# Adam Conn

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2012

### Skills

**Programming Languages:** python  $\cdot$  java  $\cdot$  c++  $\cdot$  HTML  $\cdot$  CSS

Frameworks/Libraries: Django · matplotlib · numpy · sklearn · Bootstrap

Operating Systems: Windows 8 · Mac OS · Linux/Unix

Other:

 $\label{eq:linear_linear} \begin{array}{ll} Linear\ Algebra & \cdot\ Probability & \cdot\ Basic\ Design\ Patterns & \cdot\ LaT_EX \\ Data\ Structures & \cdot\ NGS\ Technologies & \cdot\ Protein\ Purification & \cdot\ RNA-Seq \\ \end{array}$ 

#### Algorithmic Knowledge:

$\cdot$ General	· Machine Learning	· Bioinformatics
·Divide and Conquer	· Linear Regression	· Global Alignment
$\cdot$ Greedy	· Logistic Regression	· Local Alignment
·Dynamic Programming	· Support Vector Machines	$\cdot$ Genome Assembly
·Recursive	$\cdot$ Neural Networks	· Motif Finding
·Breadth First Search	$\cdot$ Decision Trees/Random Forest	$\cdot$ Gene Expression Analysis
·Depth First Search	$\cdot$ Hidden Markov Models	$\cdot$ Gene Finding
·Breadth First Search	· Boosting/Bagging Methods	•
·Djikstras	· PCA	•

#### Education

# University of California, San Diego B.S. in Bioengineering: Bioinformatics (3.5 GPA)

# San Diego City College

A.A. in Physics (3.9 GPA)

# Work Experience



Oct 2015 - Current

- Collect data using high tech 3D laser scanning to capture the architect and morphology of a plant down to micrometer precision in the form of 3D coordinate point clouds.
- Design and write machine learning algorithms to find patterns within the 3D point cloud data.
- Write programs to visually view data using matplotlib.
- Implement statistical models that approximate and predict the intricate branching structures plants undergo as a response to a specific stressful environment.
- Built an automated pipeline to analyze RNA-SEQ datasets. Involved querying and downloading data from NCBI GEO by FTP, normalizing the data, building a binary classifier, and extracting the features (genes) used to build our classifier for future research.
- Attend presentations, collaborate with other departments and institutions, present work, and write sections of articles to be submitted for publication.



2009-2013

- 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, western blots, DNA-agarose gel electrophoresis, nickel/ion-exchange/size exclusion chromatography, cell toxicology and enzyme kinetic assays.