Presentation

Investigation of the Protein Dynamics near Cell Death

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Table of Contents

Introduction

- Introduction and Goal of the Project
- Methods

First year summary

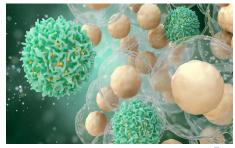
- Analysis of QENS data with Python
- Analysis of EINS data with Python
- Lectures at University of Perugia
- Neutron Scattering School

Outlook

Bibliography

Introduction: Life at extreme conditions

- During evolution: Life has adapted to extreme conditions (e.g. glacial waters, deep-sea vents)
- Mechanism of how extremophilic bacteria can thrive under extreme conditions largely uncharacterized
 but understanding is fundamental for theoretical and applicative/biotechnological prospective
- ➤ All cellular components affected by stress ⇒ Focus on proteins: Most abundant and less stable macromolecules in the cytoplasm



- Proteins unfold at high temperatures
- > Proteins live in crowded system
- > Unfolding of proteins can affect the complex network

 \Rightarrow Goal: Investigate dynamical properties of the proteins in the cytoplasm of different types of bacteria to understand the connection between the unfolding and the cell death

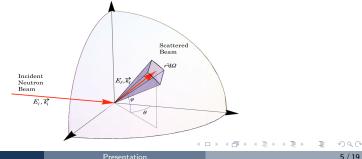
Neutron Scattering

Neutron Scattering = experimental technique for studying sample structure and dynamics by analyzing the scattering beam of neutrons

> Neutrons are characterized by their energy and momentum

$$E = \hbar \omega$$
 $p = mv = \hbar k$

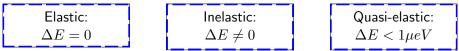
- > Thermal neutron wavelengths (Å) and energies (meV) correspond to interatomic distances and energy of thermal excitations
- > Important isotope effects, e.g. H (hydrogen), ^{2}H (deuterium) Experiment geometry:



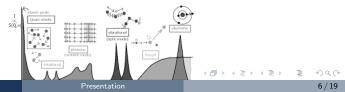
Neutron Scattering

Neutrons are scattered by nuclei in the sample exchanging momentum and energy (or only momentum)

$$\Delta E = \hbar (E_f - E_i) \quad \Delta p = \hbar (k_f - k_i) = \hbar q$$



- > Scattering intensity measured as a function of q and E.
- Contains information on sample dynamics via spatio temporal Fourier transform to the positions of the sample scattering nuclei as a function of time
- \succ Diffusive modes acting at different time-scales contribute to intensity of S(q,E)



Python Code for QENS data

Development of a Python code to fit and analyze **Quasi-Elastic Neutron Scattering** data

- **(**) Reads and fits S(E) for all q values with a model of choice
- 0 Extracts parameters of interest from the fittings, e.g. FWHM and plots as functions of q
- Fitting of certain parameters to get further information on dynamical profile

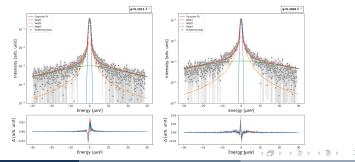
Application of the code for analysis of Psychrobacter Arcticus (Cell death temperature $T_{CD} = 295.15K$):

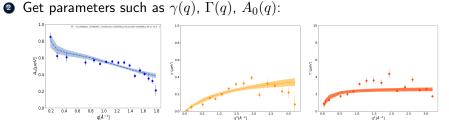
Model for the scattering function:

$$S_{\exp}(q, E) = R(E) \circledast \left[S_{AP}(q, E) + \alpha S_{D2O}(q, E) \right]$$

Model chosen for representing the average protein in the sample:

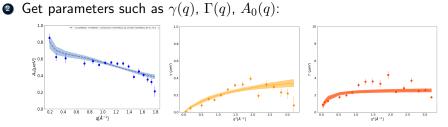
 $S_{\mathsf{AP}}(q,E) = I(q)\{L_{\gamma}(E) \circledast [A_0\delta(E) + (1-A_0)L_{\Gamma}(E)]\}$





Lorentzian widths γ and Γ can be modelled with the jump diffusion model

$$\gamma(q,T) = \frac{q^2 D_{\gamma}(T)}{1 + q^2 D_{\gamma}(T) \tau_{\gamma}(T)} \quad \Gamma(q,T) = \frac{q^2 D_{\Gamma}(T)}{1 + q^2 D_{\Gamma}(T) \tau_{\Gamma}(T)}$$



Lorentzian widths γ and Γ can be modelled with the jump diffusion model

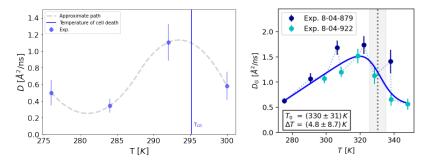
$$\gamma(q,T) = \frac{q^2 D_{\gamma}(T)}{1+q^2 D_{\gamma}(T) \tau_{\gamma}(T)} \quad \Gamma(q,T) = \frac{q^2 D_{\Gamma}(T)}{1+q^2 D_{\Gamma}(T) \tau_{\Gamma}(T)}$$

• Apply fit to all measurements in temperature to get diffusion coefficients $D_{\gamma}(T)$ and $D_{\Gamma}(T)$

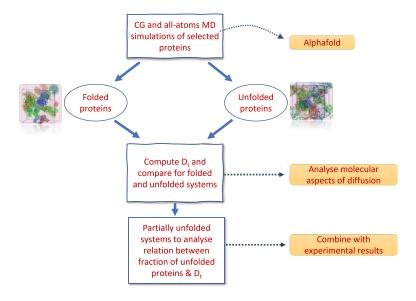
Results

- Increase of global diffusion at low temperatures and drastic decrease after T=292K shortly before cell death
- Around cell-death important reduction of the average motion of an entire protein

Comparison with E.Coli (Mesophile):



Outlook: Molecular Dynamics simulations



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Analysis of EINS data with Python

Analysis of **Elastic Incoherent Neutron Scattering** of the P.Arcticus, E.coli, A. Aeolicus

➢ For small *q*-values using the Gaussian Approximation the scattering function can be modelled as

$$S(q, E \approx 0) = \exp\left(-\frac{1}{6}\langle u^2 \rangle q^2\right)$$

where $\langle u^2
angle$ is the atomic mean square displacement (MSD)

 Reformulation gives a linear form of the logarithmic scattering function

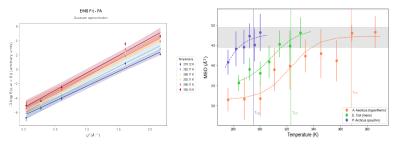
$$-6\log(S(q, E \approx 0)) = \langle u^2 \rangle q^2$$

> Fit of logarithmic scattering function to get MSD values

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Analysis of EINS data with Python

> MSD values plotted together as functions of temperature



Results:

- Common threshold and trend of the MSDs
- Reminiscent of the Lindemann criterion for solid melting, that has been verified also for powder systems
- Other Model by Hennig confirms same trend

$$-6\log(S(q,\Delta E)) = b + \langle u^2 \rangle q^2 + cq^4$$

Lectures at University of Perugia

Participation at Lectures in Physics at UniPG:

- Effective Field Theory I,II,III
- Nanosystems I,II,III (Exam)
- Teaching and Learning Physics (Exam)

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Neutron Scattering School

Participation at the 24th JCNS Laboratory Course

- Week 1: Lectures in Neutron scattering and applications + Exercise sessions
- Week 2: Visit of the Heinz Maier-Leibnitz Zentrum MLZ

Outlook

- Complete analysis of P. Arcticus, by taking further measurements at ILL and by performing all-atoms & CG MD simulations
 ⇒ Proposal sent, preparation of protein sets for simulations started
 ⇒ Reveal if there exists a set of protein that triggers arrest of the dynamics and analyse molecular aspects
 ⇒ Hypertermophile
- Complement MSD data of EINS with data of molecular dynamics simulations
 - \Rightarrow Paper writing

Summary

Lectures:

- Effective Field Theory I,II,III
- Nanosystems I,II,III (Exam)
- Teaching and Learning Physics (Exam)

Neutron Scattering School: 24th JCNS Laboratory Course

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Bibliography I

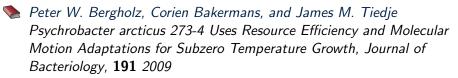


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