

# MATTHEW M. OSMOND

Postdoctoral Fellow

Center for Population Biology

University of California - Davis

mmosmond@gmail.com

mmosmond.github.io

## Academic Positions

2018- Center for Population Biology & Banting PDF, University of California - Davis  
Supervisors: **Graham Coop**, **Sebastian Schreiber**, **Andrew Whitehead**

## Education

**PhD** Zoology, University of British Columbia 2013 - 2018  
Title: *Adaptive challenges: fitness valleys and evolutionary rescue*  
Supervisor: **Sarah Otto**  
Committee: Amy Angert, Michael Doebeli, Michael Whitlock

**MSc** Biology, McGill University 2010 - 2012  
Title: *Eco-evolutionary rescue: an adaptive dynamic analysis*  
Supervisor: **Claire de Mazancourt**  
Committee: Michel Loreau, Frédéric Guichard

**BSc** Mathematics & Biology, Queen's University 2004 - 2008  
Honours title: *The meaning of female coloration in the American redstart*  
Honours supervisor: **Laurene Ratcliffe**  
Committee: Paul Martin

## Selected Awards and Fellowships

2018-2021	Center for Population Biology Postdoctoral Fellowship, UC Davis	\$125,000
2018-2020	Banting Postdoctoral Fellowship	\$140,000
2018-2020	NSERC Postdoctoral Fellowship (declined)	\$90,000
2013-2017	Alexander Graham Bell Canada Graduate Scholarship (CGS-D), NSERC	\$105,000
2011-2012	Alexander Graham Bell Canada Graduate Scholarship (CGS-M), NSERC	\$17,500
2008	Undergraduate Student Research Award (USRA), NSERC (declined)	\$4,500
2007	Undergraduate Student Research Award (USRA), NSERC	\$4,500

## Publications

9. Edwards K, Kremer C, Miller E, **Osmond M**, Litchman E, Klausmeier C. Accepted. Evolutionary stable communities: a framework for understanding the role of trait evolution in the maintenance of diversity. *Ecology Letters*.
8. Scott M\*, **Osmond M\***, Otto S. 2018. Haploid selection, sex ratio bias, and transitions between sex-determining systems. *PLoS Biology* 16:e2005609. [\* joint first authors]
7. **Osmond M**, Klausmeier C. 2017. An evolutionary tipping point in a changing environment. *Evolution* 71:2930-2941.
6. **Osmond M**, Otto S, Klausmeier C. 2017. When predators help prey adapt and persist in a changing environment. *The American Naturalist* 190:83-98. [F1000Prime Recommended]
5. **Osmond M**, Barbour M, Bernhardt J, Pennell M, Sunday J, O'Connor M. 2017. Warming induced changes to body size stabilize consumer-resource dynamics. *The American Naturalist* 189:718-725.
4. Toews D, Delmore K, **Osmond M**, Taylor P, Irwin D. 2017. Migratory orientation in a narrow avian hybrid zone. *PeerJ* 5:e3201.
3. **Osmond M**, Otto S. 2015. Fitness-valley crossing with generalized parent-offspring transmission. *Theoretical Population Biology* 105:1-16.
2. **Osmond M**, Reudink M, Marra P, Germain R, Nocera J, Boag P, Ratcliffe L. 2013. Relationships between carotenoid-based female plumage and age, reproduction, and mate colour in the American Redstart. *Canadian Journal of Zoology* 91:589-595.
1. **Osmond M**, de Mazancourt C. 2013. How competition affects evolutionary rescue. *Philosophical Transactions of the Royal Society B: Biological Sciences* 368:20120085.

## Preprints

1. Thompson K, **Osmond M**, Schluter D. 2018. Patterns of speciation and parallel genetic evolution under adaptation from standing variation. *bioRxiv* 368324. (revisions requested at *Evolution Letters*, EVL3-18-0066)

## Additional Research Experience

2017	<b>Student</b> Evolutionary Quantitative Genetics workshop (J. Felsenstein <i>et al.</i> )
2016	<b>Visiting researcher</b> University of Montpellier and CNRS (O. Ronce, T. Lenormand)
2015	<b>Student</b> Complex Systems Summer School (Santa Fe Institute)
2013	<b>Student</b> Metacommunities summer school (M. Leibold, C. Klausmeier)
2013	<b>Researcher</b> Michigan State University (C. Klausmeier, E. Litchman)
2012-2014	<b>Visiting researcher</b> University of Helsinki (S. Geritz, E. Kisdi)
2012	<b>Research assistant</b> University of British Columbia (D. Irwin)
2011	<b>Student</b> Adaptive Dynamics summer school (S. Geritz, C. Klausmeier)
2010-2012	<b>Member</b> Eco-evolutionary working group (A. Gonzalez <i>et al.</i> )
2010	<b>Research assistant</b> USGS (J. Piatt) and University of Victoria (A. Burger)
2009-2010	<b>MSc</b> (withdrew) Lakehead University (A. Mallik)

## Community Involvement

**Referee** *The American Naturalist* (6), *Genetics* (2), *Journal of Theoretical Biology* (2), *Theoretical Population Biology* (2), *Biological Journal of the Linnean Society* (1), *Ecology* (1), *Evolution* (1), *Frontiers in Ecology and Evolution* (1), *Philosophical Transactions of the Royal Society B* (1), *Journal of Statistical Mechanics* (1)

2018-       **Organizer** Center for Population Biology Tuesday Seminar, UC Davis  
 2017-2018 **Secretary** Zoology Graduate Student Society, University of British Columbia  
 2017       **Volunteer** Eco-Evo Retreat, Squamish, British Columbia  
 2016-2017 **Organizer** Let's Assume (evol. theory discussion group), University of British Columbia  
 2014       **Organizer** Vancouver Evolution Group (regional journal club), Vancouver  
 2010-2012 **Organizer** Eco-Theoretic Cafe (mathematical ecology discussion group), McGill University  
 2007       **Volunteer** Society of Canadian Ornithologists meeting, Queen's University

## Teaching Experience

2014, 2016, 2017 **Marker** Population Genetics, University of British Columbia  
 2011       **Mentor** for work-study undergraduate student, McGill University  
 2010       **Teaching Assistant** Math Models in Biology, McGill University  
 2010       **Teaching Assistant** Organismal Biology, McGill University  
 2010       **Teaching Assistant** Evolutionary Concepts, Lakehead University  
 2009       **Teaching Assistant** Ecology, Lakehead University

## Invited Seminars

**Osmond M**, Martin G, Ronce O, Otto S. 2018. Evolutionary rescue. Mathematical Biology Seminar, University of British Columbia, Vancouver, Canada.  
**Osmond M**. 2018. Evolutionary rescue: integrating ecological and evolutionary theory. Center for Population Biology, University of California - Davis, Davis, USA.  
**Osmond M**, Martin G, Otto S, Ronce O. 2016. Genetic signatures of evolutionary rescue with sex. Stochastic Models for the Inference of Life Evolution group, College de France, Paris, France.  
**Osmond M**, Otto S, Klausmeier C. 2016. When predators help prey adapt and persist. Institute National de la Recherche Agronomique, Montpellier, France.  
**Osmond M**, Otto S. 2016. Subcritical adaptation: fitness valleys and evolutionary rescue. Stochastic and Deterministic Models for Evolutionary Biology workshop, Oaxaca, Mexico.  
**Osmond M**, de Mazancourt C. 2013. Using adaptive dynamics to predict evolution and extinction in changing environments. Pacific Institute for the Mathematical Sciences, University of British Columbia, Vancouver, Canada.  
**Osmond M**, de Mazancourt C. 2011. To adapt and persist in a changing environment. Mick Follows lab, Massachusetts Institute of Technology, Boston, USA.

## Conference Presentations

- Osmond M**, Martin G, Ronce O, Otto S. 2018. Genetic paths to evolutionary rescue. Population and Evolutionary Quantitative Genetics, Madison, USA. (poster) **\*Poster award**
- Osmond M**, Martin G, Ronce O, Otto S. 2018. Predicting the genetic paths evolutionary rescue will take. Evo-WIBO, Port Townsend, USA. **\*Talk award**
- Osmond M**, Scott M, Otto S. 2017. Gametic competition, meiotic drive, sex ratio selection, and transitions between sex determination systems. Evolution, Portland, USA.
- Osmond M**, Klausmeier C. 2017. Evolutionary tipping points in changing environments. Canadian Society for Ecology and Evolution, Victoria, Canada.
- Osmond M**, Otto S, Klausmeier C. 2016. When predators help prey adapt and persist. Evolution, Austin, USA.
- Osmond M**, Klausmeier C. 2016. When predators help prey adapt and persist. Evo-WIBO, Port Townsend, USA.
- Osmond M**, Otto S. 2015. Crossing fitness-valleys without the help of Mendel: extending theory. Canadian Society for Ecology and Evolution, Saskatoon, Canada. **\*Talk award**
- Osmond M**, Otto S. 2014. Crossing fitness-valleys without the help of Mendel. Evolution, Raleigh, USA. (poster)
- Osmond M**, Otto S. 2014. Crossing fitness-valleys without the help of Mendel. Evo-WIBO, Port Townsend, USA. (poster)
- Osmond M**, Otto S. 2014. Crossing fitness-valleys without the help of Mendel. Evolution of Mating Systems, University of Jyväskylä, Jyväskylä, Finland. (poster)
- Osmond M**, Weigang H. 2012. Shorter generation times, slower evolution? Impact of life-history on evolution. Swedish Meeting on Mathematics in Biology, Lund, Sweden. (poster)
- Osmond M**, Weigang H. 2012. How life-history affects the rate of evolution. Biomathematics Day, University of Helsinki, Helsinki, Finland.
- Osmond M**, de Mazancourt C. 2012. How competition affects evolutionary rescue. Joint Congress on Evolutionary Biology, Ottawa, Canada.
- Osmond M**, de Mazancourt C. 2011. Evolutionary rescue and competition. Quebec Centre for Biodiversity Science Symposium, Montreal, Canada.
- Osmond M**, de Mazancourt C. 2011. To adapt and persist in a changing environment. Canadian Society for Ecology and Evolution, Banff, Canada. (poster)

I am a **collaborative evolutionary biologist with a broad mathematical toolset**, empowering me to ask a wide range of **questions at the intersection of ecology and evolution**. What remains constant throughout my work is a focus on **developing intuition in complex scenarios**. Here initially-counterintuitive results abound and careful mathematical analyses greatly improve **understanding and prediction of population- and community-level dynamics**.

## Evolutionary rescue

A major focus of mine to date has been **evolutionary rescue**, where sufficiently rapid genetic adaptation allows a population to persist when it would otherwise go extinct. This is a key eco-evolutionary process with important consequences for both conservation in the anthropocene and medicine in an age of increasing drug resistance.

Most theory and experiments on evolutionary rescue to date have focused on the responses of species in isolation, leaving **the effect of species interactions on rescue** an open question. Competition reduces population sizes and thus might be expected to decrease rates of adaptation and the likelihood of evolutionary rescue. On the other hand, competition can also impart strong selection, which may accelerate adaptation. During my MSc with Claire de Mazancourt (McGill, now CNRS, France) I built mathematical models to explore these contrasting effects of competition on the potential for evolutionary rescue (Osmond & de Mazancourt 2013, *Phil. Trans. B*). The analytical results showed that, while competing species will typically inhibit the rescue of a focal species by suppressing its population size, selection pressures induced by competing species – acting in the same direction as the environmental change – can more than compensate for this by accelerating adaptation in the focal species. Thus, **competition can facilitate evolutionary rescue**.

I later showed, in collaboration with Chris Klausmeier (Michigan State) during my PhD with Sally Otto (UBC), that the same conclusion holds for predators – **predators can increase their prey’s potential for evolutionary rescue** despite reducing its abundance (Osmond *et al.* 2017, *Am. Nat.*). Here I was also able to analytically demonstrate two different mechanisms by which predators can promote rescue: by a “selective push” (as in the case of competition above) and through an “evolutionary hydra effect”. This latter mechanism is surprising as it does not require predation to impose a selective pressure; predation, or even just random mortality, releases prey from density-dependence, shortening generation times and accelerating evolution. Together with my MSc work, I have thus demonstrated that **antagonistic ecological interactions can promote persistence in changing environments**, an important caveat for current approaches in conservation (e.g., predator removal) and medicine (e.g., drug resistance).

Models of evolutionary rescue are essential for predicting responses to climate change and other disturbances, yet essentially all quantitative genetic models assume the same arbitrary fitness landscape. I analytically showed that **modifying this ubiquitous assumption leads to dramatically different outcomes** (Osmond & Klausmeier 2017, *Evolution*). In particular, when selection becomes weaker with increasing maladaptation – a result commonly observed in the lab (i.e., antagonistic epistasis) – **“evolutionary tipping points” can exist, causing seemingly well-adapted populations to suddenly go extinct**. This work strongly suggests that we should use great caution when using classical quantitative genetic results to predict whether contemporary populations will persist in the face of climate change. I have since built an R package that allows researchers to look for potential evolutionary tipping points in their phenotype-fitness maps (beta version here: <https://shiney.zoology.ubc.ca/mmosmond/criticalSplines/>).

I am continuing my work on evolutionary rescue in a number of ways. Most prominently, I am developing **a theory for the genetic basis of evolutionary rescue** in a collaboration I initiated with Guillaume Martin and Ophélie Ronce (University of Montpellier, France). While

nearly all existing population genetic models of evolutionary rescue impose its genetic basis and typically assume a single mutation of a given effect is responsible, I am using branching process theory and Fisher’s geometric model of adaptation to allow greater flexibility in both the number and fitness effects of the mutations underlying rescue. My findings show that, in many instances, rescue by multiple mutations can be more likely than by a single mutation, and that the individual mutations that contribute to rescue genotypes may be nearly neutral or even deleterious in the wildtype background and thus be mistaken as hitchhikers. **This theory has already inspired an experiment with yeast** in collaboration with researchers at UBC. The experiment aims to examine the effect of demography on the genetics of adaptation while also providing a novel method to estimate the distribution of beneficial fitness effects.

Finally, in my postdoc at UC Davis with Graham Coop I am working on **methods to infer from genomic data whether evolutionary rescue has occurred** in a given population. Such methods will inform us on the frequency of evolutionary rescue in nature and will become increasingly useful as more and more natural populations are both sequenced and exposed to environmental change. Specifically, I am developing statistical tools that use genomic data before and after a population bottleneck to infer how much of the demographic recovery was due to selective sweeps. I plan to apply this approach to the collapse of Pacific Herring following the Exxon Valdez oil spill (with Andrew Whitehead, UC Davis) and/or HIV drug resistance (with Pleuni Pennings, San Francisco State). More generally, **I believe that evolutionary rescue – and eco-evolutionary dynamics more broadly – will benefit from a closer integration with genomic data and I plan to develop this line of inquiry into a mature research program.**

## Genetic background

A second theme in my work is **the impact of genetic background on evolution**. This work demonstrates how genetic backgrounds influence many processes, from adaptation to sex determination to speciation, and highlights the role of recombination and linkage in evolution.

Interactions among loci – **epistasis** – are widespread and in extreme form lead to rugged fitness landscapes, where populations can get stuck on suboptimal fitness peaks surrounded by valleys of low fitness. The problem of crossing fitness valleys is a classic one in evolutionary theory but until now assumes fair (Mendelian) transmission of alleles from one generation to the next. Meanwhile, non-Mendelian inheritance – e.g., meiotic drive, maternal inheritance, and cultural transmission – is increasingly recognized, begging the question: **How does non-Mendelian inheritance affect fitness-valley crossing?** I answered this question by analyzing a very general two-locus model using diffusion theory (Osmond & Otto 2015, *Theor. Pop. Biol.*). This allowed me to analytically quantify a number of ways non-Mendelian transmission can greatly facilitate or hinder fitness-valley crossing, pinpointing how and when undetected non-Mendelian inheritance will obscure predictions.

**Sex chromosomes** provide a genetic background with strong effects on fitness and thus evolution, including their own. Previous work on the evolution of sex chromosomes has indicated that opposing selection in males and females can lead to sex chromosome turnover, where new sex-determining alleles invade if they are in closer linkage to the loci under sexually-antagonistic selection. This theory has led to a great deal of empirical insight about the loci responsible for the rapid turnover in sex-determining factors we often see. However, so far two important factors have been ignored: 1) tight linkage between sex-determining factors and selected loci and 2) haploid selection (e.g., meiotic drive, pollen competition). In a paper Michael Scott (University College London) and I jointly first authored (Scott, Osmond, Otto 2018, *PLoS Biology*), we analytically outline how **tight linkage and haploid selection greatly expand the scenarios under which we expect transitions between sex-determining systems to occur**. These results allow loci in

previously unexpected genomic locations (e.g., on autosomes) experiencing haploid and/or diploid selection to now be implicated as drivers of sex chromosome turnover.

Hybrid fitness can be low – and **speciation** easy – due to alleles from one parent performing poorly on the other parent’s genetic background. The extent to which two populations adapt using the same mutations therefore has a great influence on the fitness of their hybrids, and thus on speciation. So far theory in this area has focused on adaptation arising from new mutation, and **the effect of standing genetic variance on hybrid fitness** is unclear. To explore this idea I wrote simulations and made analytical approximations for empiricists at UBC ([Thompson, Osmond, Schluter 2018](#), [bioRxiv](#); in review at *Evolution Letters*). The results showed that **standing genetic variation can increase the mean fitness of hybrids, making speciation more difficult**. However, this increase in fitness dissipates quickly with the degree of non-parallel selection on the parental populations, especially when many phenotypes contribute to fitness. Therefore, in complex organisms with standing variation, imperceptibly small differences in selection between populations may greatly reduce the degree of parallel genetic changes, and thus make speciation easier.

## Metabolic theory

**Metabolic scaling theory** is a powerful predictor of population-level dynamics. This largely ecological approach has given me an additional tool to explore how changing environments, especially climate change, affect interacting populations and I am currently bridging this theory with quantitative genetics to expand and improve its predictive scope.

Both metabolism and body size are expected to change with temperature and influence population dynamics, but their joint effects (including the effect of body size on metabolism) under warming have not yet been investigated. Together with a working group organized by Mary O’Connor (UBC), I led the analysis of a model combining metabolic scaling theory and the widely-observed **temperature-size rule** to ask how a consumer-resource system is affected by warming ([Osmond et al. 2017](#), *Am. Nat.*). While changes in metabolism alone are predicted to destabilize the system and therefore make extinction more likely, expected **changes in body size can reverse that prediction and stabilize consumer-resource systems under warming**.

Metabolic scaling theory often ignores evolution despite genetic variance in metabolic traits and their potentially large contribution for fitness. Evolution in metabolic traits will impact plastic changes (e.g., in body size) as well as range shifts, and thus are essential for conservation and management practices to consider. I am now in the process of adding evolution to models with metabolism and stage-structure to help William Cheung (UBC) predict **how genetic adaptation will affect the response of marine fish to warming oceans**. Preliminary findings using integral projection models show the degree to which declines in body size and drops in population growth rate are mitigated by genetic adaptation. I would like to continue **connecting metabolic theory and evolution** to improve our predictions in a changing world.

## Summary

I am a **highly collaborative theoretician with a diversity of mathematical tools to tackle questions spanning ecology and evolution**. My focus thus far has been on evolutionary rescue, impacts of genetic background on evolution, metabolic scaling theory, and combinations of these three topics. I look forward to continued discovery along these lines and many others.

I have had the great fortune of being taught by great teachers (key among them Troy Day, Eva Kisdi, and Sally Otto). Their talent has arisen from a curiosity and passion for the material, but also by a **desire to impart curiosity and passion in their students**. I recognize that being an effective teacher takes a lot of time and energy, but I am committed to it because I believe that passing knowledge on to future generations can be one of the most rewarding aspects of the job.

## Experience

I have been a **teaching assistant for a diversity of courses**. At the lower level I've taught large first year *Organismal Biology* labs at McGill and run local fieldtrips for the *Ecology* course at Lakehead. At the upper level I've led discussions for *Evolutionary Concepts* at Lakehead, run tutorials for *Math Models in Biology* at McGill, and marked assignments for *Population and Quantitative Genetics* at UBC, and guest lectured in Sally Otto's *Biomathematics* course. These experiences and many presentations (incl. 2 talk awards) have greatly improved my ability as a speaker.

In addition to these formal teaching roles I have greatly enjoyed teaching (and learning) through my **heavy involvement in discussion groups**. Most prominently, organizing the theory group at UBC was a very rewarding experience that included leading a critical analysis of all of Crow & Kimura's (1970) *An Introduction to Population Genetics Theory*. I was also happy to have a brief stint as organizer of the *Vancouver Evolution Group*, with faculty, postdocs, and students from both UBC and Simon Fraser University meeting at my house to discuss foundational topics in evolution.

I have also contributed to a collaborative learning environment in a number of other ways. For instance, I **organized a panel discussion** on "difficult scenarios and their resolution" in academia at a local ecology and evolution retreat. I have also been the **primary mentor of an undergraduate** for a 4 month internship, teaching her run simulations in R, and have enjoyed **collaborating with many empiricists**, helping them understand and perform mathematical analyses. I am now in a leadership role as the Center for Population Biology postdoc at UC Davis, where I am **organizing a weekly seminar series and a multi-day workshop**.

## Teaching

I would enjoy teaching undergraduate and graduate courses in evolution, population genetics, population biology, mathematical biology, and statistics (e.g., EEB courses 225, 319, 323, 324, 430, and 459). Whenever possible I would **keep these courses up-to-date with the current literature**, exposing students to the ever-changing nature of science and the fact there is still much to discover. I'd also be excited to **develop new courses** in these areas, especially on the topics of mathematical biology and theoretical population and quantitative genetics, where I could **teach students how to model**. It would also be fun to **add active-learning components** to new or existing courses, as I believe students best understand mathematical and statistical ideas with programs such as *R*, *Mathematica*, or *Python*, which allow them to interact with and visualize the abstract material.

## Mentoring

As I mentioned at the outset, I have been lucky to have had great mentors. In starting my own lab my goal is to emulate the aspects I have seen work best. First and foremost is **communication**; I am committed to providing quick feedback on ideas and writings, weekly meetings, and an open-door policy. Secondly, I will strive to create a **fun and welcoming environment**, allowing students to relax and ask questions. An important aspect of this approach is to create a **diverse lab**, which empowers underrepresented groups while allowing unique perspectives and new ideas to flourish.