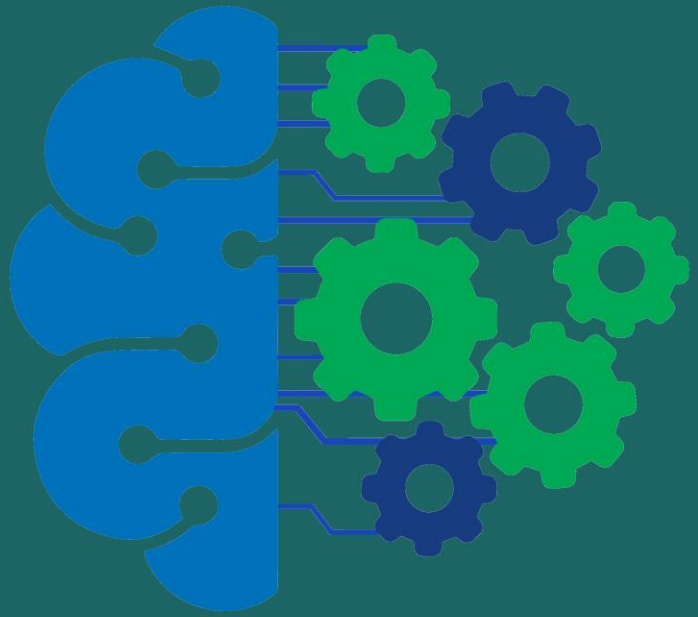
Neural networks for SAXS data analysis



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EMBL Hamburg

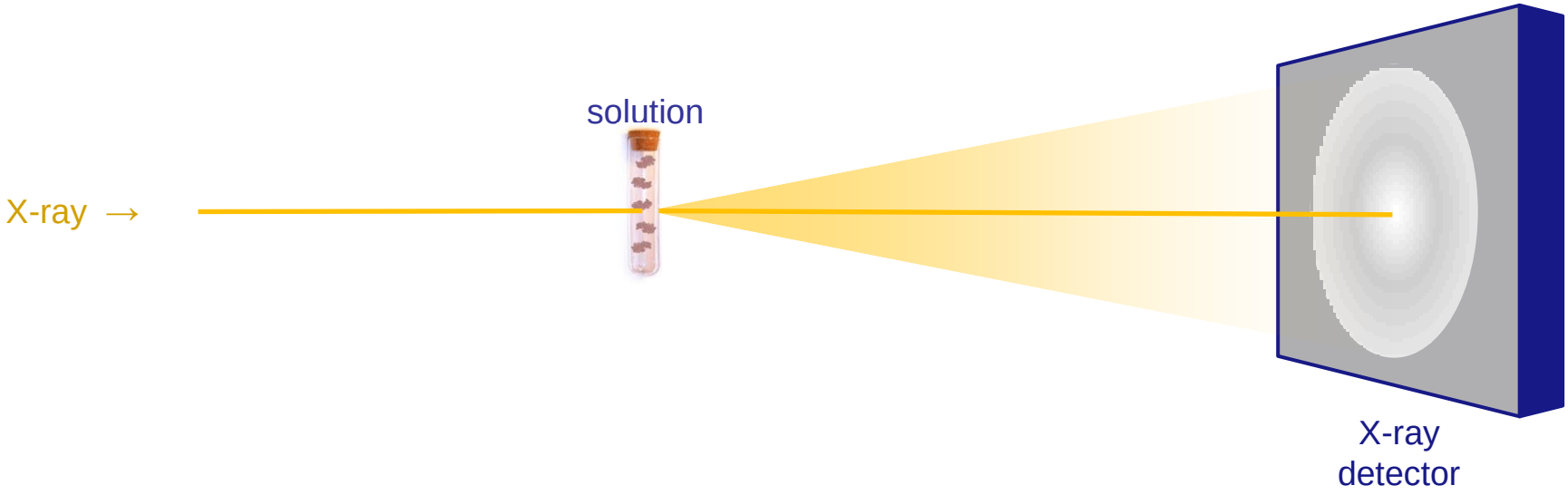
EMBL

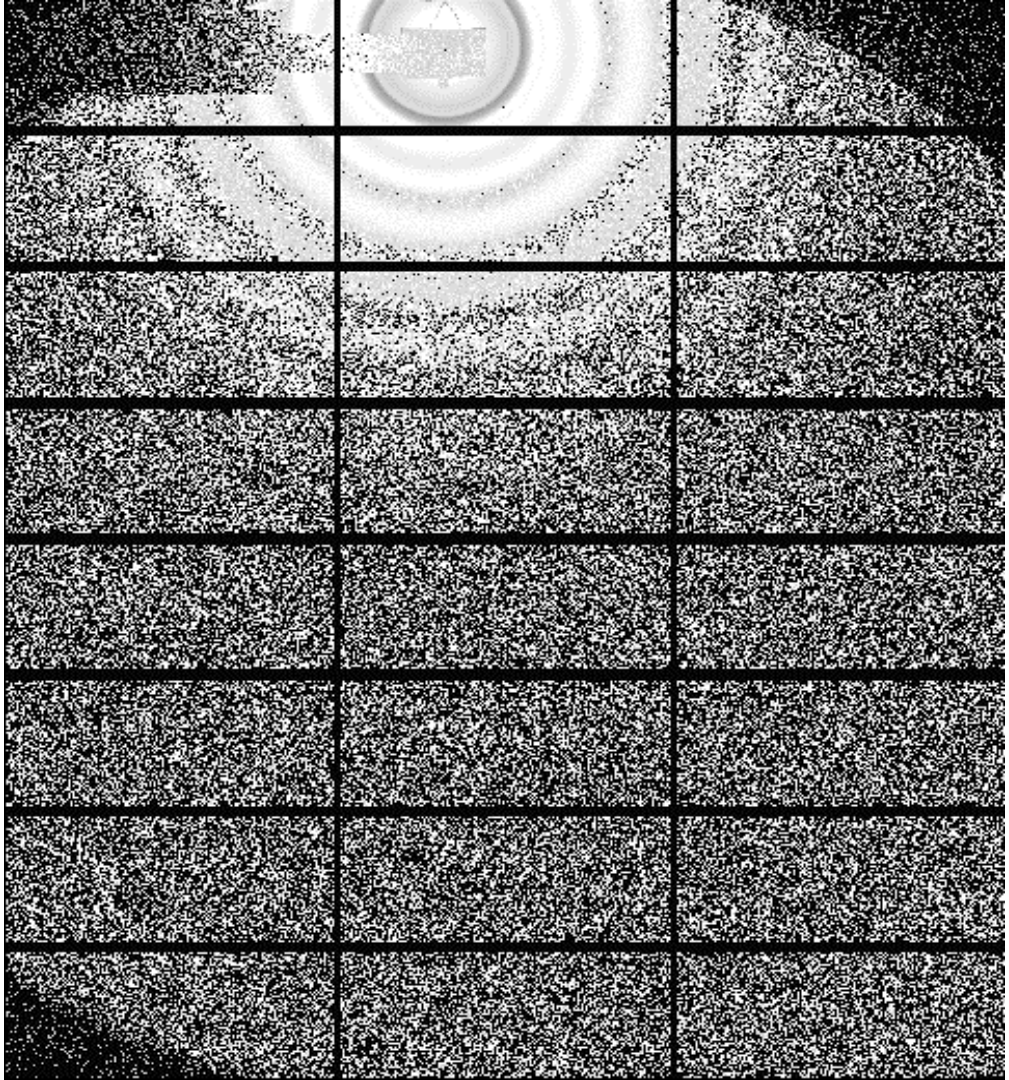
Outline

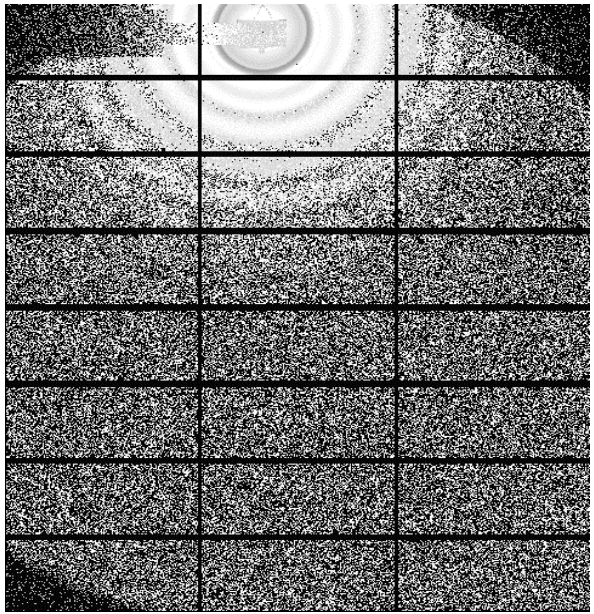
1. Small angle scattering
2. NN architecture and training set
3. Some results

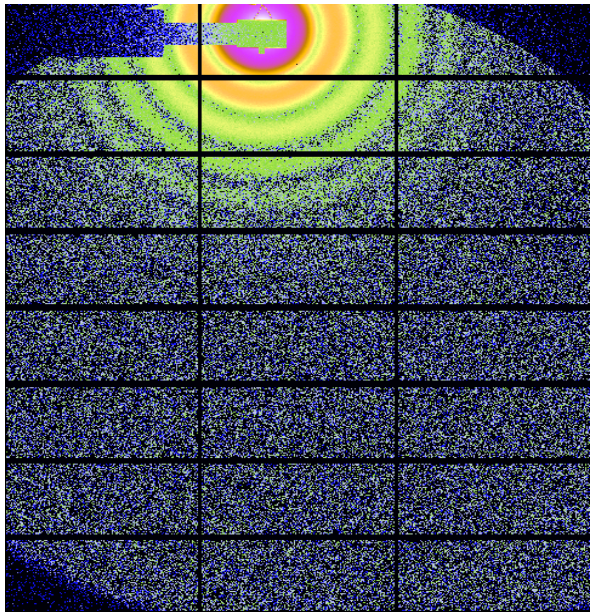
1. Small angle scattering

SAXS experiment

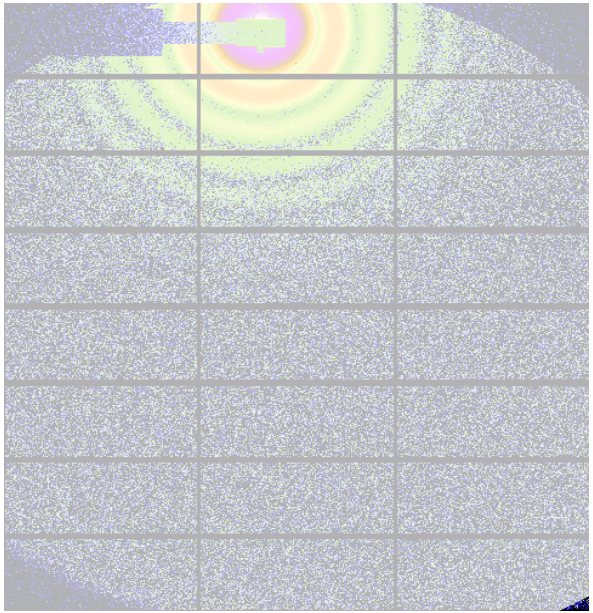


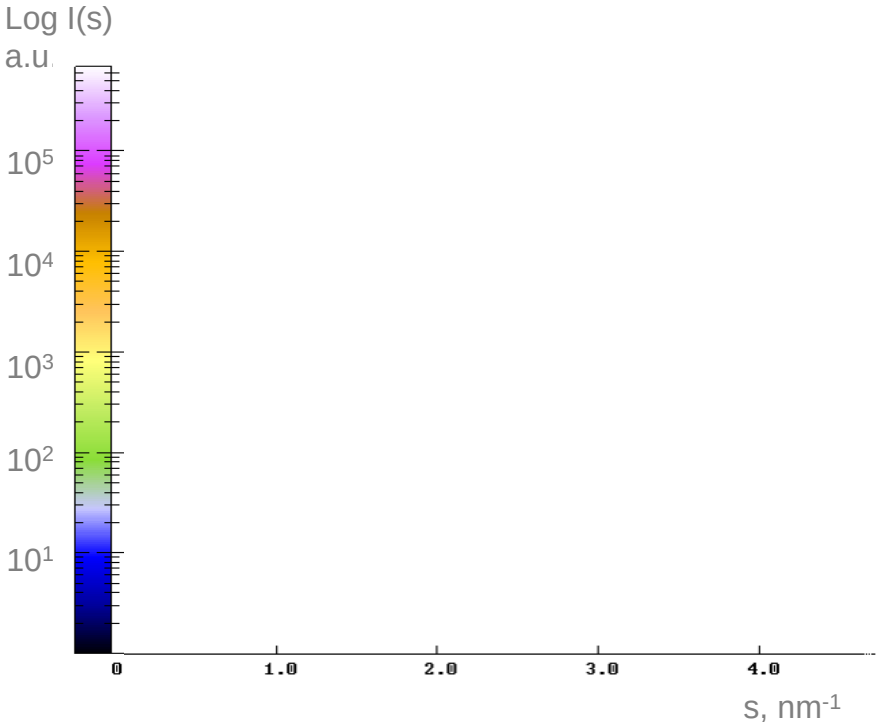




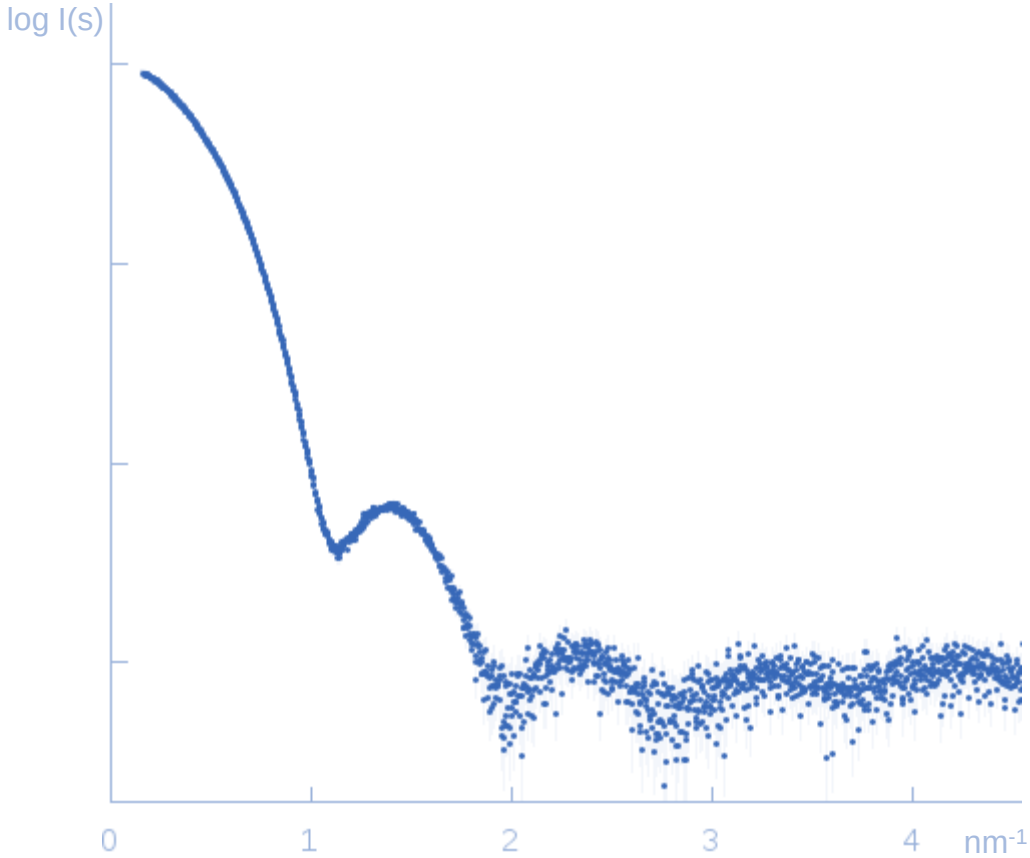

10^5
10^4
10^3
10^2
10^1

2D → 1D



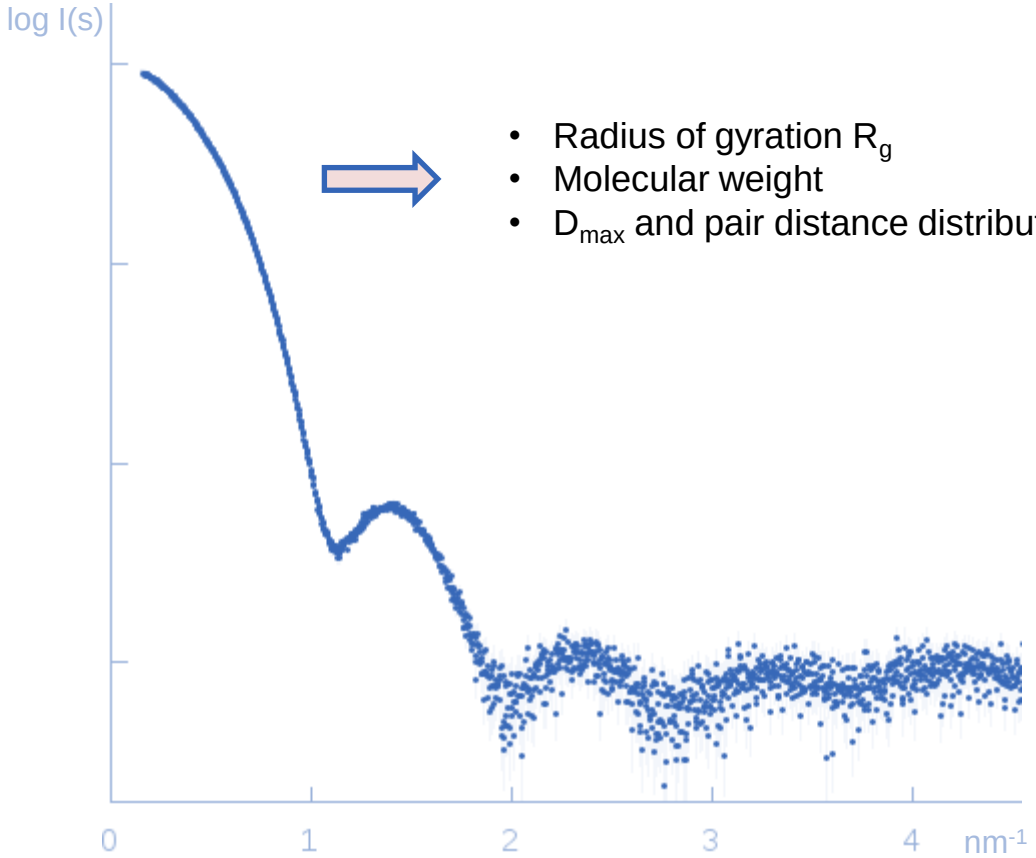


SA(X)S data



experimental SAXS pattern

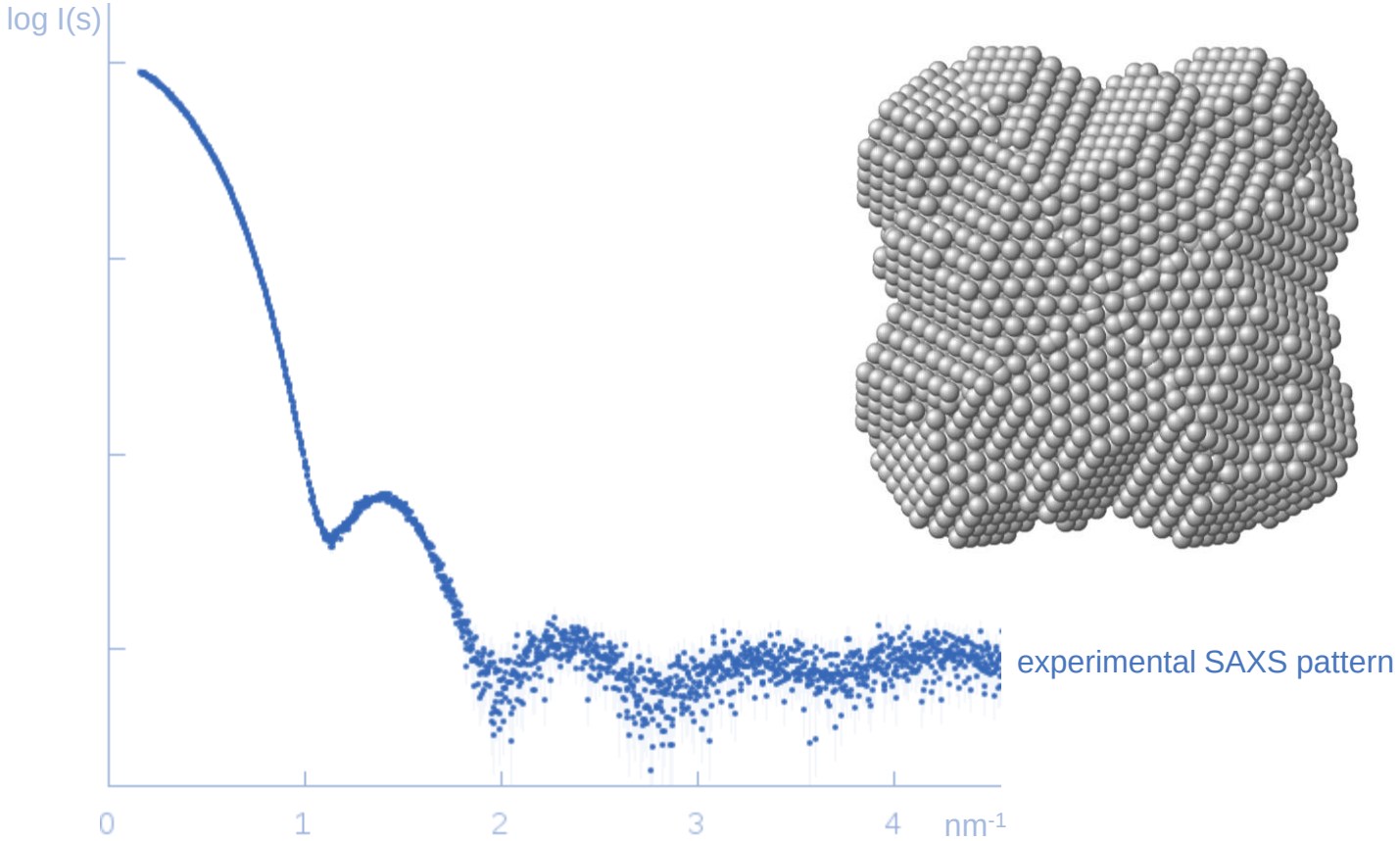
SA(X)S data



- Radius of gyration R_g
- Molecular weight
- D_{max} and pair distance distribution function

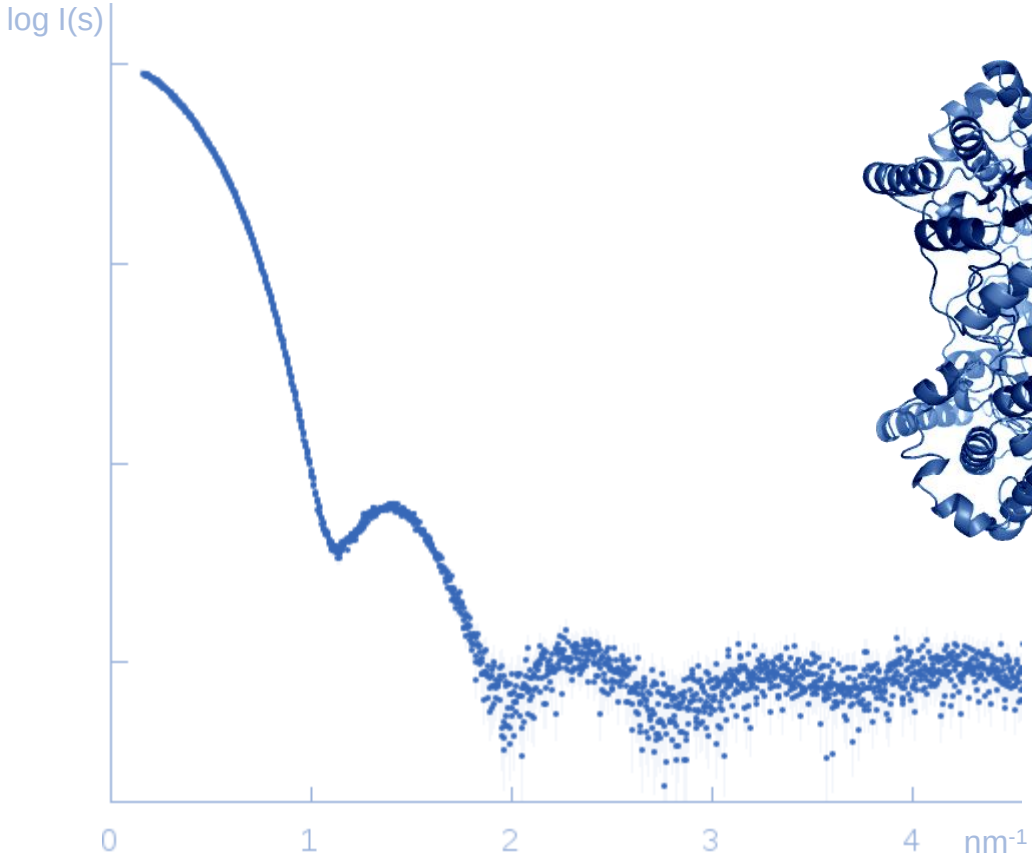
experimental SAXS pattern

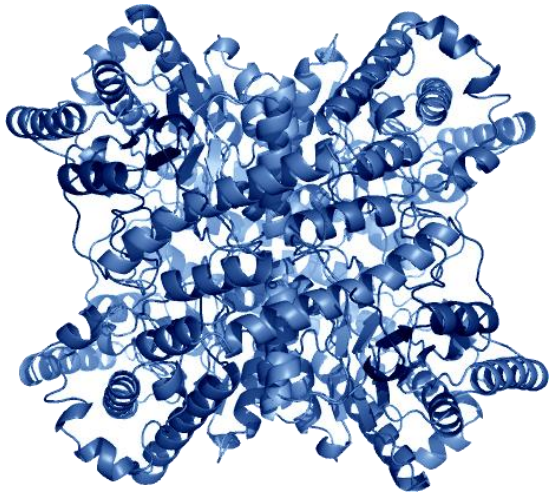
SA(X)S data



experimental SAXS pattern

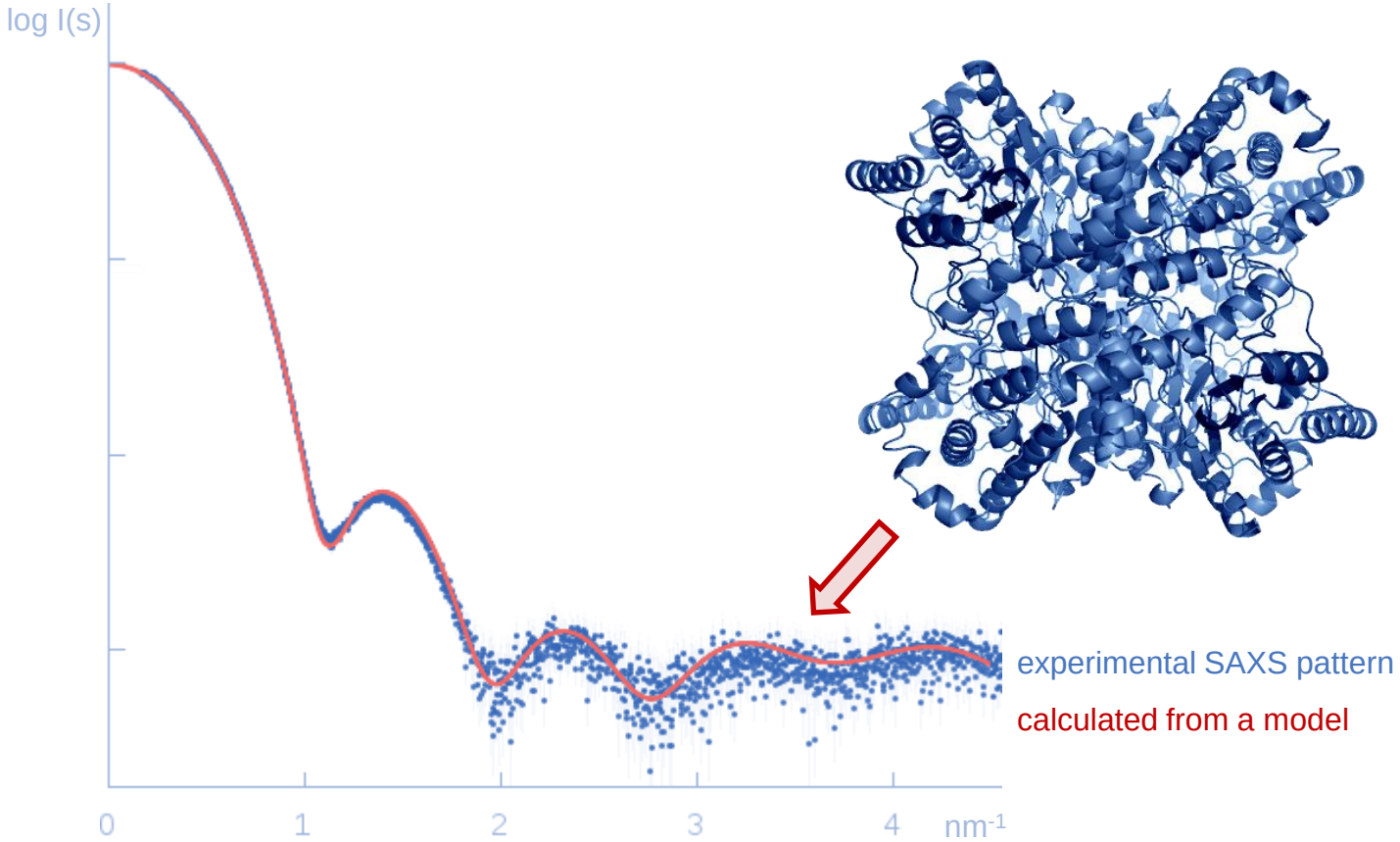
SA(X)S data





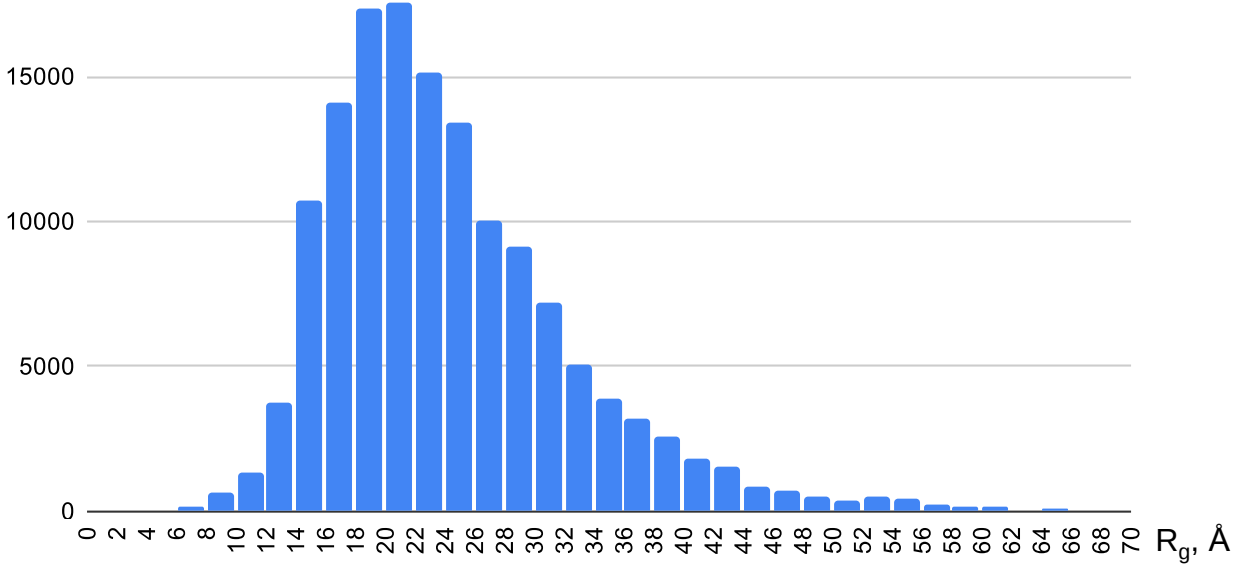
experimental SAXS pattern

SA(X)S data

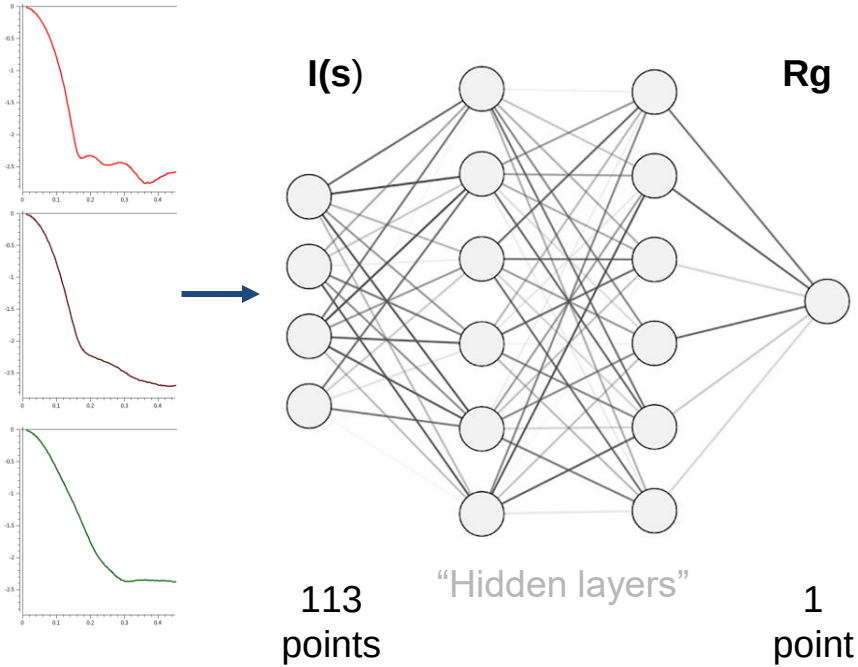

log I(s)
0
1
2
3
4
nm-1
experimental SAXS pattern
calculated from a model

2. Training set and NN architecture

Training set: > 150 000 proteins

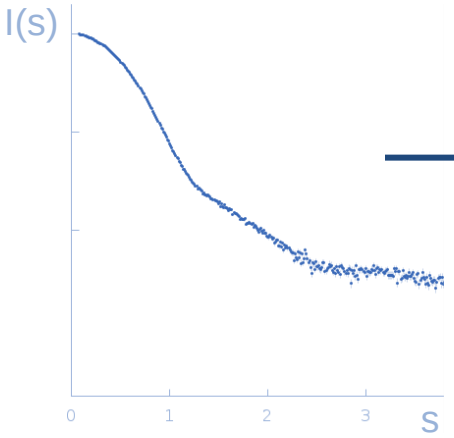


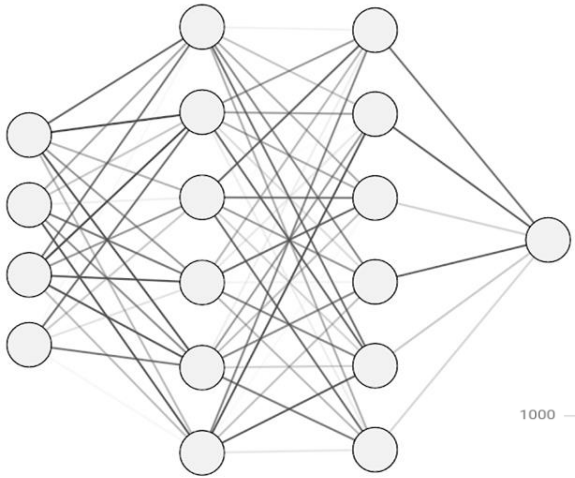
Supervised learning: thousands of I(s)-Rg pairs



Prediction:
previously unseen I(s)

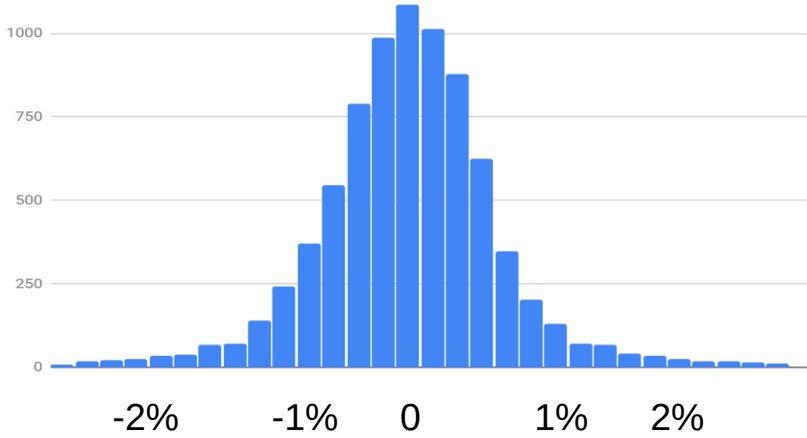
Determine R_g from SAXS data





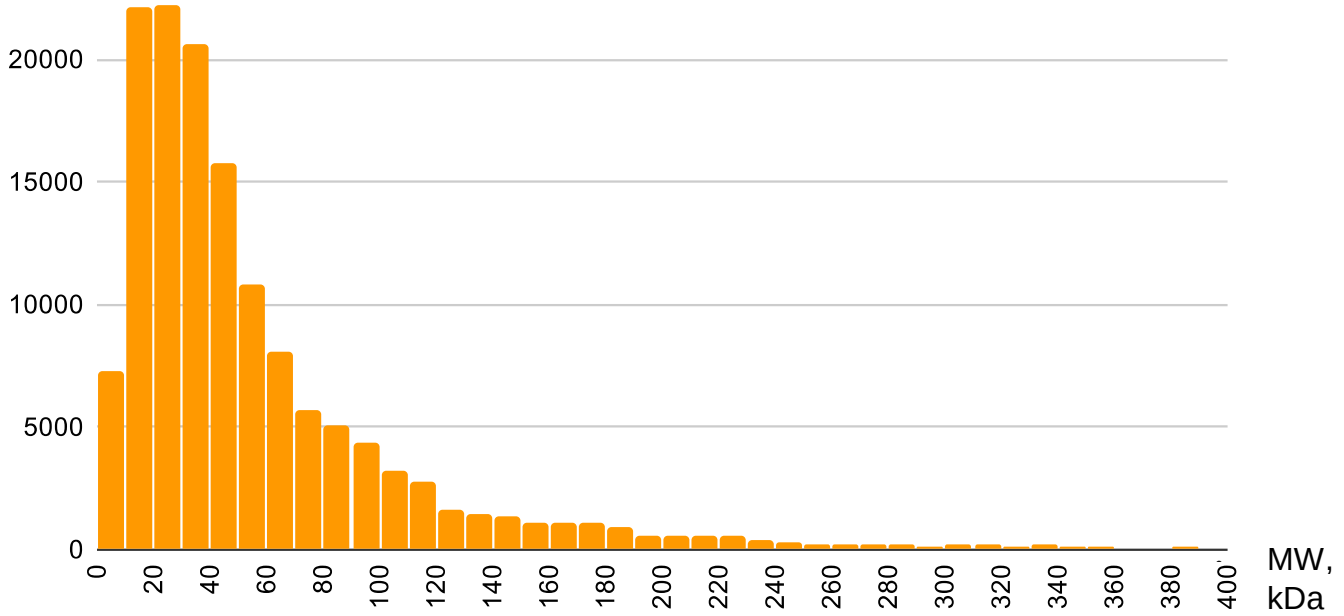
R_g

$$1 - \frac{R_g^{\,predicted}}{R_g^{\,ground\ truth}}$$

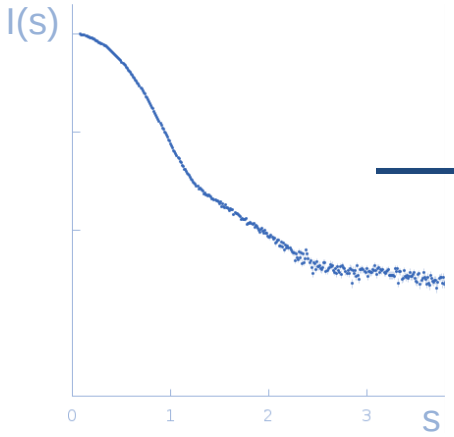


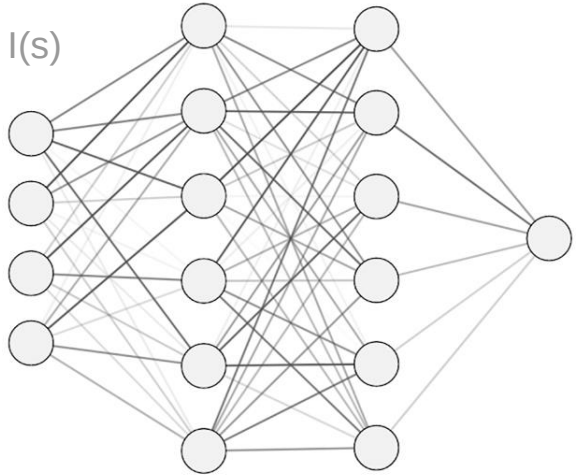
Tested on data simulated from 8192 proteins

MW distribution



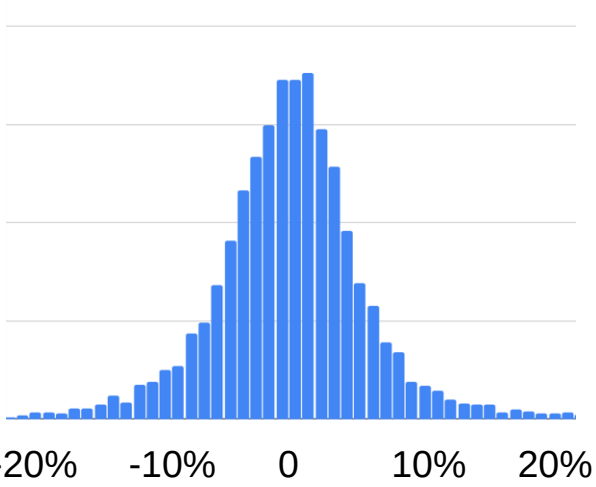
Determine ***molecular weight*** from SAXS data





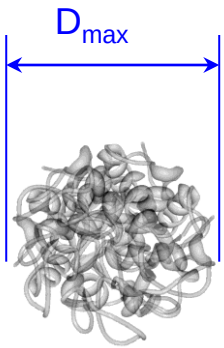
MW

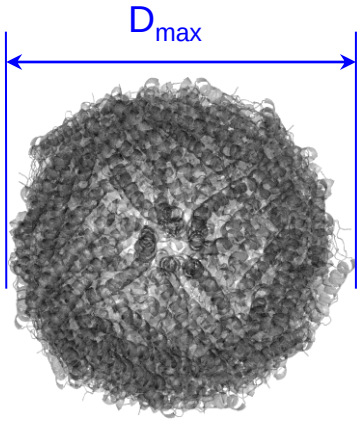
$$1 - \frac{MW^{predicted}}{MW^{ground\ truth}}$$



Tested on data simulated from 8192 proteins

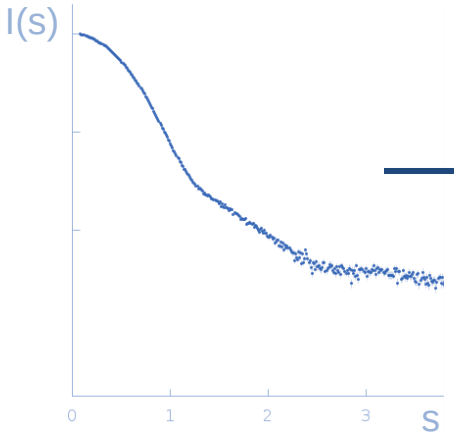
Maximum intra-particle distance of the structure (D_{max})

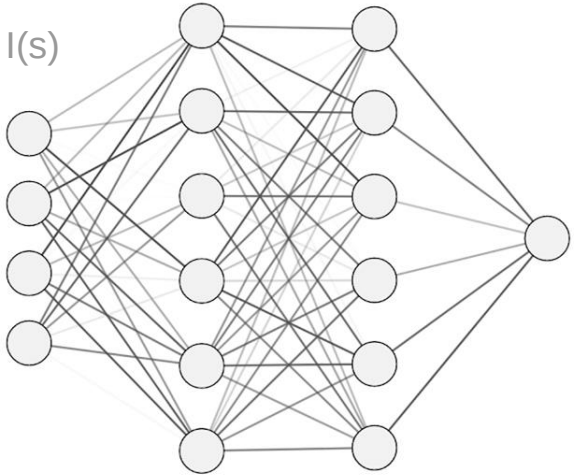




No direct mathematical way to obtain!

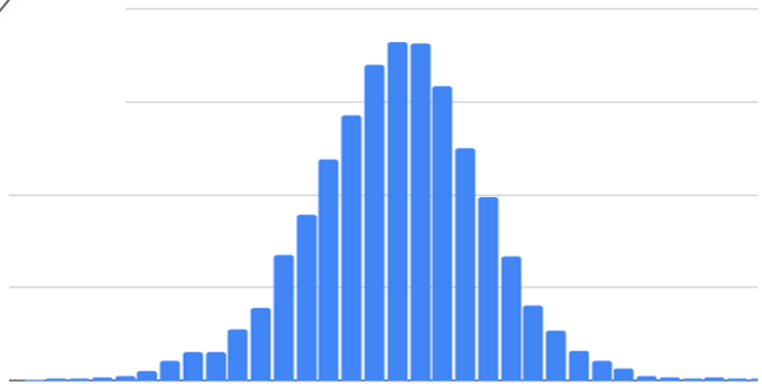
Determine D_{max} from SAXS data





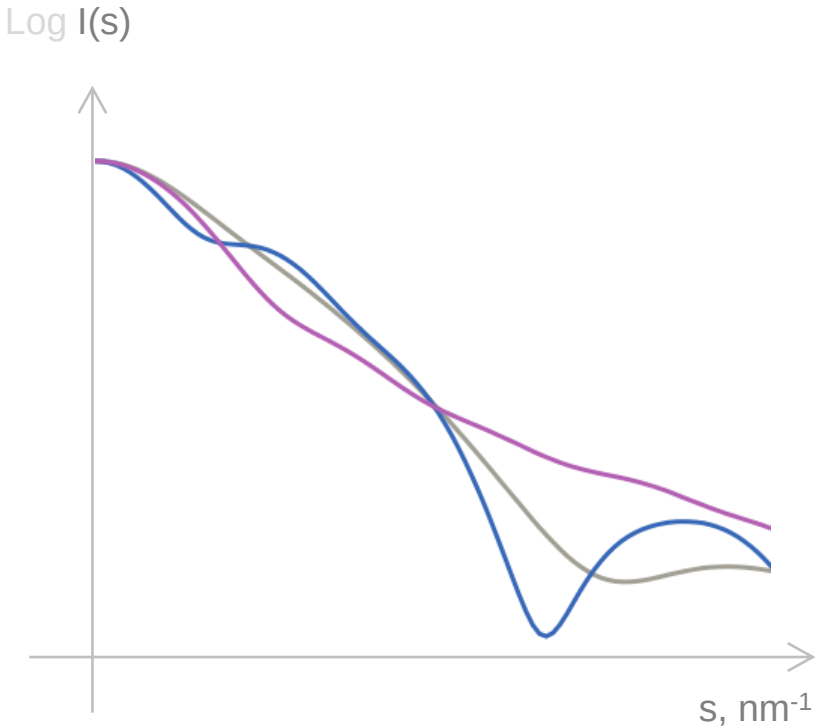
$$1 - \frac{D_{max}^{predicted}}{D_{max}^{ground\ truth}}$$

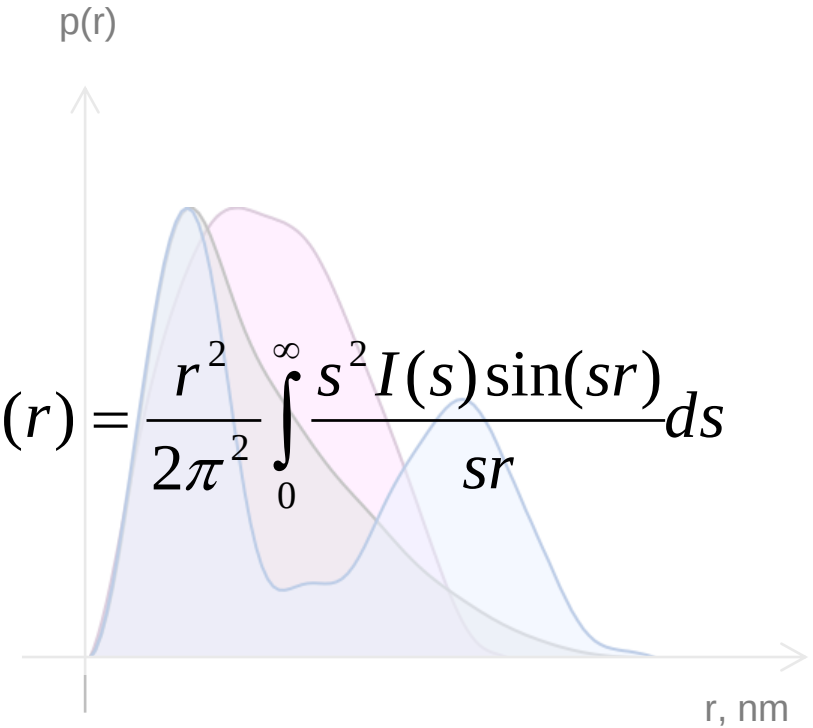
D_{max}



Tested on data simulated from 8192 proteins

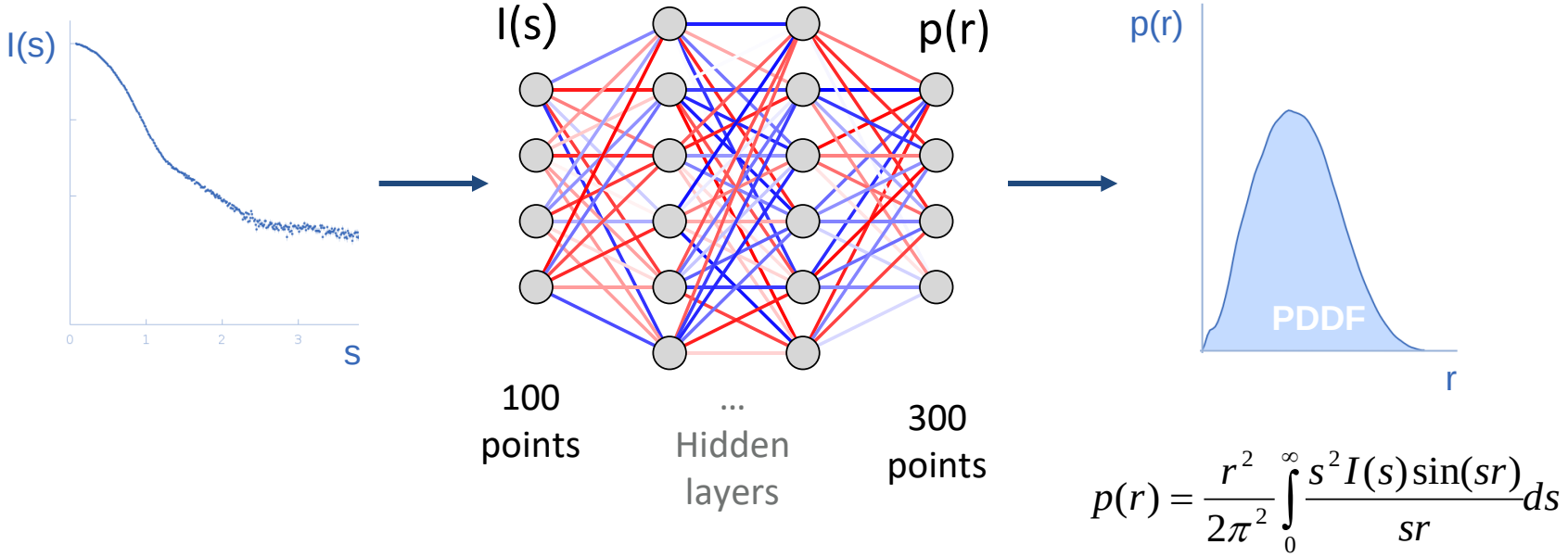
Pair-distance distribution function (PDDF)





$$p(r) = \frac{r^2}{2\pi^2} \int_0^\infty \frac{s^2 I(s) \sin(sr)}{sr} ds$$

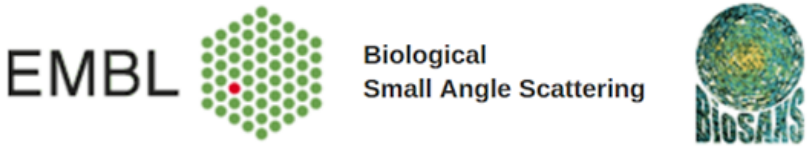
Determine ***PDDF*** from SAXS data



$$p(r) = \frac{r^2}{2\pi^2} \int_0^\infty \frac{s^2 I(s) \sin(sr)}{sr} ds$$

3. Where are we now?

https://dara.embl-hamburg.de/gnnom.php



GNNOM

Fit a PDDF p(r) to experimental data

Experimental data (*.dat) Choose File SASDF99.dat

Angular units (optional) ▼ $s = 4\pi\sin(\theta)/\lambda$

Macromolecule type protein ▼

Submit

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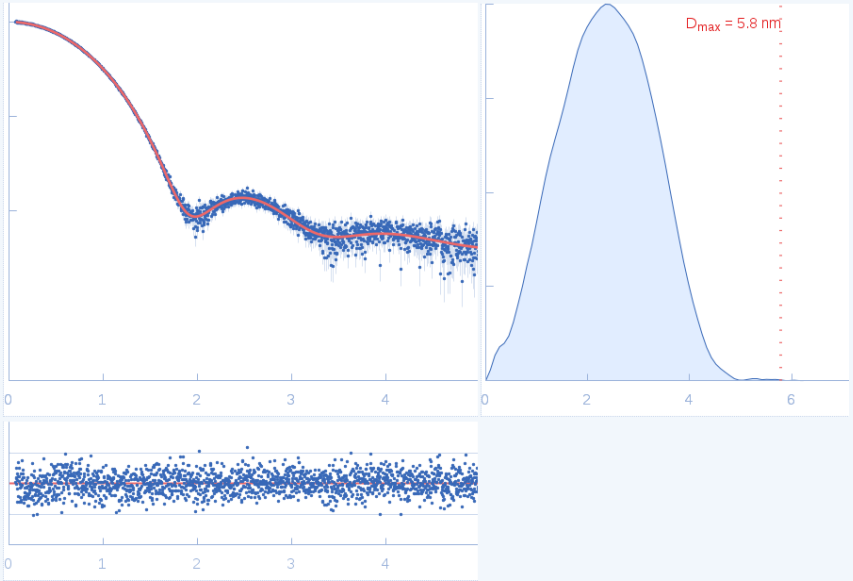
Home > Web services > DARA > SASDFP8.dat

GNNOM

SASDFP8

Predicted R_g	1.8 nm
p(r) R_g	1.8 nm
autorg R_g	1.8 nm
Predicted D_{max}	5.8 nm
p(r) D_{max}	6.2 nm
Predicted MW	23.1 kDa
χ^2	1.0

SASDFP8 – Carbonic anhydrase



Download SASDFP8.fit
Download pddf-predicted.dat

EMBL Biological Small Angle Scattering BioSAXS

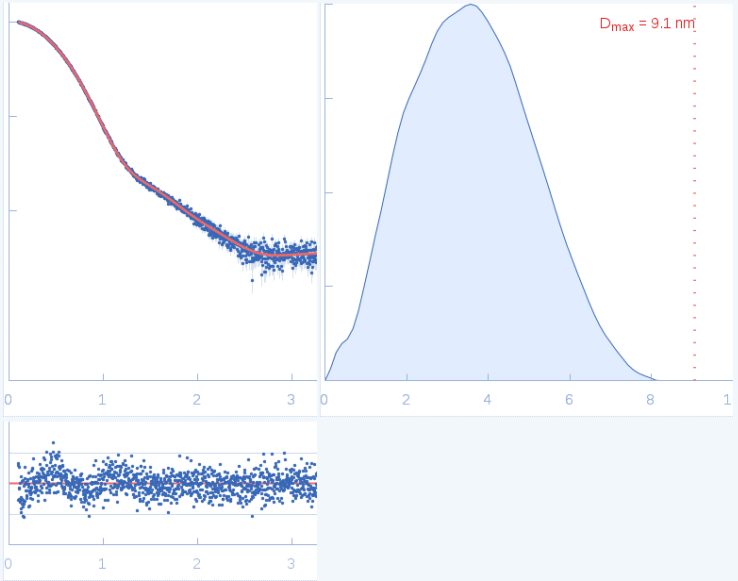
Home > Web services > DARA > SASDFQ8.dat

GNNOM

SASDFQ8

Predicted R_g	2.8 nm
p(r) R_g	2.8 nm
autorg R_g	2.7 nm
Predicted D_{max}	9.1 nm
p(r) D_{max}	8.2 nm
Predicted MW	56.7 kDa
χ^2	1.1

SASDFQ8 – BSA standard



Download SASDFQ8.fit
Download pddf-predicted.dat

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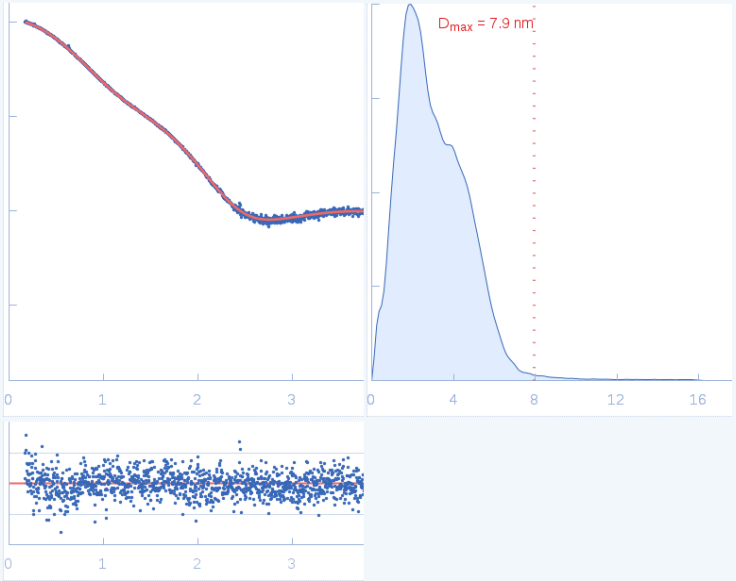
Home > Web services > DARA > SEC-LIG-Jan16-clo.dat

GNNOM

SEC-LIG-Jan16-clo

Predicted R_g	24.5 Å
p(r) R_g	24.9 Å
autorg R_g	23.9 Å
Predicted D_{max}	79.3 Å
p(r) D_{max}	16.5 Å
Predicted MW	19.3 kDa
χ^2	3.5

PDZ domain (extended)



Download SEC-LIG-Jan16-clo.fit
Download pddf-predicted.dat

EMBL Biological Small Angle Scattering BioSAXS

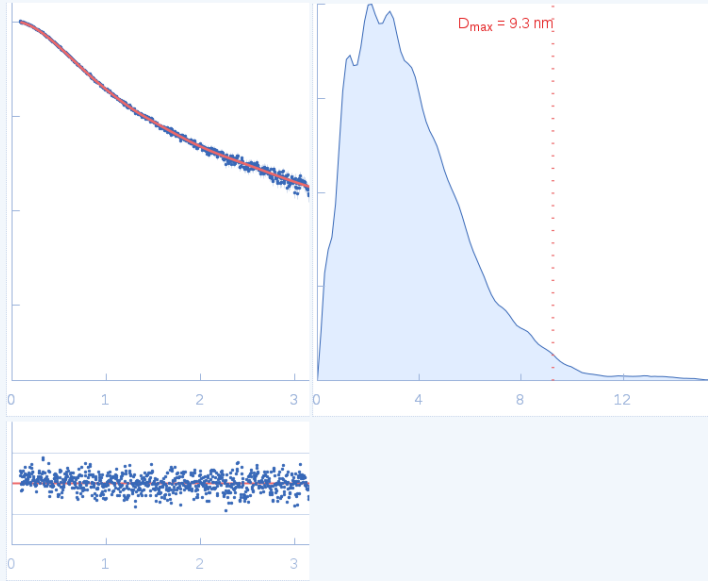
Home > Web services > DARA > Colicin-N.dat

GNNOM

Colicin-N

Predicted R_g	3.0 nm
p(r) R_g	3.0 nm
autorg R_g	2.8 nm
Predicted D_{max}	9.3 nm
p(r) D_{max}	15.8 nm
Predicted MW	19.0 kDa
χ^2	0.7

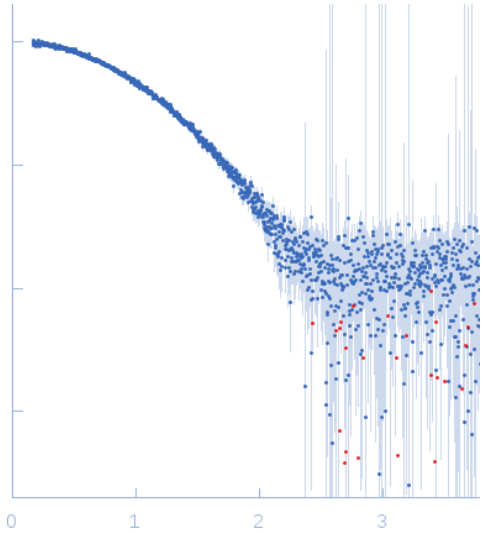
SASDC53 – Colicin N (IDP)

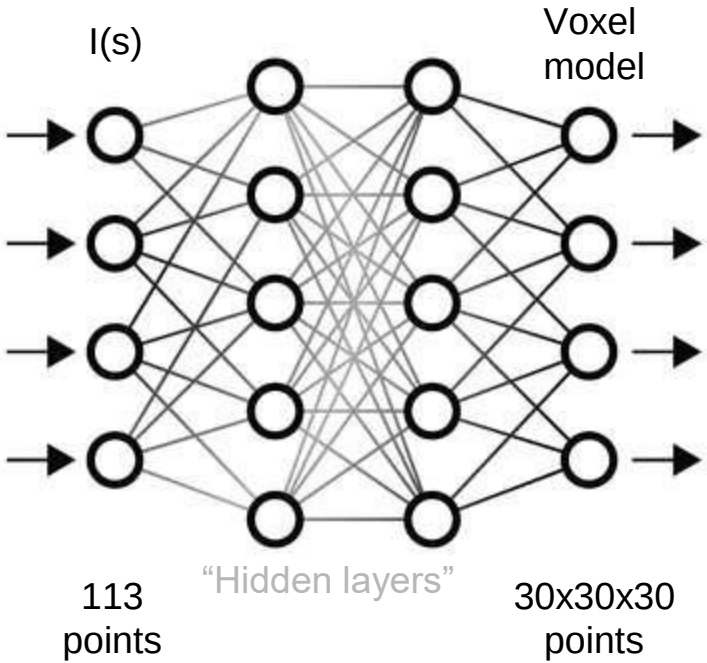


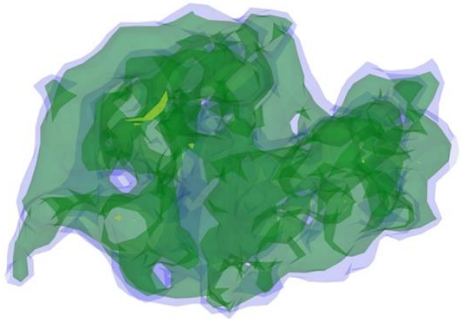
Download Colicin-N.fit
Download pddf-predicted.dat

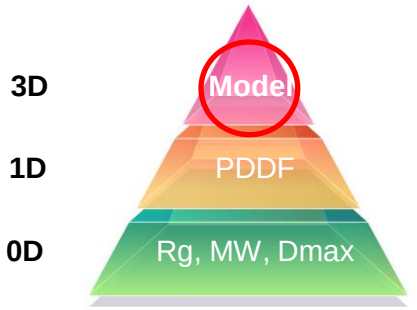
What's next?

Modelling! (3D)



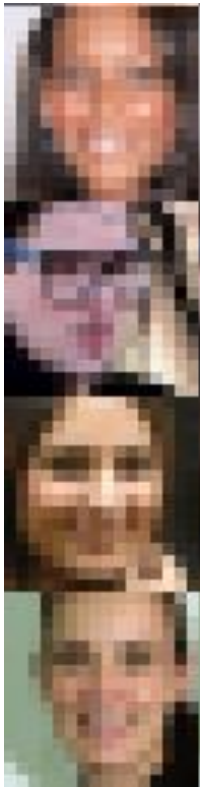






Input

Input



https://github.com/david-gpu/srez

Group members

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Taja Cheremnykh

EMBL

DESY.

BioSAXS

Keras

TensorFlow

python™

Thank you!

https://dara.embl-hamburg.de/gnnom.php

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