Xinran Li

(412)932-6740

xinranli@cmu.edu

http://xinranli.github.io/

OBJECTIVE

Obtain a summer internship in Ux design and front-end/back-end web development, software engineering, data analysis.

EDUCATION

- **Carnegie Mellon University (CMU)** , Pittsburgh, PA
- Master of Science in Computational Biology, Joint program in School of Computer Science and Mellon College of Science, overall GPA: 3.64/4.0   May 2016 (expected)
- **Sun Yat-sen University (SYSU)** , Guangzhou, China
- Bachelor of Science in Biological Science, School of Life Sciences, overall GPA: 3.6/4.0   June 2014

SELECTED COURSEWORK

Machine Learning, Bioimage informatics, Web application development, Programming for Scientists, Network Science

SKILLS

- **Programming Languages:** Python, Perl, R, Go, PASCAL, LaTeX, MATLAB
- **Web Development:** HTML5, CSS3, JavaScript, SQLite, Django, Github
- **GUI Design and Image Processing:** Adobe Photoshop, Adobe Lightroom, Adobe Dreamweaver, Adobe Illustrator, Adobe Flash, Adobe Fireworks, Painter, PaintTool Sai, CodonCodeAligner, Autodesk MAYA, SketchBookPro
- **Operating Systems:** Unix, Windows

PROJECTS

- **Built a nano-blogging social network based on Django Framework and SQLite Database**   CMU, 2015
- Built both front-end and server-side for an interactive web application including user registration and authentication, email integration for user verification, photo upload, and quasi-real-time updates.
- **Processed bioimage sequences and biological image data mining**   CMU, 2015
- Applied idea of machine learning and computer vision technique to analyze bioimage data using MATLAB.
- **Built interaction network between sncRNA and RNA-binding Proteins**   CMU, 2014
- Used R to build and visualize two interaction networks of more than 1,000 small non-coding RNA and RNA-binding Proteins interaction based on the pan-cancer and normal human cell samples data extracted from starBase.
- **Analyzed base-pair variation pattern in CRISPR-edited DNA sequence**   SYSU, 2014
- Analyzed the alignment results of sequences edited by type II CRISPR/Cas9 system from 120 samples from *EMX1* and *B2M* of 293T cell line and *CD274* and *B2M* of H441 cell line using CodonCodeAligner
- Used Perl to calculate the frequency of insertion/deletion and frameshift/inframe mutation based on the analysis above
- **Designed Graphic User interface(GUI) for Software CAST-Designe**r (Award-winning)   SYSU, 2013
- Designed Graphic materials for Computer Aided Synbio Tool - An Integrated Tool for Synthetic Biology for team SYSU-Software in 2013 iGEM competition (More details available here : http://2013.igem.org/Team:SYSU-Software)

HONORS

- Merit Fellowship (Tuition Scholarship) from Department of Biological Sciences, CMU (2014~2015 Academic year)
- Best software project and Gold Award in 2013 iGEM (International Genetic Engineering Machine) world competition: SYSU-Software team member (November 2013)

WORK EXPERIENCES

- **Graphic Designer for Grains Innovation Company**   Guangzhou,China, summer 2013
- Designed membership cards, advertisements, brochures and website interfaces