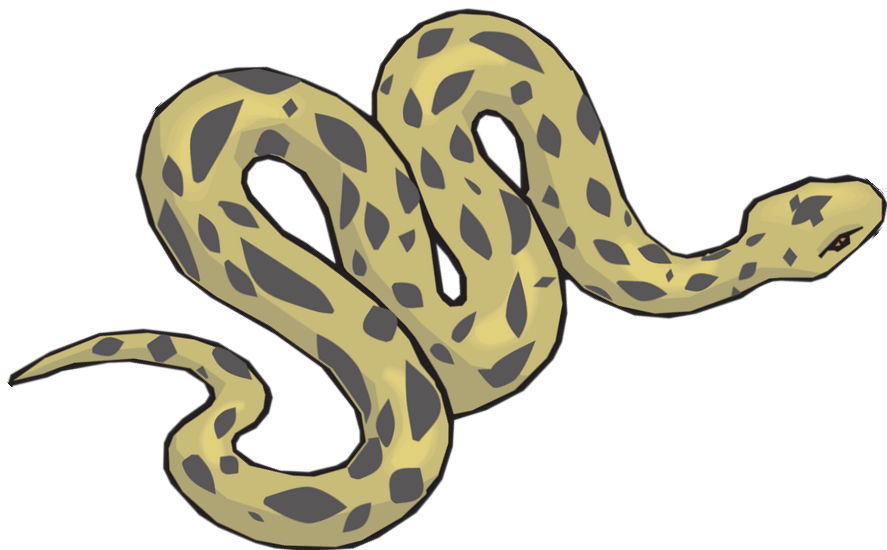
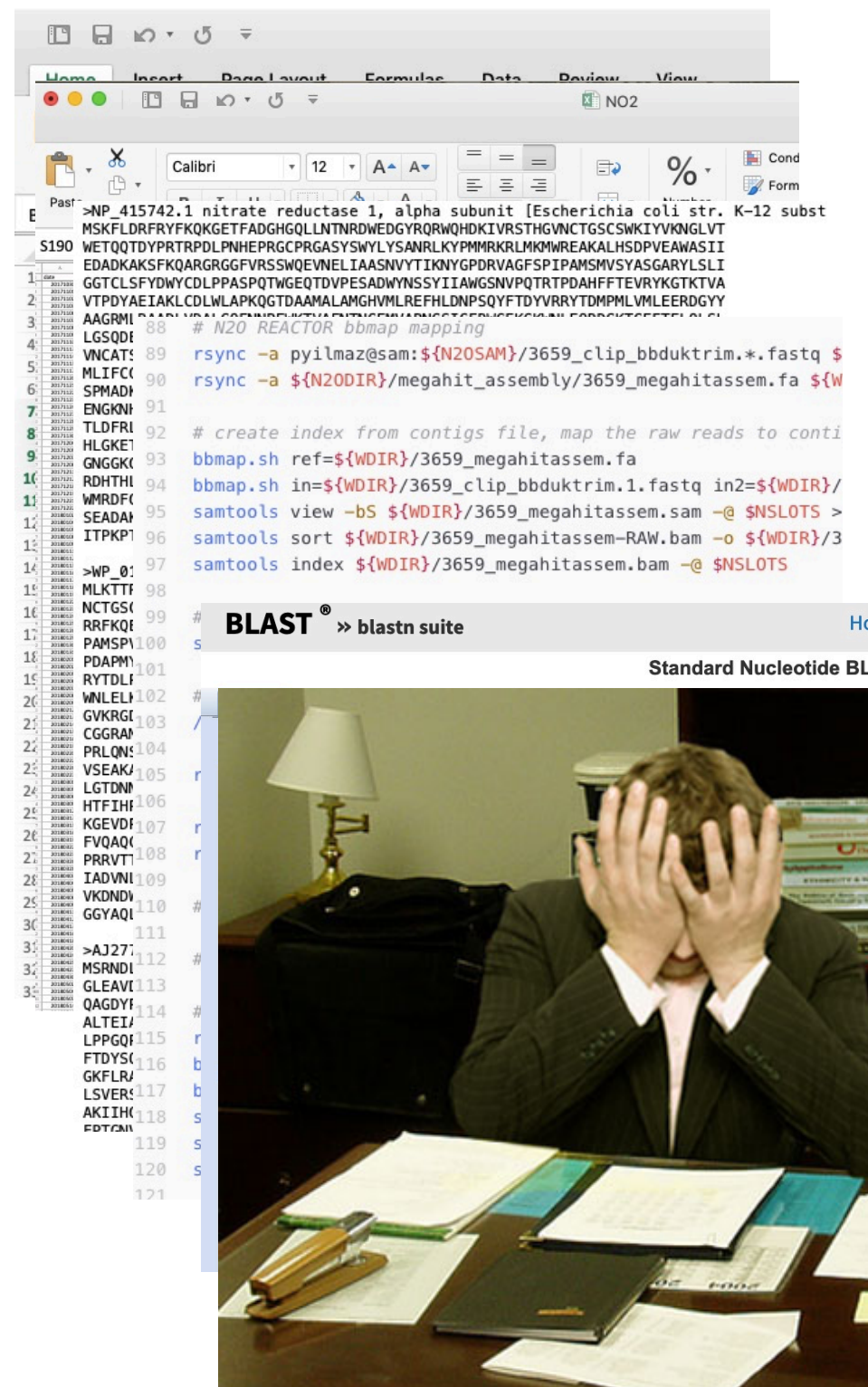


python: introduction



why programming?

are you...



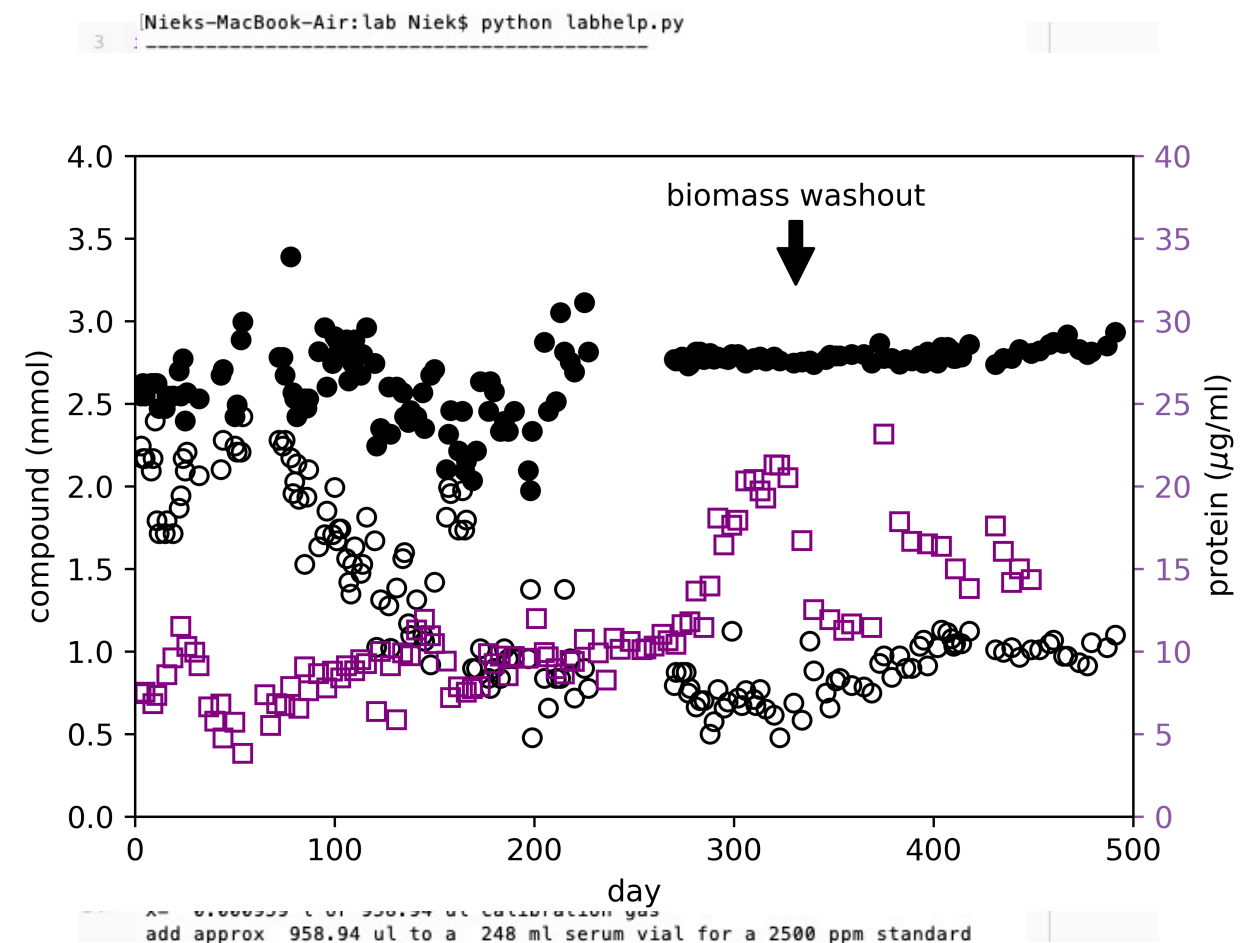
- doing endless copying and pasting?
- doing complex data analysis in massive excel sheets?
- analyzing or editing big fasta files?
- getting to the limits of your bash skills?
- manually doing tons of BLASTs?
- doing repetitive tasks over and over?

make your science better with python

- automate the boring stuff
- do reproducible science:
 - easily follow workflow from raw data to result
 - make all data alterations transparent
 - reduce mistakes

usage examples for basic skills

- change names fasta headers
- make a lab calculator
- do calculations on data
- plotting



and for experienced programmers...



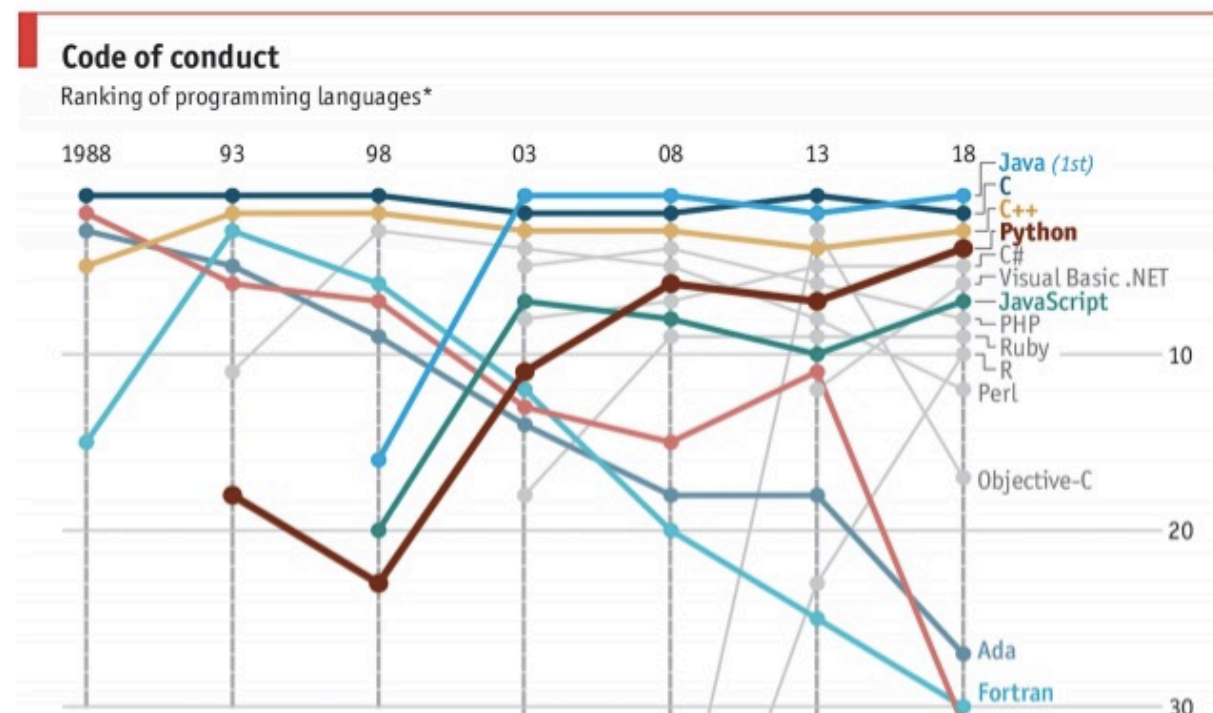
why python?

python is a good and popular programming language

Daily chart

Python is becoming the world's most popular coding language

But its rivals are unlikely to disappear



python is a good and popular programming language

- easy to learn
- but no ceiling to what you can achieve



python is relevant for our field



Analysis | Published: 14 September 2015

Detection of low-abundance bacterial strains in metagenomic data using eigengenome partitioning

Brian Cleary, Ilana Lauren Brito, Katherine Huang, Dirk Gevers, J Alm

Nature Biotechnology **33**, 1053–1060 (2015) | [Download Citation](#)

Abstract

Analyses of metagenomic datasets that are billions or trillions of bases can uncover human genomes, but naive assembly of these data requiring hundreds of gigabytes to terabytes of memory. Strain analysis (LSA), a scalable, *de novo* pre-separation of reads into biologically informed



Article | Published: 11 December 2017

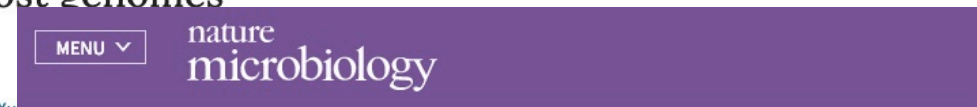
Metagenomic binning and association of plasmids with bacterial host genomes using DNA methylation

John Beaulaurier, Shijia Zhu, Gintaras Deikus, Ilaria Mogno, Xu Richardson, Ronald Canepa, Eric W Triplett, Jeremiah J Faith, Fang

Nature Biotechnology **36**, 61–69 (2018) | [Download Citation](#)

Abstract

Shotgun metagenomics methods enable characterization of microbial communities in human microbiome and environmental samples. Assembly of metagenome sequences does not require binning, so computational binning methods have been used to partition sequences into genome 'bins'. These methods can be used to predict composition, species abundance, or chromosomal



Letter | Published: 12 March 2018

Towards predicting the environmental metabolome from metagenomics with a mechanistic model

Daniel R. Garza, Marcel C. van Verk, Martijn A. Huynen & Bas E. Dutilh

Nature Microbiology **3**, 456–460 (2018) | [Download Citation](#)

Abstract

The environmental metabolome and metabolic potential of microorganisms are dominant and essential factors shaping microbial community composition. Recent advances in genome annotation and systems biology now allow us to semiautomatically reconstruct genome-scale metabolic models (GSMMs) of microorganisms based on their genome sequence¹. Next, growth of these models in a defined metabolic environment can be predicted in silico, mechanistically

course outline

course goal

whet your feet so it is easier to learn python
on your own



- **today** (13:00 - 17:00)
 - group introduction: first steps in coding
 - individual exercises: learn core programming concepts
 - time for questions
- **tomorrow** (13:00 - 17:00):
 - write your first function
 - write your first python script: change fasta headers

on github you can find...

- all course materials
- extras to get you on your way:
 - a list of good learning recourses
 - a list of excellent python packages