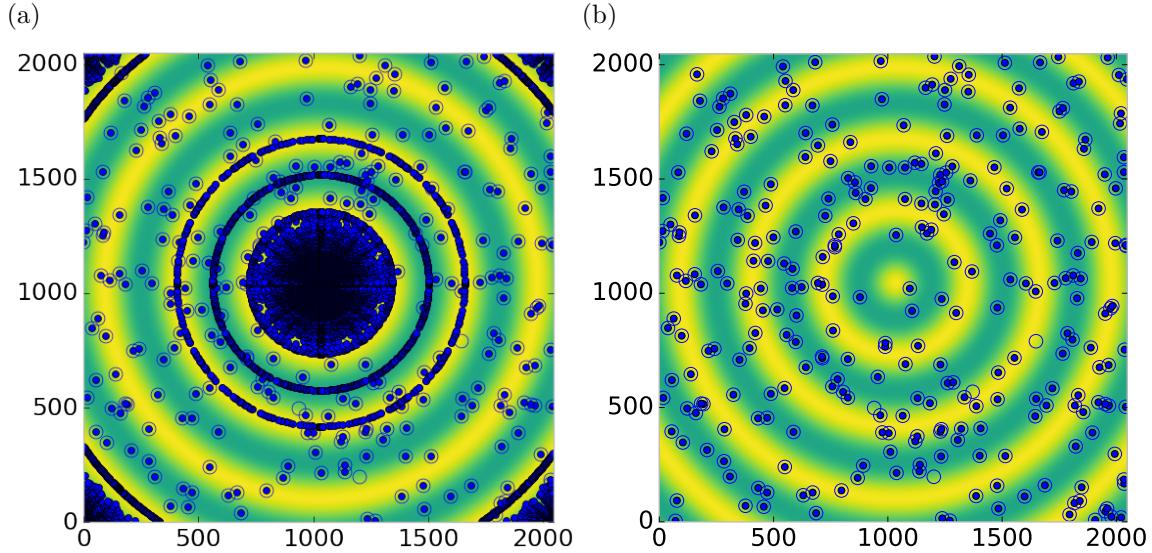


Figure 3.4: Generated dead/hot pixel masks for a detector with 300 bad pixels. a) the poorly binned mask and b) the properly binned mask

312 using the standard even bin sizes for the integration step, and one where the bin sizes
 313 are tuned to the pixel Q resolution as discussed in 3.4.

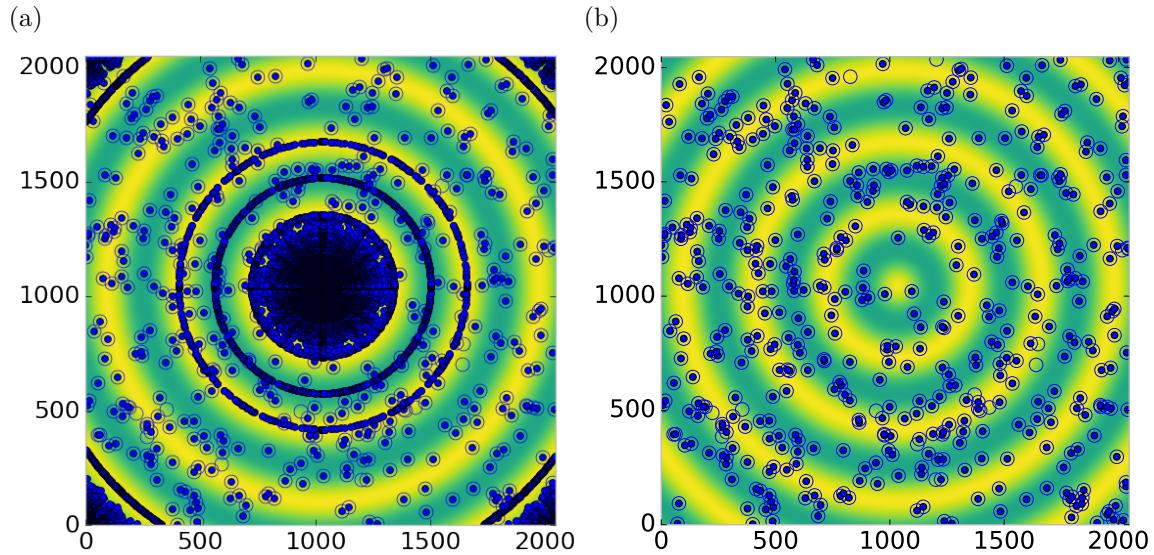


Figure 3.5: Generated dead/hot pixel masks for a detector with 500 bad pixels. a) the poorly binned mask and b) the properly binned mask

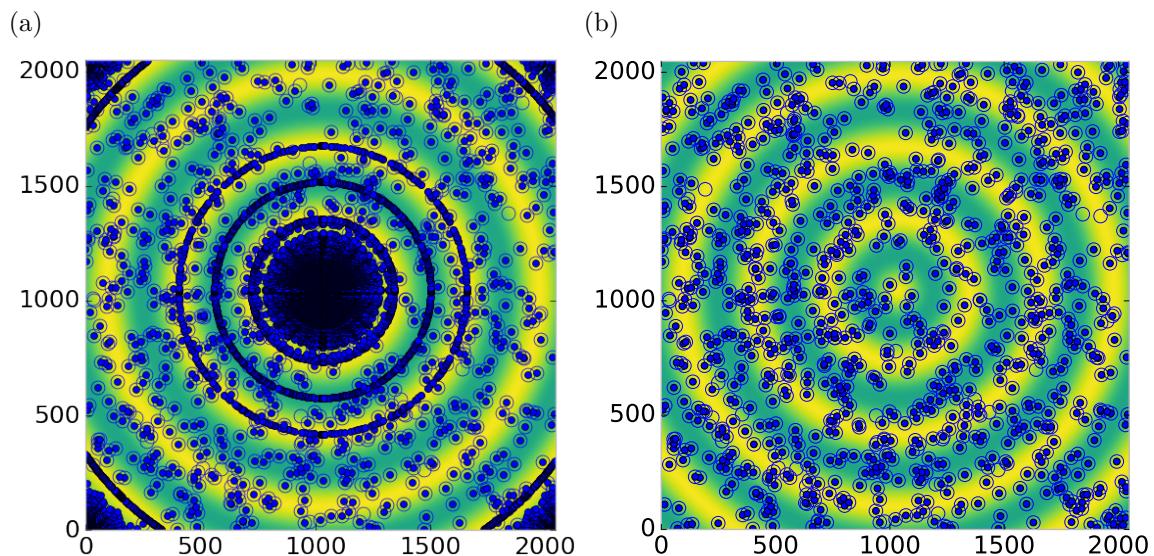


Figure 3.6: Generated dead/hot pixel masks for a detector with 1000 bad pixels. a) the poorly binned mask and b) the properly binned mask

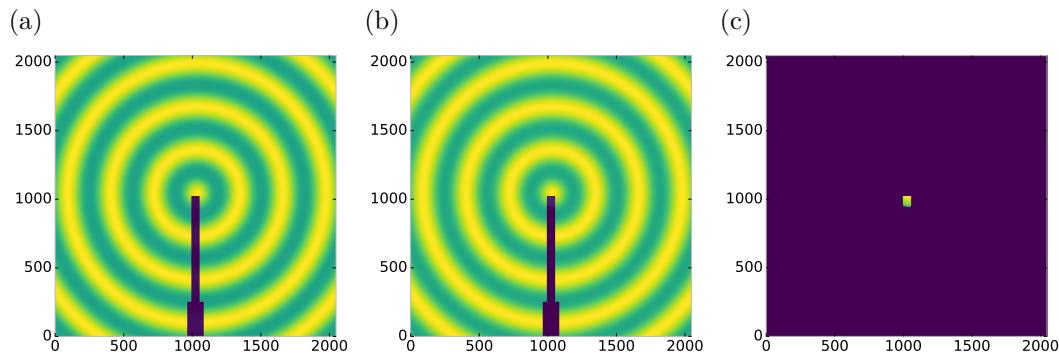


Figure 3.7: Generated beamstop holder masks for a beamstop holder with 10% transmittance. a) the raw image, b) the masked image, c) and the missed pixels

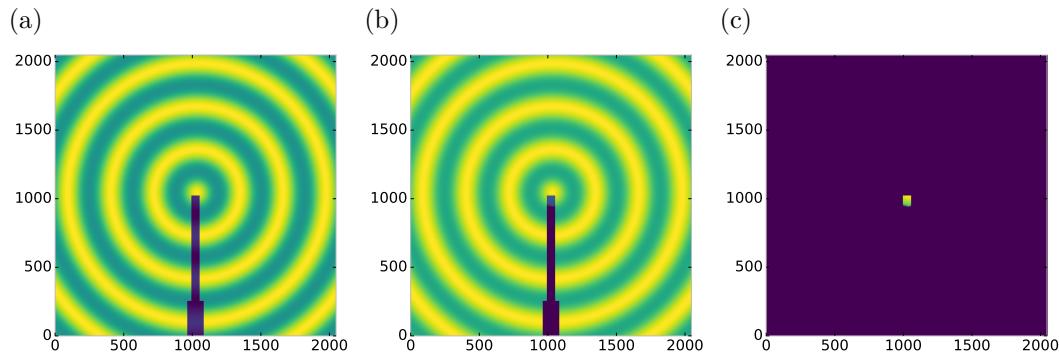


Figure 3.8: Generated beamstop holder masks for a beamstop holder with 30% transmittance. a) the raw image, b) the masked image, c) and the missed pixels

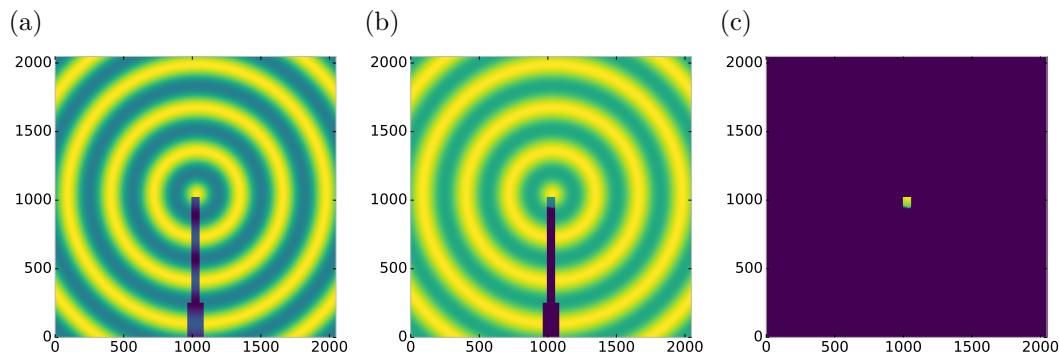


Figure 3.9: Generated beamstop holder masks for a beamstop holder with 50% transmittance. a) the raw image, b) the masked image, c) and the missed pixels

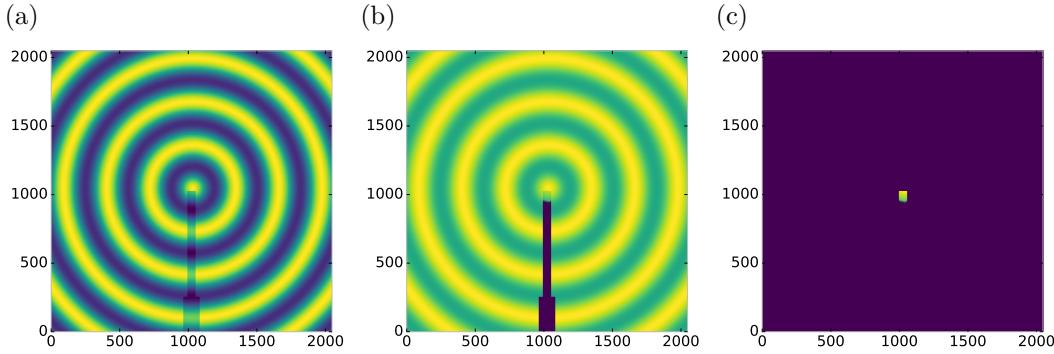


Figure 3.10: Generated beamstop holder masks for a beamstop holder with 90% transmittance. a) the raw image, b) the masked image, c) and the missed pixels

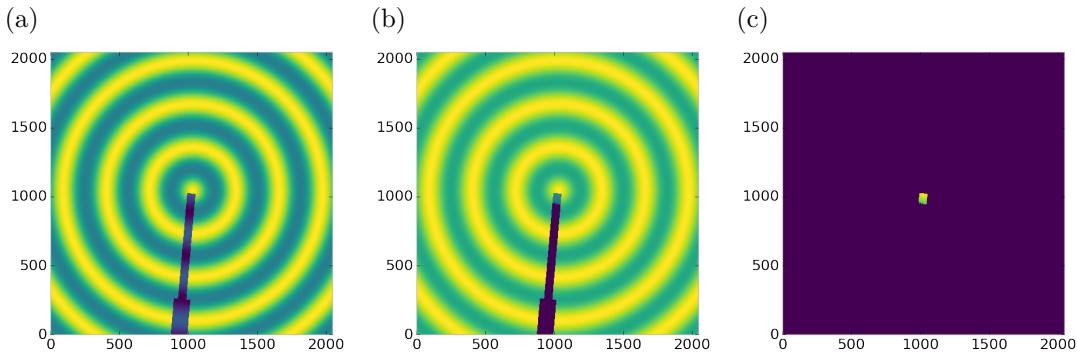


Figure 3.11: Generated beamstop holder masks which is rotated away from verticle

314 Results and Discussion

Figures 3.3-3.10 show the results of the masking algorithm on simulated images. The dead/hot pixel masking shows the importance of using the Q resolution based bin sizes as the even bin based mask have a tendency to over mask the image, removing pixels which contain valuable signal. This overmasking is caused by pixels being improperly associated with one another by the even bins. Figure 3.3 indicates that the masking algorithm, with the proper binning, masks the image perfectly, with no missed bad pixels or good pixels masked. This is not the case in figures 3.4 - 3.6 as we can see pixels which should have been masked but were not. Despite these missed pixels no pixels were improperly masked in any of the well binned images. These test cases are actually more difficult than experimental data, as the dynamic range of most

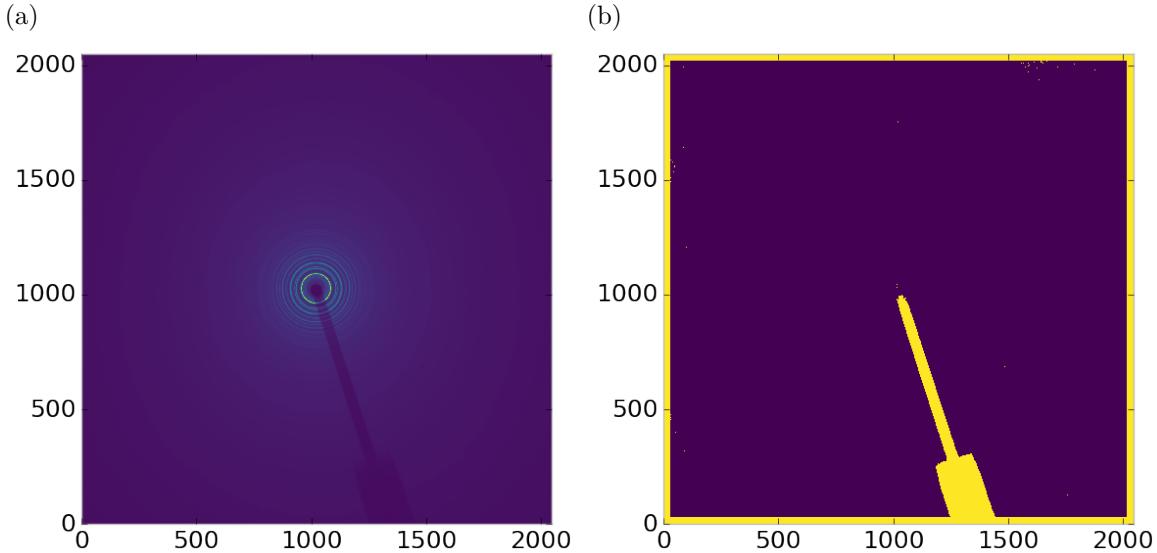


Figure 3.12: Masked experimental data. a) the raw image, b) the mask

325 detector causes the dead/hot pixels and single crystal/texture peaks to be orders of
 326 magnitude away from the desired signal.

327 The beamstop holder masks shown in figures 3.7 - 3.10, which were all run with
 328 the Q resolution binning show similar results across the transmittance range, missing
 329 only a small part of the beamstop holder near the point of incidence. Near this point
 330 the beamstop holder becomes a statistically significant part of the total number of
 331 pixels in a given ring, thus it can not be masked out using a statistical search of the
 332 rings. For most PDF and XRD studies this small area can be masked automatically
 333 by masking all the pixels who's distance from the point of incidence is smaller than a
 334 given radius r , or can be negelected outright as the area is not used in the analysis or
 335 refinement. Similar results were produced for beamstop holders which were rotated
 336 away from the vericle position, as shown in figure 3.11

337 Working with actual experimental data, obtained at the Advanced Photon Source
 338 beamline 11-ID-B, shows the difficulty of masking images which have low phonon
 339 counts. While the masking of experimental data taken with longer exposures, con-
 340 sisting of 250 .2 second shots, shown in figure 3.12 provides very sharp edges to the

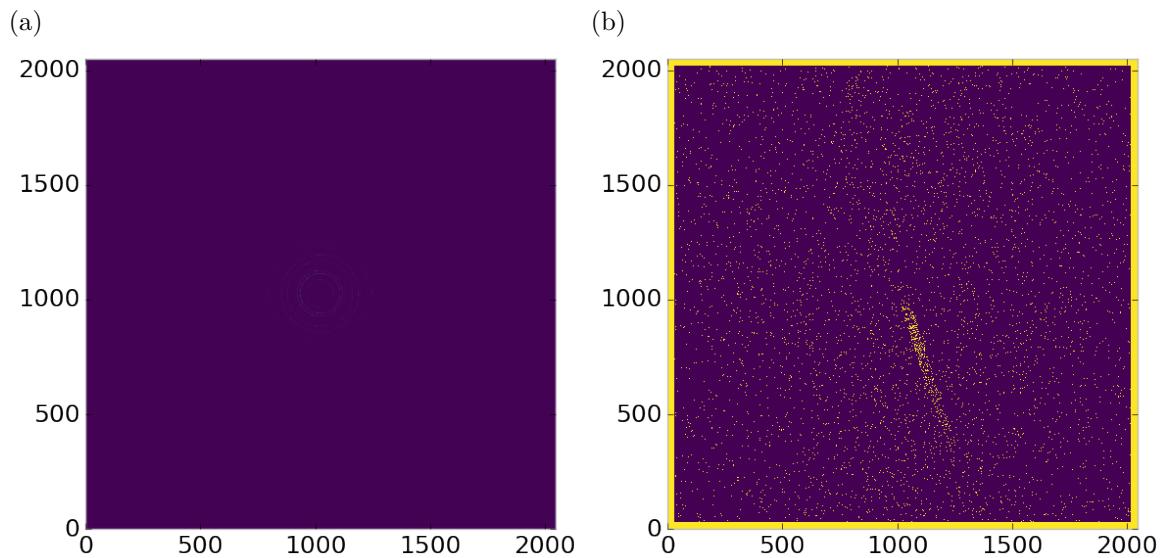


Figure 3.13: Masked experimental data with Pt single crystal signal. a) the raw image, b) the mask

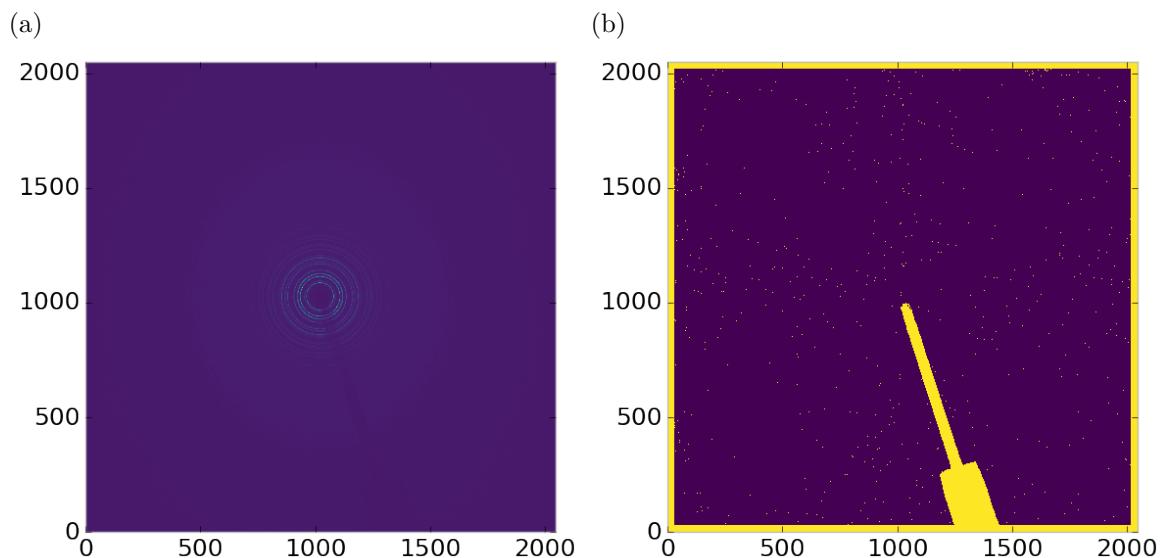


Figure 3.14: Masked experimental data with Pt single crystal signal using figure's 3.12 as a starting mask. a) the raw image, b) the mask

beamstop holder, and very little extra masking beyond the occasional dead pixel, this is not the case for the single crystal data. The single crystal data is more problematic because of its short exposure time and low flux, with 500 frame at a .1 second exposure and having shrunk the beam size. The low flux is to prevent the very strong single crystal peaks from damaging the detector. However, this causes the image to be less statistically viable than ideal, causing problems with the mask as seen in figure 3.13. This can be alleviated to some degree by using the previously generated mask as a starting mask for the single crystal image, as shown in 3.14. While the masking algorithm still produces many diffuse masked pixels, they are far fewer, this may be due to the removal of the beamstop which could have contributed to the large standard deviation in figure 3.13.

Conclusions

In this section the masking algorithm, which relies on both Q resolution based binning and a statistical approach to azimuthal symmetry, was developed. The focus of this algorithm was to remove many unwanted detector features associated with pixel defect, beamstop holder associated scattering attenuation, and single crystal/texture peaks. Simulated data was used to evaluate the beamstop holder and dead/hot pixel masking capacity, while experimental data was used to check for single crystal and texture based masking. Q resolution based binning was shown to be very important to avoid overmasking. The ability of the mask writer to mask images is somewhat limited by the overall statistical image quality, although some deficiencies can be obtained by using previously generated masks as starting points. This masking algorithm is now in use in the data processing workflow and will be available in scikit-beam soon.

364

CHAPTER 4

365

BENCHMARKING

366 4.1 PDF

367 **Au55: surface relaxed**

368 **Au55: surface disordered**

369 **Au55: amorphous**

370 **Au102: triple phase**

371 **Au147**

372 **C60**

373 4.2 PDF WITH ADPs

374

CHAPTER 5

375

ANNEALING AND AGGREGATION OF 2NM

376

AU NANOPARTICLES

377 5.1 EXPERIMENTS

378 NP Synthesis

379 X-ray Total Scattering Measurements

380 5.2 DATA PROCESSING

381 5.3 DATA ANALYSIS

382 5.4 SIMULATION

383 5.5 STRUCTURAL ANALYSIS

384 5.6 CONCLUSIONS

385

CHAPTER 6

386

PHASE CHANGES AND ANNEALING DYNAMICS OF

387

Pr_2NiO_4 AND ITS DERIVATIVES

388 6.1 EXPERIMENTS

389 **Pr_2NiO_4 Synthesis**

390 **X-ray Total Scattering Measurements**

391 6.2 DATA PROCESSING

392 6.3 DATA ANALYSIS

393 **Intra Sample Comparison**

394 **Inter Sample Comparison**

395 6.4 SIMULATION

396 **Small Box**

397 **Large Box**

398 6.5 STRUCTURAL ANALYSIS

399 6.6 CONCLUSIONS

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CHAPTER 7

401

CONCLUSION