Mapping protein interaction computatonally

Jong H. Park

Abstract

Protein interaction is an important research topic in Bioinformatics.
A novel computational method of protein interaction was developed
It shows the diverse pattern of protein protein interaction.

Curriculum Vitae

Name	: **Park, Jong Hwa**
Nationality	: Korean
First Language	: Korean (Fluent)
Second Language	: English (Fluent)
Place of Birth	: Korea, Pusan, 606-072, Youngdo-ku, Cheong Hak 2-dong, Buyoung Mansion 503
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<Education>

1986(Mar) -1987(Dec) : Veterinary Medicine, Seoul National University, Korea

1988(Jan) -1990(Jul) : Compulsory military service. Discharged as army sergeant.

1990(Jul.)-1994(Aug) : Biochemistry(1st class, Honours), Aberdeen, University, UK,
(for BSc degree)

1994(Sept)-1997(June): Protein Structure Prediction, Multiple Sequence Alignment
analysis, Genomic sequence and protein structure analysis
by computing, Centre For Protein Engineering,
MRC Centre, Hills Road, Cambridge, UK
(for PhD Degree)

1997(June)-1997(Dec) : Protein Domain Clustering, Genomic Sequence Analysis,
Assessment of sequence search algorithms.
Laboratory of Molecular Biology,
MRC Centre, Hills Road, Cambridge, UK,
(Postdoctoral)

1998(Jan) -1999(Mar) : Functional Genomics, Protein structure prediction,

Transcription regulation,

Church Lab, Genetics, Harvard Med. School, 200

Longwood Av. Boston, MA, USA

(Postdoctoral)

1999(Apr) -2000(now) : Mapping the protein universe. Liisa Holm lab,

EBI, Hinxton, UK

<list of publication>

0) Mapping Protein Family Interactions:

Intra- and Intermolecular Interaction Repertoires are Distinct

Jong Park, Michael Lappe and Sarah A. Teichmann

(submitted, 2000)

1) Estimating the significance of sequence order in protein

secondary structure prediction,

Jong Park, Sabine Dietmann, Andreas Heger, and Liisa Holm.

(2000, Bioinformatics, In press for Issue 9, 2000)

2) PDB_ISL : intermediate sequence library for protein structure assignment

Sarah A. Teichmann, Cyrus Chothia, George M. Church, and Jong Park

RECOME2000, The Fourth Annual International Conference on

Computational Molecular Biology, Tokyo, Japan, April, 2000.

3) DaliLite: A standalone program for Dali structure comparison server.

Liisa Holm and Jong Park, Bioinformatics, Issue 6, p566-667, (2000)

4) RSDB: representative sequence databases with high information content.

Jong Park, Liisa Holm, Andreas Heger and Cyrus Chothia,

Bioinformatics, (2000), May, Vol 16. Issue No. 5. 458-464

5) Sequence Search Algorithm Assessment and Testing Toolkit (SAT)

Jong Park, Liisa Holm, and Cyrus Chothia,

Bioinformatics, (2000), Vol 16. No.2, 104-110.

6) Fast and Reliable Assignment of Protein Structures to Sequences.

Sarah A. Teichmann, Cyrus Chothia, George M. Church, and Jong Park

Bioinformatics, 2000, Vol. 16, No. 2, 117-124.

7) Sequence Comparisons Using Multiple Sequences Detect Three Times as Many
Remote Homologues as Pairwise Methods.
Jong Park, Karplus, K., Barrett, C., Hughey, R., Haussler, D., Hubbard, T. and Chothia, C
Journal of Molecular Biology, 1998, Dec 11;284(4):1201-1210

8) Structural assignments to the proteins of Mycoplasma genitalium show that
they have been formed by extensive gene duplications and domain
rearrangements,
Sarah Teichmann, Jong Park and Cyrus Chothia,
PNAS., 1998, Dec 8;95(25):14658-14663.

9) DIVCLUS: an automatic method in the GEANFAMMER package that finds homologous
domains in single- and multi-domain proteins.
Bioinformatics. 1998 ;14(2):144-50.
Jong Park and Sarah Teichmann

10) Intermediate sequences find distant sequence homologues,
Jong Park, Sarah A. Teichmann, Tim Hubbard, and Cyrus Chothia,
Journal of Molecular Biology . 1997 Oct 17;273(1):349-54.

11) Protein structure prediction: Playing the fold.
Hubbard T, Jong Park, Lahm A, Leplae R, and Tramontano A.,
TIBS, 1996 Aug;21(8):279-281, (1996)

12) Hubbard,T., Tramontano,A., Barton,G., Jones,D., Sippl,M., Valencia,A.,
Lesk,A., Moult,J., Rost,B., Sander,C., Schneider,R., Lahm,A., Leplae,R.,
Buta,C., Eisenstein,M., Fjellstr^m,O., Floeckner,H., Grossman,G., Hansen,J.,
Helmer Citterich,M., Joergensen,F.S., Marchler-Bauer, A., Osuna,J., Jong Park,
Reinhardt,A., Ribas de Pouplana,L., Rojo-Dominguez,A., Saudek,V.,
Sinclair,J., Sturrock,S., Venclovas,C., Vinals,C. (1996).
Update on protein structure prediction: results of the IRBM 1995 workshop.
Folding and Design, 1, 55-63.

13) Fold recognition and ab initio structure predictions using

Hidden Markov Models and [[beta]]-strand pair potentials.

Tim Hubbard and Jong Park,

Proteins, Nov. 23(3):398-402, (1995)

Unrefereed papers:

1) Persus: A relational database and server of algorithms and subroutines

for computational biology.

Andreas Heger, Jason Johnson and Jong Park (1999)

The first Bioperl conference. Heidelberg. Germany.

2) Post-processing of Secondary structure prediction by using reverse

protein sequences.

Jong Park and George M. Church,

Critical Assessment of Structure Predictions of proteins (CASP3) meeting.

Assilomar. Dec. (1998).

<Past academic Interests>

<Bioinformatics>

Genome analysis, Functional Analysis (Bioinformatic Cell), DNA structure,

Transcription regulation, Hidden Markov Model, Protein Structure (protein folding and design),

<Ageing>

Ageing process. (DHEA, Telomerase, Free radical, hormones, Calorie reduction, DNA chip data)

<Computer science>

Computer Operating system design, Artificial Neural Network application, Chaos,

Perl, Perl/Tk,

<Other interests>

Philosophy, Mathematics, Physics, Linguistics, Psychology, Mountain Bike,

Martial Arts, Computer Hardware