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Investigating model influence on the analytical resolution of neutron reflectometry

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Neutron reflectometry is an invaluable tool for the study of biological samples due to its sensitivity to atomic nuclei and their penetrative capabilities [2] [3] [4]. The resolution of the technique as defined by the diffraction limit is at about 10 Å. However, evidence from literature would suggest that this is not the case, as articles on this technique routinely describe resolving parameters which are smaller than this [5].

Neutron reflectometry data is rarely analysed without any prior knowledge of the system i.e. what layers are present in the sample. Therefore, any analysis should always be viewed in the context of the model used. In this work, we investigate the relationship between the resolution and the choice of different models used, each with different numbers of parameters based on reasonable and justified assumptions, to describe the system under consideration. Bayesian model selection [6] [1] is used to quantify the relative quality of the models relative to each other for varied number of contrasts and the direct effect our ignorance or knowledge of the system has on the resolution.

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