

Serious Game Design Assessment Framework: Case Study 2

What is the Game About?

Locating the biological relevant native conformation of a protein is a formidable computational challenge given the very large size of the search space. Foldit players interact with protein structures using direct manipulation tools and user-friendly versions of algorithms while they compete and collaborate to optimize the computed energy.

Characters: No fictional characters, gamer can choose to have an avatar.

Music/sounds: Music on background, special sounds for different actions and congratulations events.

Visual elements: High quality computer graphics for 3D visualization of molecular structure and ways to represent it.

Setting: Microscopic world environment with atomistic resolution.

Working Title of the Game: **Foldit**

-Learning Objectives: Understand the complexity of biological molecules and how fundamental natural forces drive their folding into a unique native 3D structure that has a particular function.

-Impact - Player Experience/Feeling: Direct hands-on experience in 3D protein structure and function. Public participation in scientific research and social cause involvement as puzzles are directly linked to laboratory advances on curing diseases.

Goal: Find the 3D structure of the folded protein by solving puzzles

Action/verbs: move, rotate, wiggle, shake, mutate, remove clashes, undo unfavorable manipulations

Constraint(s): backbone packing, side chains, favorable/unfavorable interactions

Victory Condition(s): find the best scored folded structure that can add knowledge to the scientific community

Player Structure: competitive, collaborative, score ranking

Play literacy/Audience: Multiplayer online or offline game, broad audience: students all levels and general public.

Theme/Topic: Protein folding, interactions and function.

Facts and data offered: The game is part of an experimental research project developed by the University of Washington, Center for Game Science, in collaboration with the UW Department of Biochemistry.

Data: starting tutorials, chemical sequence, electronic density maps, minimized energy values (scoring). Ranking, statistics and forums.

Facts and data used: Simplified version of user-friendly algorithms from the Rosetta structure prediction methodology are used. Solutions are ranked and used in actual scientific research to design experiments and develop cures to diseases.

-GamePlay:

What Role(s) Will Players Play?

Folder: Manipulate and fold a 3D protein structure. Players working collaboratively develop a rich assortment of new strategies and algorithms; unlike computational approaches they explore not only the conformational search space but also the space of possible search strategies.

What Actions Can They Take? Fold the structure, share, get feedback and compare to other gamers to make improvements. Use spatial awareness, short term risk and recognizing dead end early.

