Adam Conn

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Summary:

- Currently a research assistant in a Computational Neurobiology Laboratory since October 2015.

- 2. 5 years doing bench work in a protein purification company.

- Published author with recent papers in Current Biology and Cell Systems.

- 2 years managerial experience for a Starbucks licensed store.

- Prior teaching experience in a program focused on Biotechnology Instrumentation.

- B.S. Degree in Bioengineering: Bioinformatics.

Skills:

- **Programming Languages**:

  - Python, Java, C++, javascript, HTML, CSS .

- **Bioinformatics**:

  - Global/local sequence alignment, De Bruijn graph assembly, Motif finding, gene prediction using HMM, familiarity with NGS technologies, and various classification/ regression machine learning algorithms.

- **Biological Applications:**

  - RNA-Seq, Chip-seq, Rad-Seq, GWAS, PCR, SDS-PAGE, protein quantification assays, genotyping, etc.

- **Software**

  - Object Oriented programming, familiarity with design patterns, and familiarity with Agile process.

- **Soft skills**

  - Demonstrated written and verbal communication, ability to communicate to both software developers and scientists, ability to connect with customers and to put their needs as a priority.

Education

 B.S. Degree in Bioengineering: Bioinformatics (3.4 GPA) 2015

Work Experience

Research Assistant: October 2015- current

- Built an automated pipeline to analyze RNA-Seq data from a sample of healthy patients of varying age in order to use the expression data to predict the age of an individual based off expression profile.

- Use of 3D laser scanning to capture plant architecture in the form of 3D xyz-point clouds. Designed and implemented statistical models to describe plant architecture. Showed similarities between branching in neurons with that of plants.

- Use of many data visualizations tools. Primarily matplotlib but also some javascript frameworks and google maps API.

- Give presentations, collaborate with other scientists, written and oral communication of our research to both other scientists and the public.

Research Associate: December 2009-May 2012

- Directly responsible for purifying native and recombinant proteins.

- Routinely worked with multiple cell lines (bacteria/insect/mammalian) to maintain, transform/transfect, ferment and harvest cells.

- Created novel cDNA libraries.

- Meticulous and detailed documentations

- Performed a wide variety of assays including PCR, RT-PCR, SDS-PAGE, west- ern blots, DNA-agarose gel electrophoresis, nickel/ion-exchange/size exclusion chro- matography, cell toxicology and enzyme kinetic assays

Publications

- A. Conn, U.V. Pedmale, J. Chory, C.F. Stevens, S. Navlakha. "Statistical Description of Plant Shoot Architecture". Current Biology. doi: http://dx.doi.org/10.1016/j.cub.2017.06.009

- A. Conn, U.V. Pedmale, J. Chory, S. Navlakha"Plant architectures reflect universal network design principles"

  (published in Cell Systems July 28, 2017)