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Human-computer interaction principles for developing web- based genomics resources

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Abstract

Genomics projects, including genome sequencing, transcriptomics, genome-wide association mapping and epigenetics assays, produce vast quantities of data. Extracting the required information from such complex datasets is a significant challenge and even where software tools do exist, these are often not intuitive or designed for non-specialist users. This dissertation details how I have applied design principles from the field of Human-Computer Interaction (HCI) to the development of intuitive bioinformatics web-based resources for exploring genomics data. In the first part of the thesis I detail the development of a specialised genomics resource that enables non-specialists who lack bioinformatics skills to access, explore and extract new knowledge from a variety of genomics data types. These tools were developed in collaboration with wet lab biologists and bioinformaticians who represent typical end-users. The tools developed have been integrated within the PlantGenIE (Plant Genome Integrative Explorer) web resource, which has been established as a platform for exploring genomics data for Populus, conifer, Eucalyptus and Arabidopsis genomics data. Even though the ability to collect, store and manage data is increasing faster due to new technologies and science, our ability to understand it remains constant. To help address this, in the second part of this dissertation I focus on the usability enhancement of tools based on the HCI and User Experience (UX) practices. To achieve this, I utilised visualisation techniques and design principles in the design process for the improvement of the PlantGenIE User Interface (UI), and applied usability methods to evaluate the UX of PlantGenIE tools. These results were then used to inform adaptations and fine-tuning of those. I show that utilisation of these research methods and practices with the development life cycle represents a framework for designing usable bioinformatics tools. Wider-scale use of these methods by future designers and developers will enable the creation of more usable bioinformatics resources.

Keywords

Affordance, Cognition, Constraints, Database, Design principles, Design process, Genomics, Human-computer interaction, Mapping, RNA-Seq, Signifiers, Specialised genomics resources, Transcriptomics, Triangulation, Usability methods, User experience, Visualisation techniques, Web resource

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