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2009 : September 2009 - New Hot Papers : Current Classics Scientist Sudhir Kumar on MEGA Integrated Software

NEW HOT PAPERS - 2009

September 2009

PDF

Sudhir Kumar talks with *ScienceWatch.com* and answers a few questions about this month's New Hot Paper in the field of Computer Science.

Article Title: MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences
Authors: Kumar, S;Nei, M;Dudley, J;Tamura, K
Journal: BRIEF BIOINFORM
Volume: 9
Issue: 4
Page: 299-306
Year: JUL 2008
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(addresses have been truncated)

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

In this paper, we have discussed the motivation, design principles, and priorities that have shaped the development of the Molecular Evolutionary Genetics Analysis (MEGA) software. We credit these attributes to be the primary reasons for the extremely high impact of the MEGA software package across a broad range of biological disciplines.

In addition to the users of MEGA, other software developers have found our design principles to be compelling, which indicate that the principles are positively influencing the design and implementation of other bioinformatics software packages.

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

This paper discusses a biologist-centric paradigm for developing software for biologists. Biologist-centric software solutions are not only user-friendly, but also emulate the common workflows and habits of biologists.

In addition, we present examples from the MEGA software which recognize that the burden is on bioinformatics software developers to inform users about the precise nature of the results generated and also to develop new applications and adapt existing ones to multiple platforms.

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

This paper presents a synthesis of knowledge on biologist-centric software designs that we've developed, which has come to be appreciated over the course of the MEGA development for a period of almost two decades. Therefore, software

developers may find some of our principles to be useful in developing effective bioinformatics software designs for biologists.

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

We initiated the MEGA software project due to our own need for employing statistical methods in the comparative analysis of DNA and protein sequences in the early 1990s. At this time, most computer programs available did not allow us to explore the primary data visually and lacked a user-friendly interface.

In order to make statistical methods available for phylogenetic analysis in a user-friendly manner, we produced a user-friendly program with a mouse/menu interface for use on early PCs in 1993. Over the last 15 years, MEGA has undergone many transformations and an extensive expansion. The most recent version of MEGA (version 5.0) is scheduled to be released later this year.

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

We are building on the successful design patterns of MEGA for a software package that responds to the requirements of biologists in this era of personal genomics and high-throughput sequencing. The need for biologist-centric solutions has become even more acute because the researchers, especially those without extensive informatics training, wish and need to analyze large and diverse datasets in their daily investigations.

Biological researchers would like to exploit the extensive genome information more effectively and efficiently while avoiding the need to navigate the complexity and size of the raw data available in public databases.

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

Perhaps not in the grand scheme of life, but within academic circles it carries social implications for the expectations that researchers and granting agencies should, and most likely will have, when it comes to using and funding bioinformatics software projects.

"We are building on the successful design patterns of MEGA for a software package that responds to the requirements of biologists in this era of personal genomics and high-throughput sequencing."

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KEYWORDS: DURANGO.

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Current Classics scientist in Computer Science, October 2007

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