Pycon 2017 Highlights

Discussing the Snake that Lives Everywhere

Notes Available on Github

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https://github.com/HarmonicHemispheres/pycon2017

The Python Landscape

Artificial Intelligence

Science

Databases

Security

Games

Finance

Our Focus Today

Data Science

Astronomy

Bio Science

Random

Python in Data Science

Jupyter Notebooks

- Widely Used
- Easily Usable
- Great for generating Reproducible Science

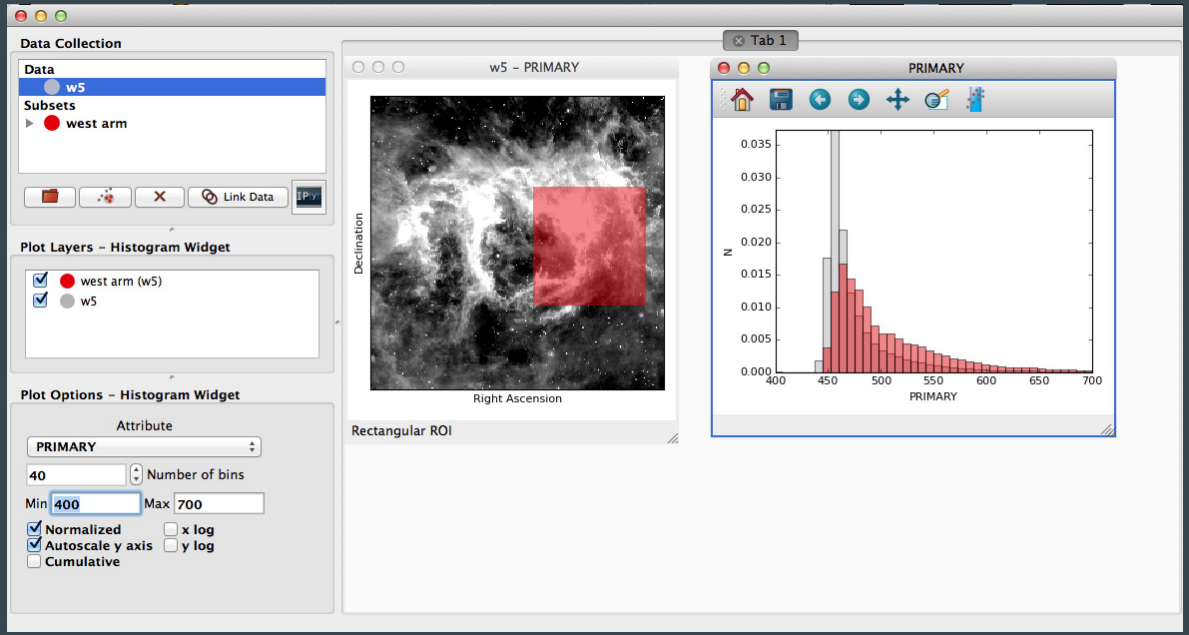
Interactive Data Analysis (Try Jupyter)

Python in Data Science

GLUEVIS

http://glueviz.org/en/stable/

Visualize sub-sets of data
across multiple visualizations



Python in Data Science

jupyter

jupyter Lorenz Differential Equations (autosaved)

File Edit View Insert Cell Kernel Help Python 3

Code Cell Toolbar: None

Exploring the Lorenz System

In this Notebook we explore the Lorenz system of differential equations:

$$\dot{x} = \sigma(y - x)$$
$$\dot{y} = \rho x - y - xz$$
$$\dot{z} = -\beta z + xy$$

This is one of the classic systems in non-linear differential equations. It exhibits a range of complex behaviors as the parameters (σ, β, ρ) are varied, including what are known as *chaotic solutions*. The system was originally developed as a simplified mathematical model for atmospheric convection in 1963.

```
In [7]: interact(Lorenz, N=fixed(10), angle=(0.,360.),
                σ=(0.0,50.0),β=(0.,5), ρ=(0.0,50.0));
```

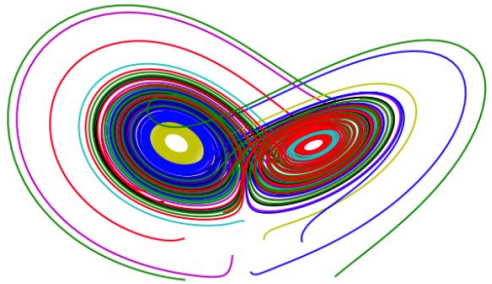
angle 308.2

max_time 12

σ 10

β 2.6

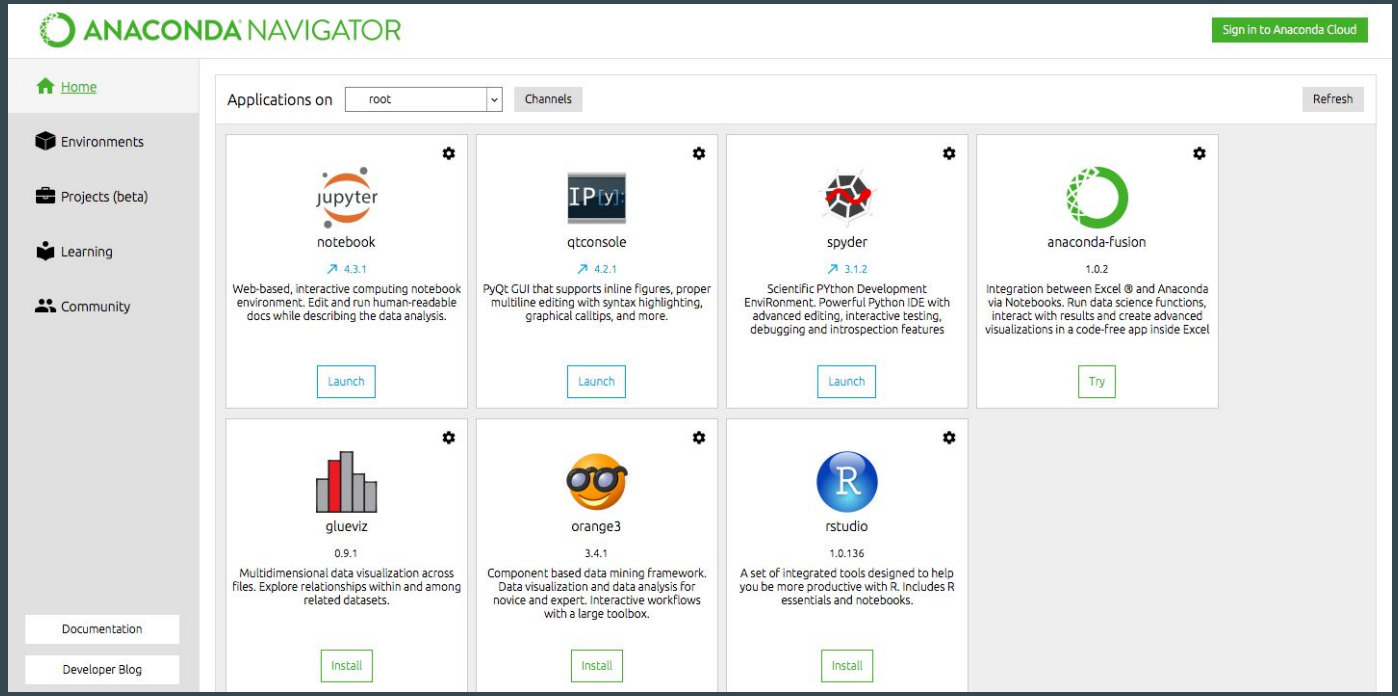
ρ 28



Python in Data Science

ANACONDA
Powered by Continuum Analytics®

A system for managing python packages and versions easily.



Python in Biology

BIOCONDA®

A library of python recipes for biology related tasks. (https://bioconda.github.io/)

abricate

downloads 384 total

Mass screening of contigs for antibiotic resistance genes

beast

downloads 227 total

BEAST is a cross-platform program for Bayesian analysis of molecular sequences using MCMC

ucsc-faalign

downloads 218 total

Align two fasta files

bioconductor-flowcl

downloads 241 total

Semantic labelling of flow cytometric cell populations.

Python in Biology

TWIST BIOSCIENCE

Our Expertise Is Synthetic DNA

BIODETECTION

Targeted resequencing

Virus

Pathogens

Metagenomics

FUNCTIONAL GENOMICS

Pathogen mode of action

Non-coding DNA

RNA editing

GENOME ENGINEERING

Gene synthesis

Genome synthesis

Biofuel & chemical production

Directed evolution

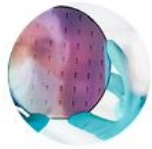
DRUGS & BIODEFENSE

Antibodies

Vaccines

shRNA

Antibiotics



DATA STORAGE

Ultra long-term

No power

High density

Python in Biology

TWIST BIOSCIENCE

April 17, 2017

Twist Bioscience Expands Agreement to Pursue Higher Density Digital Data Storage on DNA with Microsoft and University of Washington

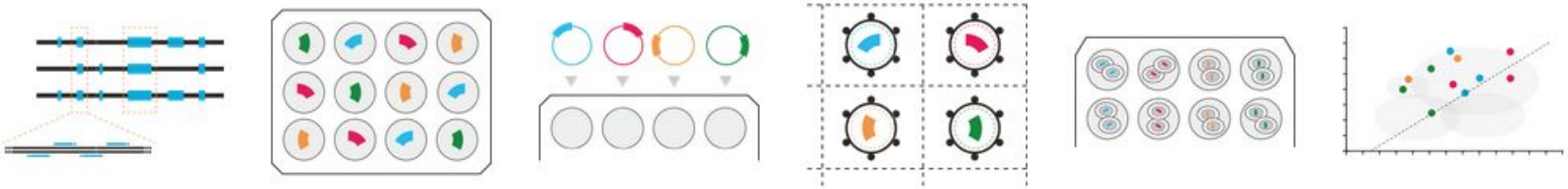
SAN FRANCISCO, Calif. – April 17, 2017 – Twist Bioscience, a company accelerating science and innovation through rapid, high-quality DNA synthesis, today announced Microsoft Corp. will purchase ten million strands of DNA from Twist Bioscience for expanded digital data storage research. The strands of DNA will be long-chain oligonucleotides used by researchers at Microsoft and the University of Washington to encode digital data at higher density. After working together for over a year, the organizations have improved storage density, thereby reducing the cost of DNA digital data storage by encoding more data per strand and increasing the throughput of DNA production.

Python in Biology

DESKTOPGENETICS

AI-POWERED GENE EDITING FROM DESIGN TO DATA

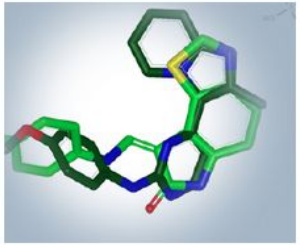
Whether you are manipulating a single gene or a hundred pathways, our specialists have the latest expertise in CRISPR to help you with anything from designing guides to analyzing and interpreting your data.



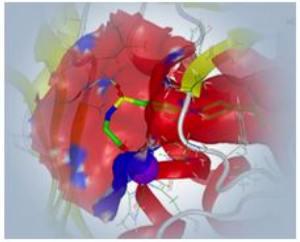
Design Manufacture Clone Package Screen Analyze

Python in Chemistry

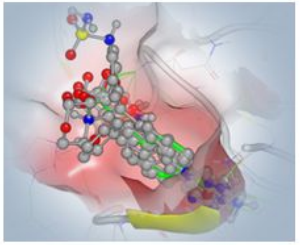
OpenEye SCIENTIFIC



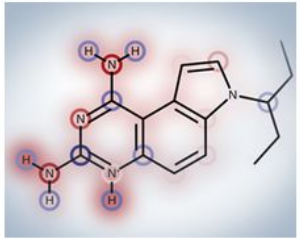
LEAD DISCOVERY



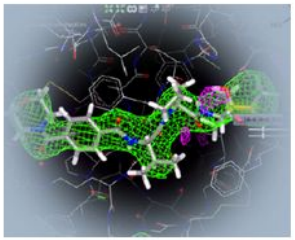
LEAD OPTIMIZATION



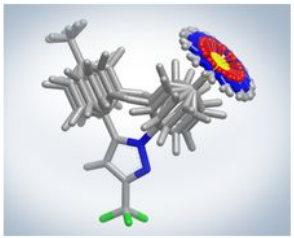
CUSTOMIZATION



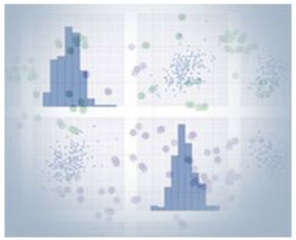
CHEMINFORMATICS



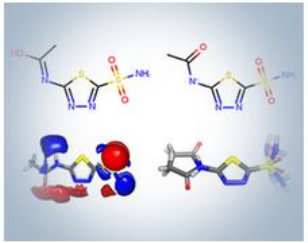
CRYSTALLOGRAPHY



DATABASES



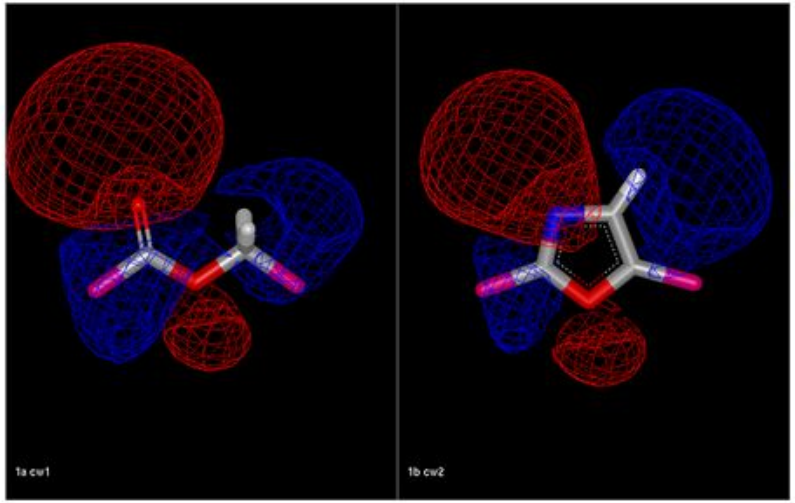
JUPYTER NOTEBOOKS



DATABASE PREPARATION

Python in Chemistry

OpenEye SCIENTIFIC



Comparison of an ester fragment and an oxazole fragment showing the electrostatic isopotential contour surfaces. The electrostatic tanimoto between the two fragments is 0.54.

BROOD

Fragment Replacement and Molecular Design

BROOD is a software application designed to help project teams in drug discovery explore chemical and property space around their hit or lead molecule. BROOD generates analogs of the lead by replacing selected fragments in the molecule with fragments that have similar shape and electrostatics, yet with selectively modified molecular properties. BROOD fragment searching has multiple applications, including lead-hopping, side-chain enumeration, patent breaking, fragment merging, property manipulation, and patent protection by SAR expansion.

For more detailed information on **BROOD**, check out the links below:

Snakes in Space

Jake Vlanderplas

scikits learn
machine learning in Python

astropy
A Community Python Library for Astronomy

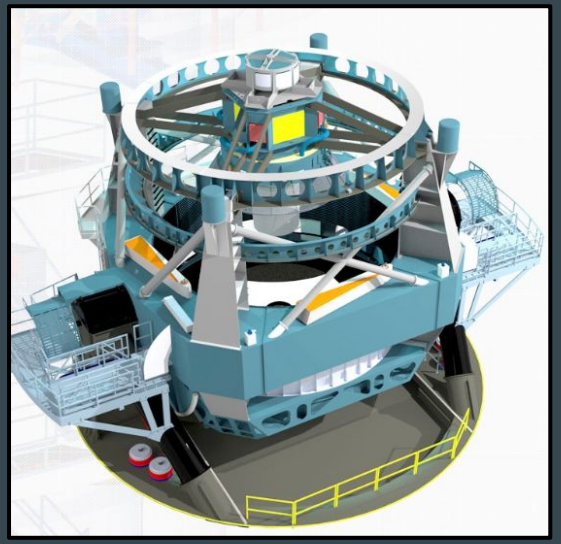
SciPy: Scientific Computing with Python

eScience Institute
ADVANCING DATA-INTENSIVE DISCOVERY IN ALL FIELDS

Snakes in Space

James Webb Space Telescope

JWST Github



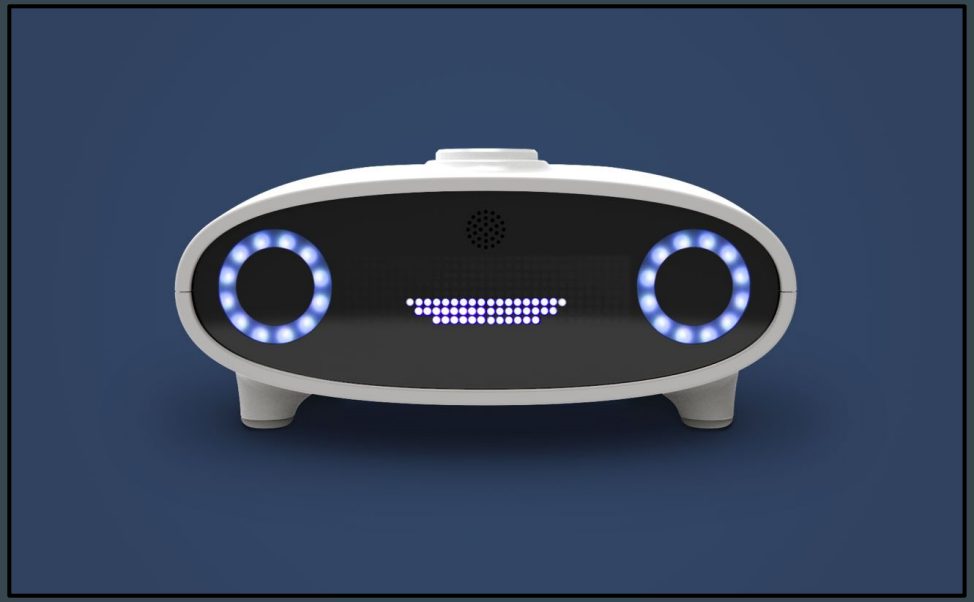
Large Synoptic Survey Telescope

LSST Github

IOT with Python & Intel

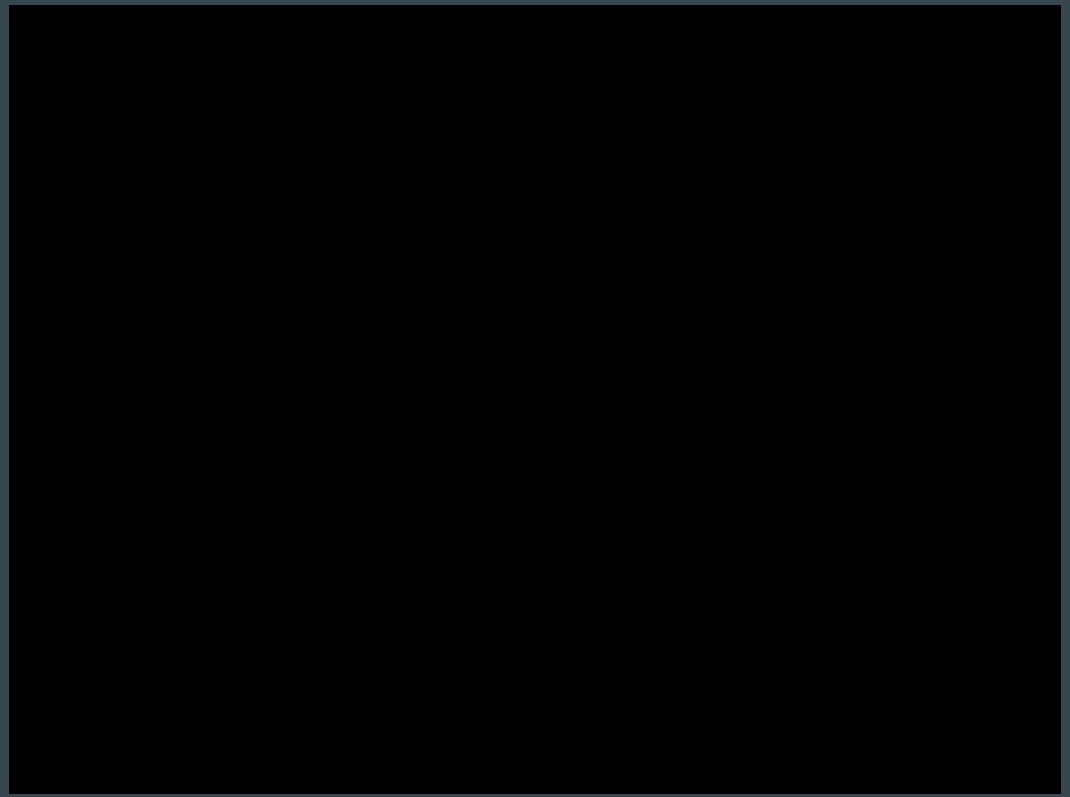
mycroft

Mycroft, the Open Source Alternative to Siri or Alexa

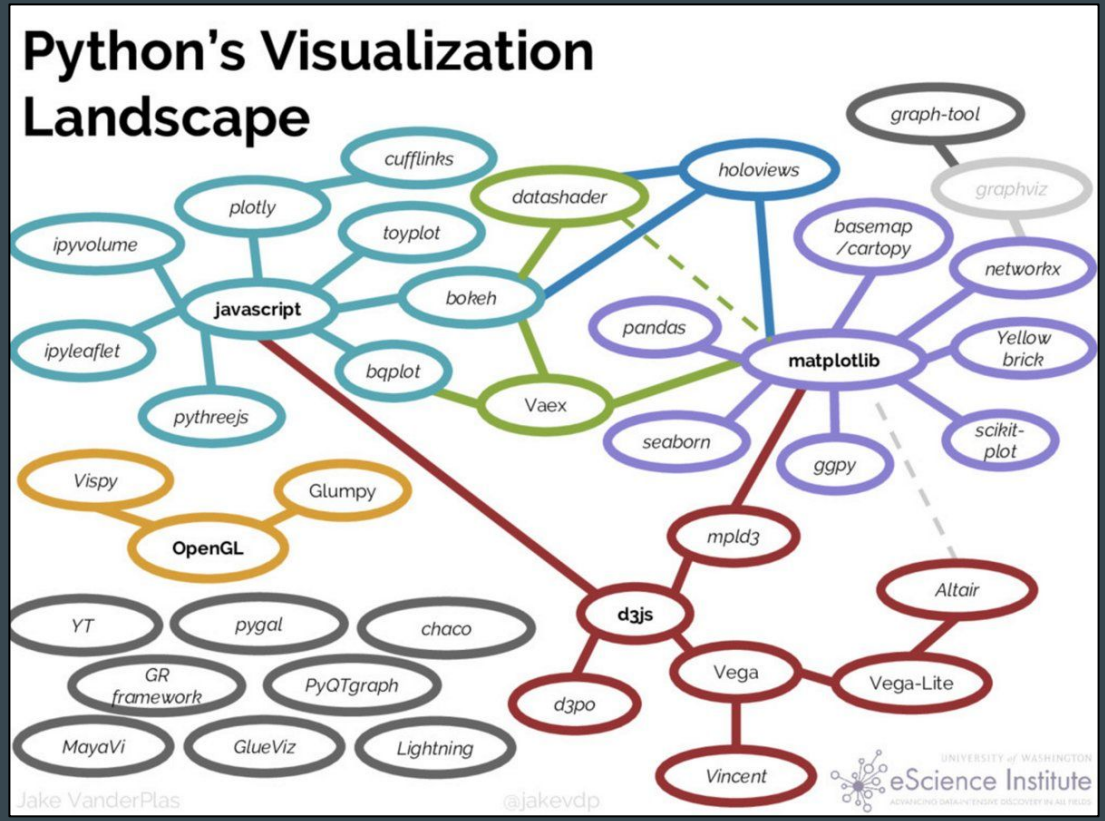


Factory Automation

Factory Automation with Python Stories about Robots, Serial Ports, and Barcode Readers



The Visualization Landscape



The Visualization Landscape

Altair

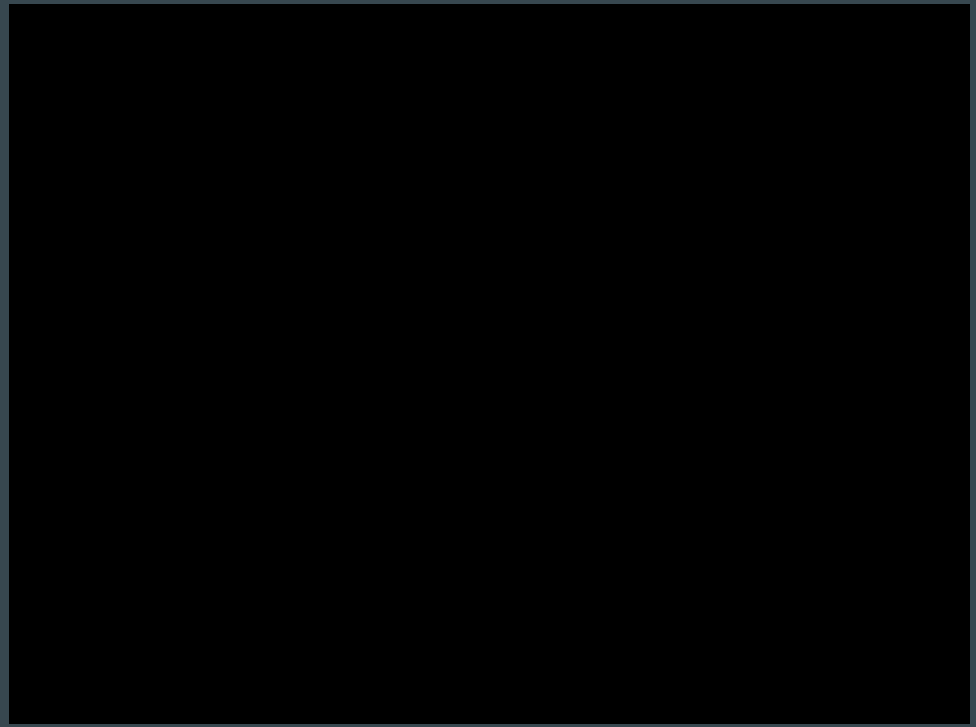
Declarative Visualization in Python

Gapminder Bubble Plot

< Layered Bar Chart | Example Gallery |

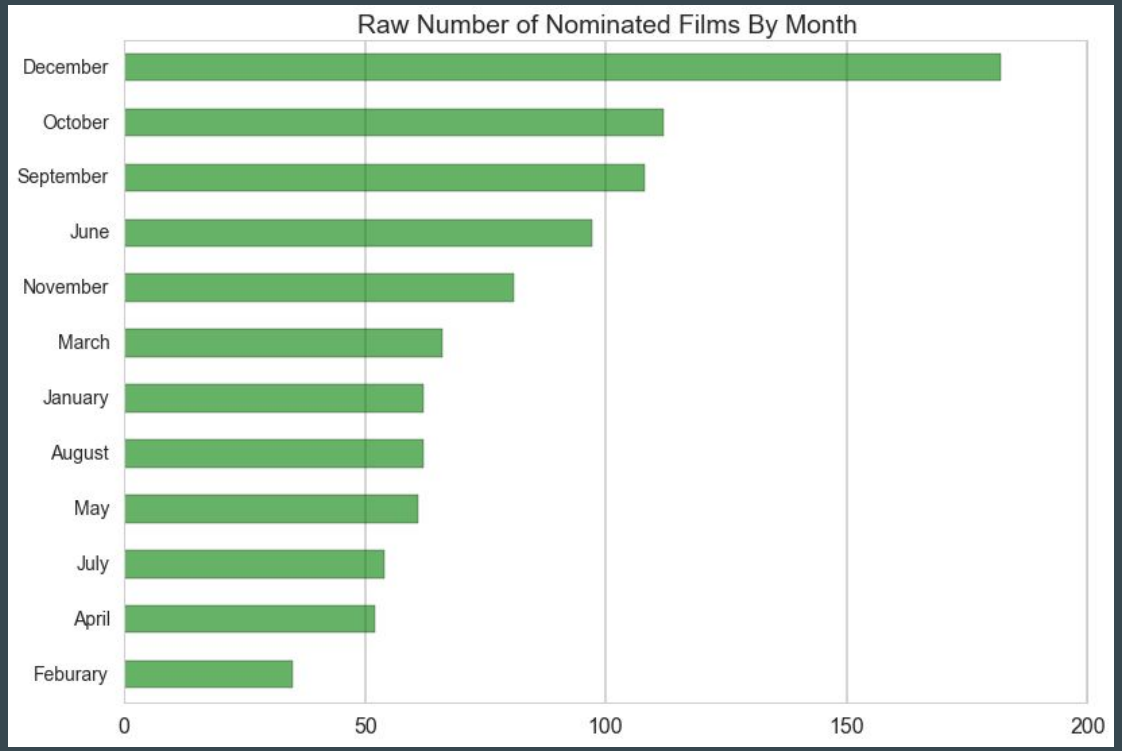
```
from altair import *

Chart(Data(
    format=DataFormat(
        type='csv',
    ),
    url='http://vega.github.io/vega-lite/d
),
    description="A bubble plot showing the
).mark_circle().encode(
    color=Color(
        value='#000',
    ),
    size='population:Q',
    x=X('income:Q',
        scale=Scale(
            type='log',
        ),
    ),
    y=Y('health:Q',
        scale=Scale(
            zero=False,
        ),
    ),
).configure_cell(
    height=300.0,
    width=500.0,
)
```



ML to Predict Oscar Winners

https://github.com/oscarpredictor/



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