

BORYANA S. KOSEVA, Ph.D.

Bioinformatics Specialist

boryanakoseva.com [in Boryana Koseva](#) [boryanakis](#)

PROFESSIONAL SUMMARY

Bioinformatics scientist with extensive experience analyzing next-generation sequencing data, passionate about leveraging cutting-edge computational tools to address biological questions. Notably:

- I have used a wide range of bioinformatic methods to address research questions from genome assembly, and annotation to differential gene expression and population genomics
- In my current role, I have worked with 13 research groups from 7 departments across campus, fostering an environment of interdisciplinary collaboration
- I have completed 19 projects, written up methods and results, and communicated findings to primary investigators and their researchers

PROFESSIONAL EXPERIENCE

Bioinformatics Specialist

K-INBRE Bioinformatics Core

[May 2017 – present](#) [Lawrence, KS](#)

- Developed, automated, and implemented pipelines to carry out analyses of next-generation sequencing (NGS) data in a Unix/Linux environment on high performance computing (HPC) clusters
- Consulted on experimental design and sequencing strategies on projects with researchers from various disciplines within the biological sciences
- Documented workflows, delivered detailed reports, and aided in manuscript preparation
- Provided bioinformatics training to several early career scientists and graduate students, both one-on-one and in short training format workshops
- Managed all workstations in the Core facility, including software installation, maintenance, and setup of new technology

EDUCATION

Ph.D., Ecology & Evolutionary Biology

University of Kansas

[2011 – 2017](#) [Lawrence, KS](#)

Dissertation: Application of RAD-seq in Evolutionary Genomics of Non-Model Organisms

Adviser: Dr. John K. Kelly

B.S., Mathematical Biology

Truman State University

[2007 – 2011](#) [Kirksville, MO](#)

Capstone: R Modules for Undergraduate Biometry

TECHNICAL SKILLS

Python R Bash git
markdown R markdown
Jupyter Notebook \LaTeX

HPC Unix Mac

DOMAIN EXPERTISE

NGS Data Quality Control ★★★★★

fastp FastQC Trimmomatic
Cutadapt Quake

Data Visualization ★★★★★

deepTools IGV R/ggplot2 Circos

Genome Assembly ★★★★★

ABYSS SPAdes SGA Velvet
SOAPdenovo

Transcriptome Assembly ★★★★★

Trinity TransABySS

Annotation ★★★★★

MAKER2 Trinotate BLAST
RepeatMasker RepeatModeler

Differential Gene Expression ★★★★★

HISAT2 kallisto featureCounts
R/DESeq2 R/Sleuth

Variant Calling ★★★★★

bwa GATK samtools bcftools

Population Genomics ★★★★★

Stacks pyRAD dDocent STITCH

Quantitative Genetics ★★★★★

R/qtl

GRADUATE RESEARCH EXPERIENCE

Center for Research Methods and Data Analysis

📅 2016 – 2017

📍 Univ. Kansas

- Worked with clients from different disciplines to manage and analyze data critical to their research goals, primarily using Python
- Developed content and lead a 6-week intensive course in Python programming for novices
- Lead short hands-on workshops on data analysis using the Python Pandas package

K-INBRE Bioinformatics Core

📅 2013 – 2017

📍 Univ. Kansas

- Lead the effort to set up the computational infrastructure of the Core
- Acted as the primary administrator of the shared computers and servers
- Performed statistical analyses of biological data using an array of bioinformatics tools

TEACHING EXPERIENCE

Certified Lead Instructor - Python, R, Bash, Git, Genomics

The Carpentries Foundation

📅 2018 - currently

- As a volunteer *Carpentries* instructor, I teach workshops introducing fundamental data science skills to researchers who are novices to programming and command line tools
- Was a lead instructor for 6 workshops at 4 different organizations

Graduate Teaching Assistant

Dept of Ecology & Evolutionary Biology

📅 2011 –2017

📍 Univ. Kansas

- Teaching assistant for 4 semesters, for classes such as Principles of Genetics (BIOL350) and graduate-level Biometry (BIOL841)

PUBLICATIONS

- B. S. Koseva, J. L. Hackett, Y. Zhou, et al. “Quantitative Genetic Mapping and Genome Assembly in the Lesser Wax Moth *Achroia grisella*.” In: *G3: Genes, Genomes, Genetics* (2019). DOI: 10.1534/g3.119.400090.
- T. Hill, B. S. Koseva, and R. L. Unckless. “The Genome of *Drosophila innubila* Reveals Lineage-Specific Patterns of Selection in Immune Genes.” In: *Molecular Biology and Evolution* (2019). DOI: 10.1093/molbev/msz059.
- B. S. Koseva, D. J. Crawford, K. E. Brown, et al. “The genetic breakdown of sporophytic self-incompatibility in *Tolpis coronopifolia* (Asteraceae).” In: *New Phytologist* 216.4 (2017), pp. 1256–1267. DOI: 10.1111/nph.14759.
- L. M. Holeski, P. J. Monnahan, B. S. Koseva, et al. “A High-Resolution Genetic Map of Yellow Monkeyflower Identifies Chemical Defense QTLs and Recombination Rate Variation.” In: *G3: Genes, Genomes, Genetics* 4.5 (2014), pp. 813–821. DOI: 10.1534/g3.113.010124.
- J. K. Kelly, B. S. Koseva, and J. P. Mojica. “The Genomic Signal of Partial Sweeps in *Mimulus guttatus*.” In: *Genome Biology and Evolution* 5.8 (July 2013), pp. 1457–1469. DOI: 10.1093/gbe/evt100.

AWARDS



Michael S. Gaines Award for Excellence in Teaching

2016

Principles of Genetics (BIOL350)



Carlín Graduate Teaching Assistant Award

2015

Principles of Genetics (BIOL350)



Kenneth B. Armitage Award for Excellence in Teaching

2015

Principles of Genetics (BIOL350)



Arthur J. Mix Summer Award

2011

Univ. Kansas Botany Endowment

REFERENCES

Available upon request