BIF101 Short Questions and mcqs from lecture 126__135

PREPARED BY UZAMA JABEEN

COMPOSED BY ZAINAB ARSHAD

UPLOADED AT

https://www.youtube.com/channel/UCh-swQpEKauZh4oSbk1z3Yg



Today I choose life. Every morning when I wake up I can choose joy, happiness, negativity, pain... To feel the freedom that comes from being able to continue to make mistakes and choices - today I choose to feel life, not to deny my humanity but embrace it.

Modeller is a for.....homology modelling

software

How many steps are included in homology modelling.

Seven

what is the first step of homology modelling

Template recognition and initial alignment

what is the second step of homology modelling

Zainab Arshad Official

Alignment correction

what is the third step of homology modelling

Backbone generation

what is the fourth step of homology modelling

Loop modeling

what is the fifth step of homology modelling

Side-chain modeling

what is the sixth step of homology modelling

Model optimization

what is the seventh step of homology modelling

Model validation

What are inputs of homology modelling

Python script file,

Sequence alignment & Template (PDB)

How Homology modelling helps predict protein structures?

By using prior structural information

Homology modelling can be done in

programmatic or automated way!

A protein fold is a

secondary structure elements

How protein fold are arranged

relative to each other in space.

What include in common fold?

Zainab Arshad Official

4-helix bundle and the TIM barrel.

How many stable folds in nature?

5,000

What should kept in mind during fold recognition?

Finding the best fit of a sequence to a set of candidate folds

Fold recognition is also known as

Threading

Fold recognition is a technique

For predicting protein structure

Fold recognition is done when

Homology modelling fail

• In the process of “Threading”, we mount an..... sequence on to the backbone of template structures in a folds library

Amino acid

The best match in Threading is computed using a

scoring function

Scoring typically involves using a Z-Score function based on

energy of a molecule

An estimate of accuracy of the predictions in Threading is based on the

confidence score of the modeling

iTASSER helps

predict function of structures output.

threading is useful For the..... with low alignment quality and identity,

Zainab Arshad Official

“Twilight Zone”

..... cannot be predicted using threading

Novel proteins

3D-1D Bowie Algorithm is proposed by

Bowie et al in 1991

3D-1D Bowie Converts 3D structure into a

1-D string profile

Part of secondary structure including
Alpha helix, and beta-sheet

Pa: j=

prob. of finding amino acid (a) in environment (j)

Pa=

probability of finding (a) anywhere

3D-1D methods convert structure and environment information into

“profiles”

Ab initio methods have **Anfinsen’s thermodynamic hypothesis** at the

center

The ab initio modelling is

Not very accurate

Limitation and defective of ab initio modelling is

• Computationally expensive

• Suitable for protein with less than 100 residues

Zainab Arshad Official

Energy released during the folding process is
computed for predicting structure

Stabilization is measured by

energy released during the folding process

Zainab Arshad Official