



Online citizen science games: Opportunities for the biological sciences



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ABSTRACT

Recent developments in digital technologies and the rise of the Internet have created new opportunities for citizen science. One of these has been the development of online citizen science games where complex research problems have been re-imagined as online multiplayer computer games. Some of the most successful examples of these can be found within the biological sciences, for example, Foldit, Phylo and EteRNA. These games offer scientists the opportunity to crowdsource research problems, and to engage with those outside the research community. Games also enable those without a background in science to make a valid contribution to research, and may also offer opportunities for informal science learning.

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1. Introduction

Citizen science is a collective term for projects that engage both professional scientists and non-scientists in the process of gathering, evaluating and/or computing various scientific data (Kostadinova, 2011). Citizen science has traditionally referred to projects which have used volunteers to collect ecological, biological or environmental data (Devictor et al., 2010). However, recent developments in digital tools and the growth of the Internet have greatly altered the citizen science landscape, increasing the number of people who are able to participate in such projects, and expanding the range of disciplines and research problems that can be addressed. A growing number of citizen science projects are conducted entirely through the Internet and participants help to analyse large sets of data that have been provided by the project scientists. These projects have been referred to as online, or virtual, citizen science (Reed et al., 2012).

2. Online citizen science

Online citizen science projects enable interested individuals to get involved with scientific research wherever there is an internet connection. Projects can take a variety of formats and the task required of the citizen scientists may vary in its level of complexity. For example, distributed computing projects simply require that participants run project software that automatically analyses 'work units' provided by the project team. For example, Folding@home (<http://folding.stanford.edu/>) is a project in which participants run algorithms that simulate

protein folding. No other active input is required. Other projects require greater cognitive involvement and participants may be asked to classify or annotate images or graphical data. For example, Cell Slider (<http://www.cellslider.net/>) asks participants to help identify cancer cells on archived cell samples. More recently, scientific research problems have been repackaged into online multi-player computer games that use stylised graphical interfaces and introduce elements of gamification such as competition between players and performance ranking.

3. Foldit

One of the first citizen science games to be developed, and perhaps one of the most successful in terms of significant results produced, is Foldit (www.fold.it). In this project, the creation of accurate protein structure models has been turned into a game, and players have been responsible for deducing the structure of proteins that have been difficult to ascertain using more conventional approaches (Khatib et al., 2011a,b). Foldit was developed at the University of Washington in Seattle by a group consisting of both biochemists and game developers. It was released to the public in May 2008. The rationale for the development of Foldit was to harness the collective problem-solving abilities of *non-experts* and to exploit a wide diversity of playing approaches to accelerate progress in understanding the three-dimensional structures of protein (Cooper, 2011). Foldit players enlist human three-dimensional problem solving skills and online manipulation tools based on computer algorithms, to produce accurate models of protein structures that have previously been unknown (Khatib et al., 2011a,b). The success of Foldit has been attributed to the diversity of playing approaches and styles, although it may also be related to the lack of expectations or biases of those who come to the game without any background knowledge of biochemistry.

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Players can play individually, or within a team, and compete against one another within a points system. Protein structures that come closest to their 'natural' configuration (that is one that requires the least amount of energy) are awarded a greater number of points. Despite the competitive aspect of the game, players also work together cooperatively and collaboratively to solve the protein puzzles. Players interact through real-time internet relay chat (IRC) during the game with any other individual who is playing and individual teams have their own IRC channels where members of the same team can work together. Players can also have real-time interaction with the scientists and developers of Foldit through regular IRC 'chats' where new tools or new science puzzles can be discussed, or issues with the game interface or software can be highlighted.

Foldit is a complex game and can be difficult to learn compared to other multiple-player online games (Andersen et al., 2012). Before a player can compete and work on protein puzzles where the structure is unknown (known in Foldit as 'science puzzles'), he/she is presented with a series of tutorial or 'intro' puzzles (32 in total) that guide them through the various game tools available. These are based on proteins where the structure is already known. Once confident with the tools and the general layout of the game, a new player is then able to play the science puzzles (Fig. 1). A player does not have to complete all the tutorial puzzles before playing the science puzzles, although new players are often advised by more experienced players on the IRC to complete them if they want to play the game effectively. A number of more experienced players are active in helping those new to the game and may guide them through the learning process.

The majority of people who play Foldit have little or no background in biochemistry (Khatib et al., 2011a,b), yet some have become adept at the game and have helped to develop a novel approach to understanding the science of protein folding. Indeed, Foldit has had some success

which has resulted in a number of publications (Eiben et al., 2012; Khatib et al., 2011a; Khatib et al., 2011b). Perhaps the most significant of these is based on the efforts of Foldit players to 'solve' the structure of the Mason-Pfizer monkey virus (M-PMV) retroviral protease, a simian AIDS-causing monkey virus. While biochemists have attempted to elucidate the structure of this molecule for a number of years, two teams of Foldit players were able to construct an accurate model using the game interface in three weeks (Khatib et al., 2011b). These two teams of Foldit players were included in the list of authors on the subsequent paper.

The efforts of Foldit players have also led to a significant improvement in algorithms used to predict protein structures, and players have remodelled the backbone of a computationally designed Diels–Alderase, thus enhancing its activity and interaction with substrates (Khatib et al., 2011a; Eiben et al., 2012). Foldit players were included collectively in the list of authors in both of these publications.

Consequently, Foldit has received much attention from journalists and science communicators, and a number of articles have been published praising Foldit for its approach to collaboration with non-expert citizens, 'crowdsourcing science', and with opening up the scientific research process to 'the masses' (Hand, 2010; McGonigal, 2011).

4. Other online citizen science games: Phylo and Eterna

Phylo (<http://phylo.cs.mcgill.ca/>) was developed by computer scientists and biologists at McGill University and released in 2010. It uses comparative genomics as the basis of a Tetris-like game and utilises human pattern recognition skills to address the Multiple Sequence Alignment problem (Kawrykow et al., 2012). Players attempt to match up coloured blocks that represent nucleotide sequences from both coding and regulatory areas of genes from different animal species

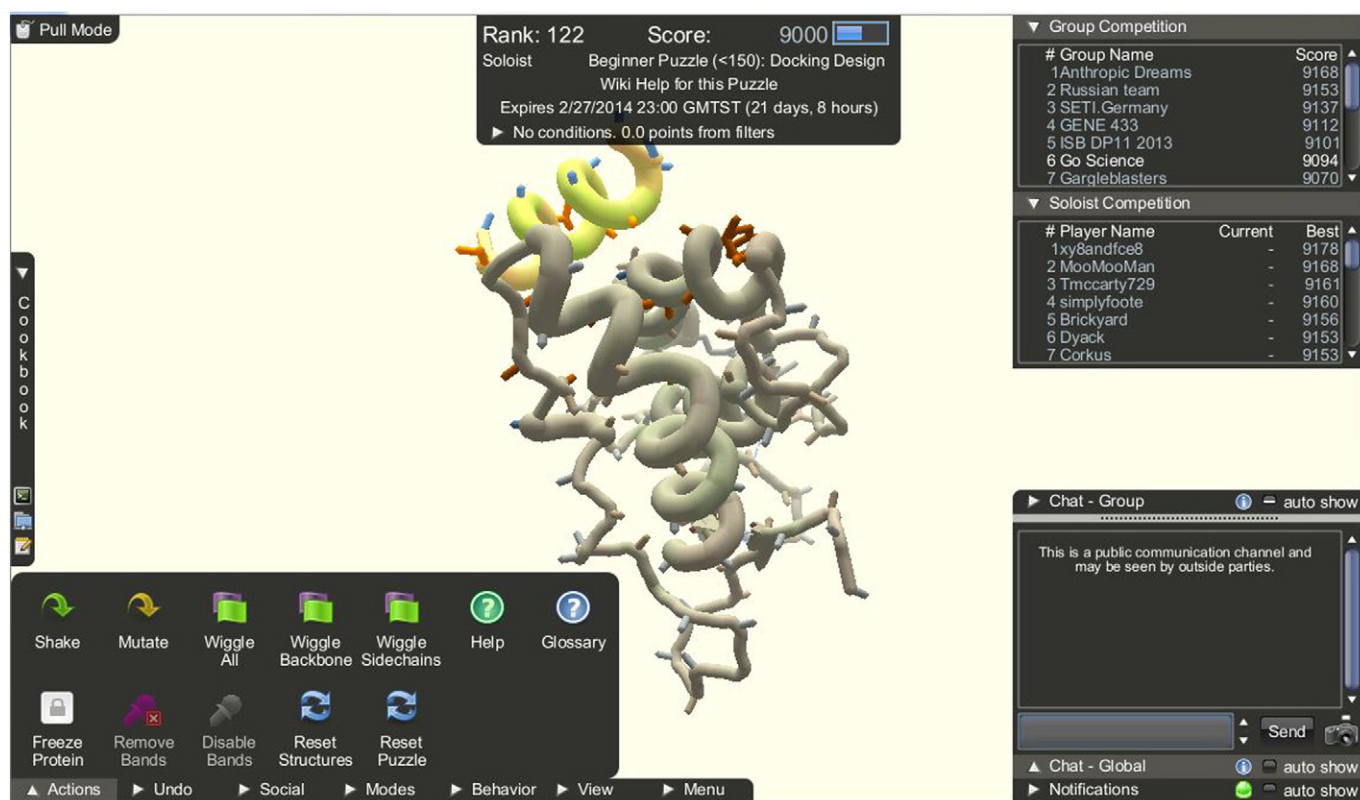


Fig. 1. Foldit science puzzle. The game tools are visible in the bottom left-hand corner, the rank of all players taking part in this puzzle is displayed in the top right-hand corner, and the internet relay chat (IRC) window is in the bottom right-hand corner.

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