

Shannon EK Joslin, PhD

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SUMMARY

Computational Genetics PhD with 9 years of experience teaching, 4+ years running research programs, and domain expertise across Molecular & Cellular Biology, Ecological & Environmental Biology, and Vertebrate & Invertebrate Biology.

QUALIFICATIONS

- Strong **scientific communication** skills as a lecturer, conference speaker, and peer-reviewed author.
- Program and **project leadership experience for asynchronous work groups** in federal agencies, university teaching teams, international workshops, scientific projects, and student groups.
- **Subject matter expert** in population genetics, genomics, bioinformatics, genome assembly, evolutionary biology, mammalian ecology and zoology, conservation genetics, data-intensive biology and workflow systems.
- **Strong technical skills** developing custom database solutions (ESRI, SQL, MSAccess) and automated bioinformatics pipelines (snakemake), and expertise in virtual environments (conda), workload managers (slurm), data visualization (R, RStudio) and version control (Git/Github).
- Fluency in **high performance computing clusters, cloud computing** (AWS), and **programming** (python, R, bash, Markdown, perl).
- **Technical skills** in genomic analyses (GWAS, PCA, MDA, genome assembly) next and third generation technology (shotgun sequencing, RAD-Seq, ddRADSeq RNASeq, Illumina, PacBio, Hi-C) and wet lab molecular genetic methods (DNA extraction, polymerase chain reaction, gel electrophoresis, RADSeq library prep, qPCR, Qubit fluorometry)

EDUCATION

2016 - 2023 **PhD**, Genetics at *University of California, Davis* (GPA: 3.96/4.0)
2008 - 2012 **BS**, Genetics at *University of California, Davis* (GPA: 3.54/4.0)

EXPERIENCE

National Park Service - Conservation Data Architecture Lead March 2021 - August 2025
Terrestrial Wildlife Program – Yosemite National Park

- **Program leadership** – Led a team of biologists in mapping temporal and geographic seasonality of bats utilizing cliffs and tracking the spread of a fungal pathogen, *Pseudogymnoascus destructans*, lethal to bat populations.
- **Educational outreach and scientific communication** – Grew Big Wall Bats program by translating scientific findings into public-facing educational materials, developing a framework and defined vocabulary for standardized data collection and enlisting community driven observations.
- **Method development** – Pioneered novel methods for studying cliff-dwelling wildlife now utilized across the United States and Canada to gain fundamental ecological knowledge of how bats utilize cliffs and high-angle terrain.
- **Data infrastructure development** – Owned and directed the database creation, management, and visualization for 5 distinct wildlife programs. Digitized and streamlined data collection and automated quality assessment and control to efficiently analyze and disseminate information to the NPS, researchers, partners, and funding sources.

Computational Genomics Doctoral Researcher

September 2016 - December 2023

Genomic Variation Lab - University of California, Davis

- **Genome assembly** – Developed pipelines to assemble vertebrate and invertebrate genomes of endangered species.
- **Population genetics** – Analyzed population structure, genetic differentiation (F_{st}), relatedness (IBD), with ANGSD, Structure, Plink softwares utilizing Bayesian statistics and maximum likelihood approaches.
- **Evolutionary genetics** – Used coalescent theory to estimate historical & contemporary effective population size (N_e), investigated genomes for sex-specific markers.

Bioinformatics Curriculum Coordinator

Summer 2017 - 2020

Lab for Data Intensive Biology - University of California, Davis

- **Graduate level curriculum development** – Developed open-source, version controlled, collaborative, workshop materials for an internationally attended Data Intensive Biology Summer Institute ANGUS (Analysis of Next-Gen Sequencing) bioinformatics workshop for post-doc's, professors and research professionals.
- **Graduate level instruction** – Co-developed curriculum and taught graduate level course: "GGG298 Tools to Support Data-Intensive Research".

Research Assistant in Comparative Genetics

November 2008 - November 2012

Feline Genetics Lab - University of California, Davis

- **Molecular genetics lab work** – Expertise in Sanger sequencing, microsatellites, gel electrophoresis, PCR, DNA extraction, and NGS library prep and creation.
- **Computational & comparative genetics** – Carried out genome wide association studies, principle component analysis, Bayesian clustering, and multi-dimensional scaling analysis. Employed UCSC Genome Browser, GenBank, NCBI Genome Browser.

Research Assistant in Evolutionary Genetics

Summer 2017 - 2019

Evolutionary Ecology Fly Lab - University of California, Davis

- **Invertebrate studies** – Led *Wolbachia* fecundity study investigating effects of infected status on fertility of *Drosophila melanogaster*.
- **Statistical analysis** – Linear regression, (ANOVA, Wilcoxon Rank-Sum)

PUBLICATIONS

Joslin SEK. "Chromosome-Scale Genome Assembly and Investigation of the Hypomesus transpacificus Genome for Sex-Specific Markers, and Association of the Lactase Persistence Haplotype Block With Disease Risk in Populations of European Descent" Dissertation University of California, Davis, 2023.

Blair SRK, Schreier A, Escalona M, Finger AJ, **Joslin SEK** ... and Hull J. "A chromosome-level reference genome for the Versatile Fairy Shrimp, *Branchinecta lindahli*." Journal of Heredity, 2023.

Blair SRK, Schreier A, Escalona M, Finger AJ, **Joslin SEK** ... and Hull J. "A draft reference genome of the Vernal Pool Fairy Shrimp, *Branchinecta lynchi*." Journal of Heredity, 2023.

Blair SRK, Hull J, Escalona M, Finger AJ, **Joslin SEK** ... and Schreier A. "The reference genome of the Vernal Pool Tadpole Shrimp, *Lepidurus packardii*." Journal of Heredity, 2022.

Campbell MA, **Joslin SEK** ... and Finger AJ. "Polygenic discrimination of migratory phenotypes in an estuarine forage fish." G3 Genes — Genomes — Genetics, 2022.

Joslin SEK, ... Lemay DG. "Association of the lactase persistence haplotype block with disease risk in populations of European descent." Frontiers in Genetics, 2021.

- Reiter T, Brooks PT, Irber L, **Joslin SEK**, Reid CM, Scott C, Brown CT, Pierce-Ward NT. "Streamlining data-intensive biology with workflow systems." GigaScience, 2020.
- Standage D, Aliyari A, Cohan LJ, Crusoe MR, Head T, Irber L, **Joslin SEK**, and Brown CT. "khmer release v2.1:software for biological sequence analysis." JOSS, 2017.
- Gandolfi B, Alhaddad H, Affolter VK, Brockman J, HAggstrom J, **Joslin SEK** ... and Lyons LA. "To the root of curl: a signature of a recent selective sweep identifies a mutation that defines the Cornish Rex cat breed." PLoS ONE, 2013.
- Gandolfi B, Alhaddad H, **Joslin SEK** ... and Lyons LA. "A splice variant in KRT71 is associated with curly coat phenotype of Selkirk Rex cats." Scientific Reports, 2013.