

# Kyle Fletcher Ph.D

Assistant Project Scientist, University of California Davis, Genome Center.

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[Google Scholar](#)

## PROFILE

Innovative and collaborative computational biologist with over six years of experience in (meta)genomics and bioinformatics. I enjoy developing solutions to biological questions using big data and computational approaches. I work across several interdisciplinary, cross-institutional teams to assemble and annotate the genomes of eukaryotic microbes called oomycetes. In addition, I collaborate on projects studying the genomes of fungi, bacteria, animals, and plants.

## EDUCATION AND APPOINTMENTS

<b>2020 to present</b>	<b>Assistant Project Scientist (Bioinformatics), <i>UC Davis Genome Center</i>, (Michelmores lab)</b>
<b>2016 to 2020</b>	<b>Postdoctoral Scholar (Bioinformatics), <i>UC Davis Genome Center</i>, (Michelmores lab)</b>
<b>2011 to 2015</b>	<b>Ph.D. Molecular Biology, <i>University of Aberdeen, UK</i> (Küpper and Van West labs)</b>
<b>2007 to 2010</b>	<b>B.Sc. (Hons) Biological Sciences, <i>Queen's University of Belfast, UK</i></b>

## KEY BIOINFORMATIC SKILLS

- *De novo assembly*: (Meta)Genome, Transcriptome,
- *Taxonomic assignment of metagenomic sequences*.
- *Annotation and functional prediction*: Genes, ORFs, Repeats, Pseudogenes, and Horizontal gene transfer.
- *Phylogenetics*: Multi-species coalescence
- *Pipeline development*: AFLAP, VCFvariance
- *Association testing*: GWAS, QTL, Fine mapping
- *Differential gene expression analysis*: EdgeR
- *Candidate gene analysis*
- *Variant calling*: SNPs, SNVs
- *Public database use*: NCBI, Pfam, UniProt, SILVA
- *Next-generation sequencing*: Illumina, PacBio, Oxford Nanopore, Aviti, Hi-C, GBS, cDNA (long and short read)
- *Molecular marker development*: Allele specific PCR, RFLPs, structural variation.
- *Unix operating systems*: Linux
- *Programming languages*: Bash, R, Perl, Python
- *Version control*: Git
- *HPC scheduling*: SLURM
- *Data visualization*: Figures, Genome Browsers
- *Statistics*: Linear modelling, Clustering
- *Teaching, Leadership, and Communication*

## PROFESSIONAL EXPERIENCE

**2016 to present: Postdoctoral Scholar then Assistant Project Scientist, UC Davis, Michelmores lab.**

- *Assembled genomes of 14 species of oomycete, including 5 to chromosome-scale. These include microbial pathogens of lettuce, spinach, and corn.*
- *Taxonomic classification of metagenomic data.*
- *Assembled transcriptomes (short-read and long-read data).*
- *Developed and deployed computational pipelines for linkage analysis (AFLAP) and detection of polyploidy (VCFvariance).*
- *Mentored seven scientists in distinct bioinformatic projects.*
- *Contributed to five successful, annual grant submissions (one project) and coordinated the semi-annual reports.*
- *Completed a Professors for the Future fellowship to develop leadership skills.*
- *Presented six posters and nine oral presentations at conferences and seminars.*
- *Published five papers as first author, two papers as middle author.*
- *Collaborated with scientists at the USDA, Texas A&M, University of Arkansas, International Crops Research Institute for the Semi-Arid Tropics (India), and private companies.*

**2011 to 2015: Ph.D. student, University of Aberdeen, UK (Küpper and Van West labs).**

- *Worked between two labs to characterize the phylogenetic affiliation of oomycetes which infect marine algae, using molecular biology, phylogenetics, and light and electron microscopy.*
- *Conducted an 18s rRNA amplicon analysis of organisms associated with marine algae from a global collection in search of oomycete sequences (Qiime and SILVA).*
- *Mentored two scientists in molecular biology and microbiology projects.*
- *Presented two posters and six oral presentations at conferences.*
- *Published three papers as first author, four as middle author.*
- *Collaborated with and visited the labs of scientists at the Scottish Association of Marine Sciences – UK, Stazione Zoologica – Italy, Station Biologique de Roscoff – France, and Kongju National University – South Korea*

## KEY PUBLICATIONS (Full list of publications available at Google Scholar)

**Fletcher et al.** Ancestral chromosomes for the Peronosporaceae inferred from a telomere-to-telomere genome assembly of *Peronospora effusa*. *Molecular Plant Microbe Interactions* (2022). <https://doi.org/10.1094/MPMI-09-21-0227-R>

**Fletcher et al.** Variance of allele balance calculated from low coverage sequencing data infers departure from a diploid state. *BMC Bioinformatics*. (2022). <https://doi.org/10.1186/s12859-022-04685-z>

**Fletcher et al.** AFLAP: Assembly-Free Linkage Analysis Pipeline using k-mers from whole-genome sequencing data. *Genome Biology* 22, 115 (2021). <https://doi.org/10.1186/s13059-021-02326-x>

## OTHER

- U.S. driver's license.