Human Computation and
The Wisdom of Clouds

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Luis von Ahn
Hours per year, world-wide, spent playing computer solitaire: 9 billion

Hours spent building the Panama Canal: 20 million (less than a day of solitaire)
The New York Times

Years 1851-1980 were fully digitized, start to finish, in 2009!
Your partner has suggested 3 labels.

- off-limits
  - building
  - hotel
  - car
  - cars
  - sky

- my labels

- zoom out
Games for scientific discovery

David Baker
Rosetta@home
Protein Folding, Design, and Docking

BOINC Application version 480 [workunit: ]

Searching... Accepted

1.5% Complete
CPU time: 0 hr 18 min 54 sec
Jack Schorbrun - Total credit: 1000 - RAC: 500
Baker Lab
Rosetta@home v4.8 http://boinc.bakerlab.org/rosetta/

Stage: Ab Initio
Step: 9821
Accepted RMSD: 11.12
Accepted Energy: -29.31936
What's New

Small Update

We've posted a small update today, here's what's in it:

- Some stability fixes, particularly with crashes when canceling recipes.
- Improvements to scoring of sequence alignment. The scores of your existing alignments will change in the Sequence Alignment Tool due to this, but it won't affect your actual scores for the puzzles.

http://fold.it/portal/
BootsMcGraw
Global Soloist Rank: #6
Global Soloist Score: 3784
Cases

Profile

Name: BootsMcGraw
Location: Dallas, Texas USA
Started Folding: 12/03/08
About me: An educated redneck here, from Dallas, Texas.

When I was in grad school in 1965 at the State University of New York at Buffalo, my master’s thesis was to construct and present a computer program that predicted secondary structures (helix, sheet, loop) of proteins based on their amino acid sequences. Tertiary structure (i.e. folding) prediction was a pie-in-the-sky fantasy.

Imagine my delight; a quarter century later, to find out that not only are people determining tertiary structures of proteins, but they’ve made a “game” of it.

Hobbies: Licensed Massage Therapist, also a photographer, videographer, and webmaster. I have studied health and nutrition for over twenty years. Ask me my opinions about the subject.

Group: Contenders
Public Solves Protein Structure

Players of an online game that allows users to adjust how proteins are folded have solved a decade-long protein structure mystery.

By Jef Akst | September 18, 2011

A small group of diverse individuals living on at least three continents, who call themselves The Contenders, have solved the structure of a protein that has stumped scientists for more than 10 years. And they did so from the comfort of their own homes, playing on online protein folding game called Foldit.
Crowdsourced national security

[Peter Lee, DARPA]
40th Anniversary of the Internet

29 Oct – Announced
5 Dec – Balloons Up

$40k Prize

[Peter Lee, DARPA]
Games for learning

Abstract

Refraction is a new puzzle game for teaching fractions. The game is not obviously a lesson in fractions, but requires knowledge of fractions to succeed. We built this game in cooperation with experts in learning, early mathematics, virtual manipulatives, and game design. In Refraction, the player must partition lasers in order to power spaceships containing various animals who have gotten stuck in space, as shown in Figure 1. These animal spaceships all require different fractions of the lasers, and the player is given several pieces that split and bend the lasers to reach the animals and satisfy these requirements. These mechanics can be used to teach many important fraction concepts, such as equal partitioning, addition, multiplication, mixed numbers, improper fractions, and common denominators. The game itself is instrumented so that it records everything the player does, allowing teachers and researchers to analyze play data.
Games for scientific discovery

http://games.cs.washington.edu/

Games for learning
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