**Adam Conn**

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**Summary:**

* 1.5 years as research assistant in Computational Biology Laboratory at the Salk Institute.
* 2. 5 years of DNA, RNA, protein, and cell culture experience in industry.
* 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 with focus on Bioinformatics at UCSD.

**Skills:**

* **Programming Languages**: Python, Java, C++, javascript, HTML, CSS.
* **Biological Applications:** His-tag purification, ion-exchange chromatography, size-exclusion chromatography, DNA isolation, restriction digest, transformations, transfections, PCR, insect/ bacterial cell fermentations,
* **NGS applications:** Solid understandings of sequence by synthesis and downstream applications such as De Novo assembly, whole-genome sequencing, RNA-seq, ChIP-seq, single/paired end sequencing, as well as current challenges of short-read sequencing.
* **Software:** Object Oriented Programming, familiarity with MVC and other design patterns, familiarity with Agile.
* **Bioinformatic Algorithms:** Burrows-wheeler alignment, global/ local alignment, genome assembly with de Bruijn graphs, and gene prediction with HMM’s.
* **Machine Learning Algorithms:** linear regression, logistic regression, SVM’s, decision trees, random forests, and Bayesian analysis.
* **Other:** Linear algebra, probability, unit testing, linux/ windows, REST, Django, GIT, and MySQL.

**Publications:**

* A. Conn, U.V. Pedmale, J. Chory, C.F. Stevens, S. Navlakha. “A **Statistical Description of Plant Shoot Architecture**”. *Current Biology: 27(14) pg 2078-2088e3, July 6, 2017.* DOI:http://dx.doi.org/10.1016/j.cub.2017.06.009.

# A. Conn, U.V. Pedmale, J. Chory, S. Navlakha. “**High-Resolution Laser Scanning Reveals Plant Architectures that Reflect Universal Network Design Principles**” *Cell Systems: 5(1) pg 53-62, July 26, 2017.* DOI: h[ttp://dx.doi.org/10.1016/j.cels.2017.06.017](http://dx.doi.org/10.1016/j.cels.2017.06.017)

**Education:**

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

 *A.A. Degree in Physics (3.9 GPA) 2012*

**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.
* Designed and implemented statistical models to describe plant architecture, and the plasticity of the architecture when exposed to different growing conditions using high-precision laser scanning.
* Use of many data visualizations tools. Primarily matplotlib but also some javascript frameworks and google maps API.
* Give presentations, collaborate with other scientists, and communicate our research to both other scientist as well as the public.



*Research Associate: December 2009-May 2012*

* Directly responsible for purifying native and recombinant proteins.
* Routinely worked with multiple cell lines (bacteria/ insect) to maintain, transform/ transfect, ferment and harvest cells.
* Created novel cDNA libraries.
* Meticulous and detailed documentation.
* Performed a wide variety of assays including PCR, RT-PCR, SDS-PAGE, western blots, DNA-agarose gel electrophoresis, nickel/ion-exchange/size exclusion chromatography, cell toxicology and enzyme kinetic assays



*Starbucks License Store Manager: May 5, 2007-January 2010*

* Managed a small team of ~5 employees to design and execute world class customer satisfaction.
* Met sales goals, and ordered products and tracked inventory through POS system.