



Thank you for stopping by! In my next role I'm hoping to combine my extensive experience as Molecular Biologist in drug discovery along with my knowledge, interest and excitement to use computational tools.

Through my career I have conducted research on several disease states and their biological underpinnings. This involved attention to detail, trouble shooting and good communication skills. In support of my assay development efforts at Amgen and Caraway, I used scripting languages to read, manipulate and visualize high dimensional data in an automated way. This allowed for the advancement of projects by producing data rapidly followed by thorough analysis.

Since the downturn in the biotech industry, I have been keeping abreast of new technologies thru online learning. The following slides have summarized that journey. As with my previous employment, I would bring a can-do attitude to your organization and look forward to leveraging these skills to achieve your departmental goals. Thank you for your time and attention.

Sincerely

Jabbar Campbell

# NGS

Certification	Area	Topics	Tools
✓	<a href="#">Next Generation Sequencing</a>	Extraction---QC---RNA/CDNA---library prep—end repair Amplification types (Emulsion vs Bridge) Platforms (Seq by ligation, Ion torrent semiconductor , Illumina Reversible terminator) Variant analysis(indel SNPS)	NGS Overview
✓	<a href="#">Functional Genomics (Microarray to RNA-Seq) Data Analysis</a>	Raw read---QC---Trimming—alignment—reporting Microarray analysis	NCBI, Linux, E-util, SRA tools (fastqc, bowtie, samtools, htseq) GEO2R
✓	<a href="#">Case Studies in Functional Genomics   edX</a>	Raw read---QC---Trimming—alignment—reporting Poisson and negative Binomial distributions Epigenetics/ Methylation (illumina 450, Bisulfate ,CHIP-seq)	Linux, TCGA, GEO Bioconductor (Star, Deseq, Limma, Minifi, Bumphunter )
NA	<a href="#">Genomics in the Cloud</a>	HPC, Google Cloud, Virtual machines, mounting buckets, Containerization, Variant calling (*.vcf), reference mode (*.qvcf), BSQR, VQSR, joint vs single sample calling, Workflows for... Germline vs Somatic Variants, Copy Number Variants, Parellization	Gsutil, Docker, GATK, Spark, IGV, Cromwell, wdl, json, PAPI, TERRA
NA	<a href="#">Getting started — Nextflow 23.10.0 documentation</a>	Raw read---QC---Trimming—alignment--reporting	NEXTFLOW
NA	NEXTFLOW summit	Building a pipeline, containerization	NEXTFLOW, nf-core
NA	<a href="#">Nextgenerationsequencinghq.com</a>	Raw read---QC---Trimming—alignment--reporting	SRA, FastQC, EA-utils, MIXCR R(immunoarach)

# Data Science and Machine Learning

Certification	Course	Topics	Tools
✓	<a href="#">Statistics in R</a>	Quantiles, Normal Distributions, Skew, QQplots, p-values, t.tests, Monte Carlo Simulations, Statistical Power, Permutation, Chi square & Fisher Tests for Contingency Tables, Correlation	R
✓	<a href="#">Introduction to vector databases using Milvus   Udemy</a>	Milvus (Vector Databases), PyMilvus commands, Generation and storage of vector embeddings from raw image or text data for similarity search	Pymilvus, tensorflow, Pytorch, API
✓	<a href="#">HarvardX  Data Science and Machine Learning</a>	Bayesian Statistics, Prediction, Regression, LOWESS, Cross Validation, KNN models, Monte Carlo simulations & Bootstrapping, Linear Discriminant Analysis, Matrix Decomposition(SVD)	R (caret)
✓	<a href="#">Pytorch Basics for Machine learning  edX</a>	Tensors, Derivatives, Gradient Descent, Linear , Nonlinear and Logistic Regression	Pytorch
✓	<a href="#">Deep Learning Fundamentals with Keras</a>	Neural Network architecture, input functions, Node Activation functions, Convolution Networks, Recurrent networks, Deep Learning, Autoencoders	Keras, Pytorch, Tensorflow

# Engineering

Certification	Course	Topics	Tools
✓	<a href="#">Udemy Course The Git &amp; Github Bootcamp</a>	Git Syntax	GitBash
✓	<a href="#">Udemy Course Bash Scripting and Shell Programming (Linux Command Line)</a>	Bash and Linux Syntax	BASH
✓	<a href="#">Course: Data Engineering for Beginners with Python and SQL   Udemy</a>	Creating in a Python interactions with a SQL database thru an API	VsCode, Python review, SQL (postgres, sql-shell) APACHE(KAFKA,PULSAR,AWS-KINESIS) Postman(API)
✓	<a href="#">Git Lab CI: CI/CD and Devops for Beginners   Udemy</a>	Web/cloud deployment, yaml pipelines in gitlab, containerization, AWS, beanstalk, java, Unit testing	YAML, json, surge.sh, Gatsby, node,js, postman, gradle, newman
✓	<a href="#">Python Programming GUI, Database and System Design   Udemy</a>	Common data types, case logic, looping, functions, class objects, inheritance, GUI interfaces, System Design	Python, Tkinter, Primordious, SQLite

# Project Experience by Company

Company	Area	Project	Tools
Academia	Neuroscience	DNA cloning, Genotyping	NCBI Blasts, PCR oligos
Amgen	Neuroscience	High Content Imaging, Histology	Gene data Screener
		HTS- electrophysiology	R
		HTS - FRET	R, Python, SHINY
Caraway	Biomarker Discovery	HTS-High Content Imaging and ELISA	R, Python (seaborn) SHINY
		RNA-Seq	R, Bioconductor, (GEO2R, QUASR, DESEQ2,) AWS
		Mass Spec	R, Bioconductor (ViseoGO)
		Lipidomic	R, Bioconductor (indeed)
		3d Organoid Cyst Swelling	R (EBImage)
...in progress	Neuroscience	ALS Pathology Imaging	Milvus, Pymilvus, Pytorch

# Community and Events

## Workshop: Charting human biology using AI for Precision Health & Precision Medicine



### Location

238 Main Street, Cambridge, MA, 02139

6th floor conference space where [Bayer's](#) office is located.

You shared feedback on April 30. Your feedback helps make the Meetup experience better for everyone.

# DNAnexus®

 **Boston Computational Biology and Bioinformatics Meetup**  
Public group

📅 Thursday, April 18, 2024  
6:00 PM to 8:00 PM EDT  
[Add to calendar](#)

📍 Portico Brewing  
101 South St - Somerville, MA  
How to find us  
Look for a friendly group of nerds near the BCBB sign.

[Event Chat](#)



## Boston Computational Biology and Bioinformatics Meetup

📍 Cambridge, MA, USA

👤 3,785 members · Public group

👤 Organized by [Matthew Eaton](#) and 5 others

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