

## Research Article

# ImageJS: Personalized, participated, pervasive, and reproducible image bioinformatics in the web browser

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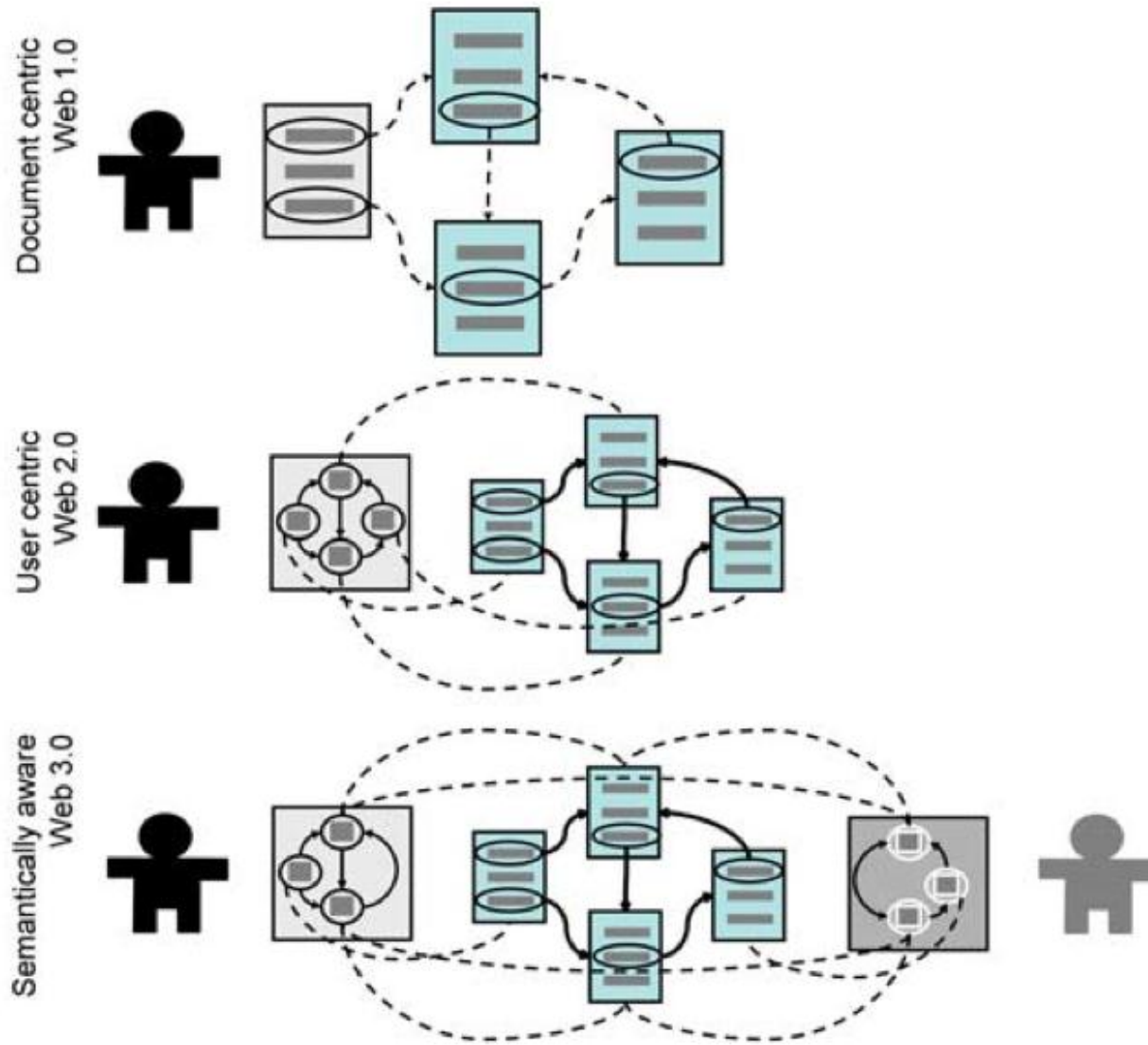
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Deus FH, R Stanislaus<sup>1</sup>, DF Veiga, C Behrens, II Wistuba, JD Minna, HR Garner, SG Swisher, JA Roth, AM Correa, B Broom, K Coombes, A Chang, LH Vogel, JS Almeida (2008) A Semantic Web management model for integrative biomedical informatics. *PLoS ONE*. Aug 13;3(8):e2946 [PMID: 18698353].

# Fractal MapReduce decomposition of sequence alignment

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## Abstract

### Background

The dramatic fall in the cost of genomic sequencing, and the increasing convenience of distributed cloud computing resources, positions the MapReduce coding pattern as a cornerstone of scalable bioinformatics algorithm development. In some cases an algorithm will find a natural distribution via use of *map* functions to process vectorized components, followed by a *reduce* of aggregate intermediate results. However, for some data analysis procedures such as sequence analysis, a more fundamental reformulation may be required.

### Results

In this report we describe a solution to sequence comparison that can be thoroughly decomposed into multiple rounds of *map* and *reduce* operations. The route taken makes use of iterated maps, a fractal analysis technique, that has been found to provide a "alignment-free" solution to sequence analysis and comparison. That is, a solution that does not require dynamic programming, relying on a numeric Chaos Game Representation (CGR) data structure. This claim is demonstrated in this report by calculating the length of the longest similar segment by inspecting only the USM coordinates of two analogous units: with no resort to dynamic programming.

### Conclusions

The procedure described is an attempt at extreme decomposition and parallelization of sequence alignment in anticipation of a volume of genomic sequence data that cannot be met by current algorithmic frameworks. The solution found is delivered with a browser-based application (webApp), highlighting the browser's emergence as an environment for high performance distributed computing.

### Availability

Public distribution of accompanying software library with open source and version control at <http://usm.github.com> [webcite](#). Also available as a webApp through Google Chrome's WebStore <http://chrome.google.com/webstore> [webcite](#): search with "usm".

JavaScript faster than C ?

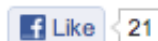
## Science News

... from universities, journals, and other research organizations

### Angry Birds Meets Bioinformatics

*ScienceDaily (July 20, 2012)* — For years researchers have been looking for ways to improve patient care by making better use of health information. So far, Big Data and Web 3.0, techie terms for massive stores of patient data and a unified global system to analyze it -- have not realized their full potential in medical research.

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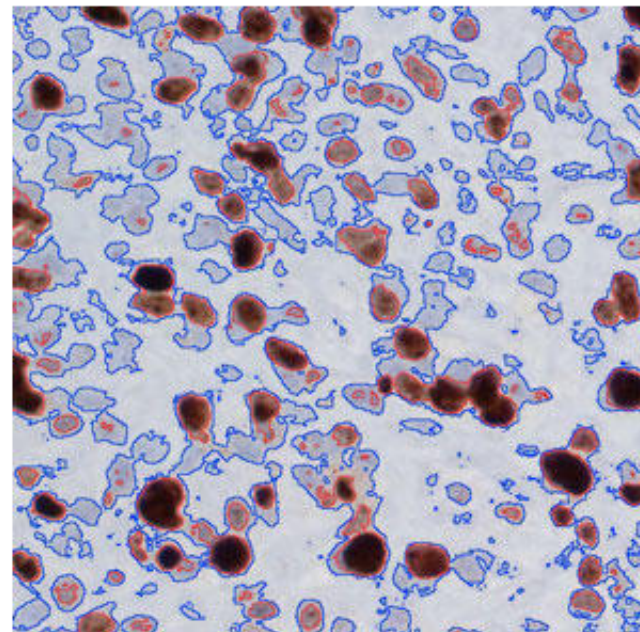
#### See Also:

#### Health & Medicine

- [Today's Healthcare](#)
- [Diseases and Conditions](#)

Meanwhile, you can cruise your favorite app store for hundreds of Web applications that analyze data, in many cases to create a smartphone game. No need to buy pricey hard drives or software packages. Ironically, the market asked Web browsers, the part of your computer that talks to the internet, to do so many things in recent years that this cheap, universal computing environment became an analytical powerhouse, especially when you network browsers together in "clouds."

Bioinformatics experts have looked on with envy, wishing they too had



*This snapshot is the result of using an ImageJ's module to determine how fast brain cancer cells are growing. The darks blots are the nuclei of cells dividing as part of the high-speed abnormal growth seen in tumors. (Credit: Image courtesy of University of Alabama at Birmingham)*



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