

- [ScienceWatch Home](#)
- [Inside This Month...](#)
- [Interviews](#)

- [Featured Interviews](#)
- [Author Commentaries](#)
- [Institutional Interviews](#)
- [Journal Interviews](#)
- [Podcasts](#)

Analyses

- [Featured Analyses](#)
- [What's Hot In...](#)
- [Special Topics](#)

Data & Rankings

- [Sci-Bytes](#)
- [Fast Breaking Papers](#)
- [New Hot Papers](#)
- [Emerging Research Fronts](#)
- [Fast Moving Fronts](#)
- [Corporate Research Fronts](#)
- [Research Front Maps](#)
- [Current Classics](#)
- [Top Topics](#)
- [Rising Stars](#)
- [New Entrants](#)
- [Country Profiles](#)

About Science Watch

- [Methodology](#)
- [Archives](#)
- [Contact Us](#)
- [RSS Feeds](#)

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TRACKING TRENDS & PERFORMANCE IN BASIC RESEARCH

[Interviews](#)
[Analyses](#)
[Data & Rankings](#)

2009 : February 2009 - Fast Breaking Papers : Valadi K. Jayaraman, Bhaskar D. Kulkarni, Piyushkumar Mundra, Madhan Kumar, and Krishna Kumar Kandaswamy

FAST BREAKING PAPERS - 2009

February 2009



Valadi K. Jayaraman, Bhaskar D. Kulkarni, Piyushkumar Mundra, Madhan Kumar, and Krishna Kumar Kandaswamy talk with *ScienceWatch.com* and answer a few questions about this month's Fast Breaking Paper in the field of Engineering.



Article Title: Using pseudo amino acid composition to predict protein subnuclear localization: Approached with PSSM

Authors: Mundra, P;Kumar, M;Kumar, KK;Jayaraman, VK;Kulkarni, BD

Journal: PATTERN RECOGNITION LETT

Volume: 28

Issue: 13

Page: 1610-1615

Year: OCT 1 2007

* Natl Chem Lab, Chem Engn & Proc Dev Div, Dr Homi Bhabha Rd, Pune 411008, Maharashtra, India.

* Natl Chem Lab, Chem Engn & Proc Dev Div, Pune 411008, Maharashtra, India.

SW: Why do you think your paper is highly cited?

Nuclear proteins operating in related pathways, or those that share common functionality, tend to be localized in specific compartments within the nucleus. Protein subnuclear localization prediction has tremendous biological significance as the mislocalization of proteins can lead to genetic diseases and cancer. Our support vector machine-based methodologies have yielded more accurate predictions.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

This paper studies different methods for extracting knowledge from sequence information in the form of features for machine learning algorithms. These include evolutionary information in the form of position specific scoring matrix (PSSM) features, pseudo amino acid composition features (as proposed by Kuo-Chen Chou at the Gordon Life Science Institute in San Diego) and five factor solution score features (as derived by William R. Atchley of the Department of Genetics at North Carolina State University) using nearly 500 amino acid properties.

SW: Would you summarize the significance of your paper in layman's terms?

Our methodology can speed up the process of protein annotation and



subsequent relevant discoveries.

SW: How did you become involved in this research, and were there any problems along the way?

We have been working on important *in-silico* predictions of protein and gene functions for the past several years and found this particular problem to be potentially crucial. We found that the biggest difficulty was in determining how to choose a relevant dataset. Hong-Bin Shen and Kuo-Chen Chou's previous work on this issue, at the Institute of Image Processing and Pattern Recognition of Shanghai's Jiaotong University, led to our utilization of their same dataset, which demonstrated excellent prediction results.

Top to bottom:
Bhaskar D. Kulkarni,
Piyushkumar Mundra,
and Krishna Kumar
Kandaswamy

SW: Where do you see your research leading in the future?

Considering its biological implications, we believe more research attention will be diverted towards protein subnuclear localization prediction problems. Newer methods for mathematically representing protein sequences may be proposed to further increase prediction accuracy.

SW: Do you foresee any social or political implications for your research?

Our work could speed up the nuclear protein annotation process, which may help the medical community, particularly those individuals working in the fields of human genetics and cancer research.

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Krishna Kumar Kandaswamy

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Keywords: nuclear proteins, protein subnuclear localization prediction, mislocalization of proteins, support vector machine-based methodologies, machine learning algorithms, position specific scoring matrix, pseudo amino acid composition features, five factor solution score features, protein subnuclear localization prediction problems, nuclear protein annotation process.

 PDF

[back to top](#) 

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