Silas Tittes

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EDUCATION

University of Colorado at Boulder

- PhD. – Ecology and Evolutionary Biology — Aug 2014 – May 2019
  Advisers: Prof. Nolan Kane, and Prof. Nancy Emery
  - Dissertation: Predicting evolution and inferring its consequences
- Bachelor of Arts – Ecology and Evolutionary Biology — May 2008 – Dec 2012
  Adviser: Prof. Andrew Martin
  - Honors Thesis (*Magna Cum Laude*): Flea genetic diversity in Gunnison's Prairie Dog colonies and its implications for flea transmitted diseases

RESEARCH EXPERIENCE

University of California Davis

- Postdoctoral Researcher, Department of Evolution and Ecology — May 2019 – present
  Supervisor: Prof. Jeffrey Ross-Ibarra

University of Colorado at Boulder

- Professional Research Assistant, Ecology and Evolutionary Biology — Aug 2014 – Aug 2013
  Supervisor: Prof. Nolan Kane
- Undergraduate Research Student, Ecology and Evolutionary Biology — May 2009 – Aug 2012
  Supervisor: Prof. Andrew Martin

SKILLS

R, R Markdown, R Shiny, Bash, Python, HPC, Snakemake, Nextflow, SLiM, Stan, Keras, Docker, Pandoc, LaTeX, git, GitHub, and Googling Stackoverflow.

AWARDS & SCHOLARSHIPS

- Excellence in Teaching Award — 2019
  CU Boulder, Ecology and Evolutionary Biology
- Ling-Ju Harn Fellowship — 2014
  $18,000
- Undergraduate Research Opportunities Program — 2010
  $1,000
- Edith Scates Memorial Scholarship — 2008
  $1,000
- Lion's Club International Scholarship — 2008
  $500

SOFTWARE

- Python package: mop
  Simple tool for capturing alignment regions with sufficient quality for genotyping.
- R package: rdmc
  Implements convergent adaptation models of Lee and Coop (2017).
- R package: performr
  A probablistic Hierarchical Bayesian model to predict performance curves across multiple groups (i.e. lines, populations, taxa, etc.).
- R package: pomodoror
  A writing productivity application.

TEACHING

INSTRUCTOR

- Apple Genomics, CU Boulder — Spring 2018
  I designed and taught Apple Genomics as an upper-division undergraduate elective course focused on the assessment of genetic diversity and classification of Boulder county apples trees. Starting from leaf samples students learned DNA extraction and QC; the development of custom pipelines for DNA sequence alignment, genotyping, and calling variants; and the use of several software packages to assess population structure and genetic diversity. This project is ongoing and is now led by several of the students that took the course.

TEACHING ASSISTANT

- Phylogenetics / Comparative Biology, CU Boulder — Spring 2019
- Evolutionary Biology, CU Boulder — Fall 2016 - 2018, Spring 2017, Summer 2017

- Genetics, CU Boulder — Spring 2015, Summer 2015, Spring 2016
- Genomics, CU Boulder — Fall 2015

COURSE DEVELOPMENT

- Population Genetics web applications — Summer 2017
  I developed a series of R shiny based web applications used to teach undergraduate fundamental concepts in Population Genetics. These are free to use and available on GitHub, and are used regularly in several population genetics courses in several countries.

HACKATHONS, WORKSHOPS, AND MEETUPS

HACKATHONS

- Ross-Ibarra Lab Snakefest (organizer), UC Davis — August 2019
  I organized a one day hackathon to develop a Snakemake based pipeline for aligning short reads, calling and filtering SNPs.
- PanAnd (attendant), Cornell University — June 2019
  I attended a five day hackathon hosted by the Bucker lab at Cornell University. I explored methods to identify conserved non-coding regions using multi-species alignments of DNA shape statistics.

WORKSHOPS

- Workshop: msprime (attendant), UC Davis — December 2018
  I attended a three day workshop hosted led by Kevin Thornton introducing msprime and related tools for coalescent based population genetic simulations.

MEETUPS

- Meetup: R-ladies Boulder Meetup (attendant), Boulder, CO — Monthly (starting September 2019)
  I attend the monthly R-ladies Boulder Meetup to practice, learn, and develop new R language skills in an inclusive environment.

PUBLICATIONS

JOURNALS

[16] MB Hufford, A Seetharam, …, S Tittes, …, RK Dawe. De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes (2021). *Science*.

[15] NB O'Hara, SJ Franks, NC Kane, S Tittes, JS Rest. Evolution of pathogen response genes associated with increased disease susceptibility during adaptation to an extreme drought event in a *Brassica rapa* plant population (2021). *BMC Ecology and Evolution*.

[14] S Tittes. rdmc: an open source R package implementing convergent adaptation models of Lee and Coop (2017). (2020). *G3*.

[13] R Wooliver, S Tittes, SN Sheth. A resurrection study reveals limited evolution of thermal performance in response to recent climate change across the geographic range of the scarlet monkeyflower. (2020). *Evolution*.

[12] AA Comeault, J Wang, S Tittes, K Isbell, S Ingley, AH Hurlbert, DR Matute. Genetic diversity and thermal performance in invasive and native populations of African fig flies. (2019). *Molecular Biology and Evolution*.

[11] K Carscadden, M Mcdermott S Turbek, S Tittes, AP Martin. Building bridges: An active learning lesson in evolution and collaboration. (2019). *Journal of College Science Teaching*.

[10] C Weiss-Lehman, S Tittes, NC Kane, R Hufbauer, BA Melbourne. Riding the wave: genomic signatures of gene surfing and selection in experimental range expansions. (2019). *Philosophical Transactions of the Royal Society B*.

[9] S Tittes, JF Walker, L Torres-Martinez, NC Emery. Grow where you thrive, or where only you can survive? An analysis of tolerance curve evolution in a clade with diverse habitat affinities. (2019). *The American Naturalist*.

[8] CS Smith, E Scordato, S Tittes, S Taylor, D Vergara. Book Review: Molecular Population Genetics. Matthew Hahn. (2019). *Molecular Ecology*.

[7] CS Smith, S Tittes, JP Mendieta, E Collier-zans, H Rowe, LH Rieseberg, NC Kane. (2018). Genetics of alternative splicing evolution during sunflower domestication. *Proceedings of the National Academy of Sciences*.

[6] Q Gao, NC Kane, B Hulke, S Reinert, C Pogoda, S Tittes, J Prasifka. (2017). Genetic architecture of capitate glandular trichome density in florets of domesticated sunflower (*Helianthus annuus L.*). *Frontiers in plant science*.

[5] DJ Gray, H Baker, K Clancy, RC Clarke, K deCesare, J Fike, MJ Gibbs, F Grotenhermen, NC Kane, KG Keepers, DP Land, RC Lynch, JP Mendieta, M Merlin, K Muller-Vahl, CS Pauli, BJ Pearson, B Rhan, TC Ruthenberg, CJ Schwartz, S Tittes, D Vergara, KH White, RN Trigiano. (2016). Current and future needs and applications for *Cannabis*. *Critical Reviews in Plant Sciences*.

[4] D Vergara, H Baker, K Clancy, KG Keepers, JP Mendieta, CS Pauli, S Tittes, KH White, NC Kane. (2016). Genetic and genomic tools for *Cannabis sativa*. *Critical Reviews in Plant Sciences*.

[3] RC Lynch, D Vergara, S Tittes, KH White, CJ Schwartz, MJ Gibbs, TC Ruthenburg, K deCesare, DP Land, NC Kane. (2016). Genomic and chemical diversity in *Cannabis*. *Critical Reviews in Plant Sciences*.

[2] SJ Franks, NC Kane, NB O'Hara, S Tittes, JS Rest. (2016). Rapid genome-wide evolution in *Brassica rapa* populations following drought revealed by sequencing of ancestral and descendant gene pools. *Molecular Ecology*.

[1] S Tittes, NC Kane. (2014). The genomics of adaptation, divergence and speciation: a congealing theory. *Molecular Ecology*.

CONFERENCES

[6] S Tittes. (2020). Evolutionary genetics of lots of grass. *UC Davis, Center for Population Biology, Seminar*, remote

[5] S Tittes. (2020). Local Adaptation in Maize landrace and *parviglumis* populations. *Zeavolution*, remote

[4] S Tittes, NC Emery. (2018). A novel Bayesian inference method to model tolerance curves. *The American Society of Naturalists*, Montrey, CA

[3] S Tittes C Weiss-Lehman, NC Kane, R Hufbauer, BA Melbourne. (2017). Surfing in pools of beetles: using replicated landscape experiments to disentangle signatures of selection and drift. *Evolution*, Portland, OR

[2] NB O'Hara, SJ Franks, NC Kane, S Tittes, Amidi-Abraham G, JS Rest. (2014). Genomic signatures of rapid evolution in drought response and disease susceptibility in an annual plant, *Brassica rapa*. *Society for Molecular Biology and Evolution*, Puerto Rico

[1] SJ Franks, NC Kane, NB O'Hara, S Tittes, JS Rest. (2014). Genome-wide analysis reveals rapid genetic changes in natural *Brassica rapa* populations following drought. *Evolution*, Raleigh, North Carolina

[*CV compiled on 2021-08-09*]