

Nicholas G. Crawford

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EDUCATION

BOSTON UNIVERSITY

PH.D. EVOLUTIONARY BIOLOGY
Grad. 2013 | Boston, MA

SAN DIEGO STATE UNIVERSITY

M.S. EVOLUTIONARY BIOLOGY
Grad. 2007 | San Diego, CA

UNION COLLEGE

B.S. BIOLOGY
Grad. 2001 | Schenectady, NY

SKILLS

COMPUTATIONAL

Languages:

Python (10+ years) • R • SQL • HTML • CSS

Python modules:

Pandas • Scipy • Numpy • iPython •
Matplotlib • Biopython • Pysam • Rpy2
• Pybedtools • Flask/Django

Genomics tools:

GATK • Tophat/Cufflinks • Beagle •
Bowtie2 • STAR • Samtools • Vcftools •
Bedtools • Blast • Blat • Annovar •
GREAT • GOrilla • EMMAX • Pylmm •
WASP • PLINK • Velvet • IGV • UCSC
Genome Browser • NCBI • Ensembl

MISCELLANEOUS

Wetlab (10+ years) • Linux/Unix •
Word • Excel • PowerPoint • \LaTeX • Fish
& Reptile Sampling

LINKS

Github:// [ngcrawford](#)
StackOverflow:// [nickcrawford](#)
LinkedIn:// [ngcrawford](#)
Twitter:// [ngcrawford](#)

OBJECTIVE

I am interested in a Computational Biologist position that utilizes my extensive experience in whole genome sequence analysis and transcriptomics.

EXPERIENCE

POST-DOCTORAL FELLOW | TISHKOFF LAB

2014 – Present | University of Pennsylvania, Philadelphia, PA

- GWAS on 5M Illumina arrays and secondary fine-mapping analyses on 133 whole genome sequences to identify novel pigmentation genes and loci in African populations.
- Customized and ran an allele-specific expression analysis pipeline on 150 whole-blood transcriptomes as part of a larger collaborative project.
- Supervised three undergraduates.

POST-DOCTORAL FELLOW | CALIFORNIA ACADEMY OF SCIENCES

2013 | San Francisco, CA

- Phylogenomic analysis of target enriched short-read Illumina sequences to infer relationships among turtle lineages.
- Constructed a computational pipeline to analyze reduced representation RAD-tag libraries.

LABORATORY TECHNICIAN | SAVANNAH RIVER ECOLOGY LAB

2007 | Aiken, SC

- Designed and optimized microsatellite libraries in a variety of non-model organisms.

RESEARCH TECHNICIAN | BOSTON BIOCHEM

2001 – 2003 | Cambridge, MA

- Purified E1 ubiquitin ligase and assorted 6-his and GST-tagged proteins.
- Ran an E. coli bioreactor.

PUBLICATIONS

SELECTED FROM 15 TOTAL (see: [google scholar](#))

- **Nicholas G. Crawford** et al., 2016. Genetic Basis of Pigmentation in Africans. *In Prep.*
- **Nicholas G. Crawford***, James F. Parham*, Anna B. Sellas, Brant C. Faircloth, Travis C. Glenn, Theodore J. Papenfuss, W. Brian Simison. 2014. A phylogenomic analysis of turtles. *Molecular Phylogenetics and Evolution*, 83, 250-257.
- Marcus R. Kronforst, Matthew E. B. Hansen, **Nicholas G. Crawford**, Jason R. Gallant, Rob J. Kulathinal, Durrell D. Kapan, Sean P. Mullen. 2013. Hybridization reveals the evolving genomic architecture of speciation. *Cell Reports*, 5, 1-12.
- **Nicholas G. Crawford**, Brant C. Faircloth, John E. McCormack, Robb T. Brumfield, Kevin Winker, Travis C. Glenn. 2012. More than 1000 ultraconserved elements provide evidence that turtles are the sister group of archosaurs. *Biology Letters*, 8(5), 783-786.
- **Nicholas G. Crawford**. 2010. SMOGD: Software for the Measurement of Genetic Diversity. *Molecular Ecology Resources*, 10: 556-557. (**Cited 500+ times**).