



Arnaud Martin, Post-Doctoral Researcher
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George Washington University – Department of Biology

Faculty Position in Evolutionary Developmental Biology

Dear colleagues and search committee members,

I am pleased to submit my application as a prospective Assistant Professor at the George Washington University. I am a developmental biologist by training, and I further specialized in evolutionary studies of the genotype-phenotype map, in particular in non-model organisms of ecological interest. I am particularly interested in the generative mechanisms of evolutionary change and use **a combination of comparative, genomic and developmental tools in lepidopterans** to tackle how the genetic properties of living systems underlie biodiversity. Working at the intersection of development, evolution and molecular genetics, I am particularly interested in general phenomena such as morphological evolution, convergence, adaptive radiations, and I have accumulated a quite unique knowledge of butterfly development that is widely recognized by a diverse body of collaborators. While my prime ambition is to produce experimental results prone to diffusion in lecture slides and textbooks, I am also keen to stir fundamental debate in evolutionary genetics by providing an original and panoramic view of the field. For instance, I recently obtained \$270,000 to conduct **meta-analyses of the phenomenon of convergent genetic evolution across Eukaryotes**, and my work on this topic (see *Evolution* 2013) aims at unifying fields together rather than focusing on a particular taxonomic group.

Similarly, I worked with a wide range of animals (not just butterflies) and in labs spanning both molecular and organismal levels of investigation. I thrive in environments intellectually as diverse as the Department of Biology at GWU, and I see a strong synergistic potential with several research groups (eg. in general lepidopterology with John Lill, evolutionary genetics with Mollie Manier, and in the study of morphological radiations with several groups). I am also excited by the relative proximity of peppered moth field sites in the Appalachian forests, as well as by the department SEM facility and greenhouses. On more experimental grounds, I am typically inclined to cross-disciplinary interaction, and would like to contribute shared equipment in microscopy and molecular biology that will foster crossovers between labs. I will develop a novel model organism using next-generation tools I am already using successfully (**CRISPR genome editing, RAD-sequencing**), and I expect this expertise will be of strategic importance for other faculty members who want to develop the potential of their organisms of interest. Finally, I am interested in promoting the access of minorities to scientific careers via my teaching responsibilities and roles as a research supervisor, and in using the charisma of butterfly wing patterns to reach broad audiences with my work.

Best Regards,

Arnaud Martin

Curriculum Vitae

French citizen, 31 years old

CONTACT

Arnaud Martin

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APPOINTMENTS AND EDUCATION

- | | |
|-------------------|--|
| June 2014-present | Post-Doctoral Researcher, II
University of California - Berkeley
Advisor: Nipam Patel |
| 2012-2014 | Post-Doctoral Researcher, I
Cornell University / University of California - Irvine
NSF-IOS grant <i>Identity and Function of Heliconius Mimicry Genes</i>
to Robert Reed (PI). Host lab and co-advisor: Thomas Schilling |
| 2007-2012 | Ph.D. in Biological Sciences - Evolutionary Genetics group
University of California – Irvine
Thesis: The developmental genetics of color pattern evolution in
butterflies. Advisor: Robert Reed |
| 2006-2007 | Master in Molecular and Cellular Biology - with Honors
Ecole Normale Supérieure de Lyon
Thesis: Development and diversity of rodent palatal rugae profiles
in rodents. Advisors: Vincent Laudet, Sophie Pantalacci |
| 2003-2006 | License in Molecular and Cellular - with Honors
Ecole Normale Supérieure de Lyon / Université Lyon I |
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AWARDS AND GRANTS

Smithsonian Institute of Tropical Research	Ernst Mayr Fellow 2011	\$5,000
University of California, Irvine	Chancellor's Club Fellow 2012	\$10,000
Society of Developmental Biology	West Coast Best Talk Award 2013	\$1,000
John Templeton Foundation	Main PI on Funded Grant (2014-2017)	\$271,645
<i>Genomic Hotspots of Evolution: pervasive Paths of Least Resistance behind Phenotypic Variation.</i> Administered by co-PI (Virginie Orgogozo) at Institut Jacques Monod, CNRS Paris.		

PEER-REVIEWED PUBLICATIONS

16 articles, 480 citations (h-index = 9)

*: equal contributions

Martin A, Reed RD. *Wnt* signaling underlies evolution and development of butterfly wing pattern symmetry systems. *Developmental Biology*. In press; doi: 10.1016/j.ydbio.2014.08.031

Gallant JR, Imhoff VE, **Martin A**, Savage WK, Chamberlain NL, Pote BL, Peterson C, Smith G, Evans B, Reed RD, Kronforst MK, Mullen SP. Ancient homology underlies adaptive mimetic diversity across butterflies. *Nature Communications* 2014 September; 5(4817)

Kunte K*, Zhang W*, Tenger-Trolander A, Palmer D, **Martin A**, Reed RD, Mullen SP, Kronforst MR. *Doublesex* is a mimicry supergene. *Nature* 2014 March; 507(7491):229-32

Martin A, McCulloch KJ, Patel NH, Briscoe AD, Gilbert LE, Reed RD. Multiple recent co-options of Optix associated with novel traits in adaptive butterfly wing radiations. *EvoDevo* 2014 Feb; 5:7

Orgogozo V, **Martin A**. Evolution and Development: Genes and Mutations underlying Phenotypic Variation. *Oxford Bibliographies Online: Evolutionary Biology* 2014 Jan; doi: 10.1093/obo/9780199941728-0003. Review

Martin A, Orgogozo V. The loci of repeated evolution: a catalog of genetic hotspots of phenotypic variation. *Evolution* 2013 May; 67: 1235–1250. Review

Martin A, Papa R, Nadeau NJ, Hill RI, Counterman BA, Halder G, Jiggins CD, Kronforst MR, Long AD, McMillan WO*, Reed RD*. Diversification of complex butterfly wing patterns by repeated regulatory evolution of *WntA*. *Proceedings of the National Academy of Sciences USA*. 2012 Jul; 109(31):12632-7

The Heliconius Genome Consortium. A butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature*. 2012 Jul; 487(7405):94-8

Reed RD*, Papa R*, **Martin A**, Hines HM, Counterman BA, Pardo-Diaz C, Jiggins CD, Chamberlain NL, Kronforst MR, Chen R, Halder G, Nijhout HF, McMillan WO. *optix* drives the repeated convergent evolution of butterfly wing pattern mimicry. *Science*. 2011 Aug; 333:1137-1141

Martin A, Reed RD. *wingless* and *aristaless2* define a developmental ground plan for moth and butterfly wing pattern evolution. *Molecular Biology and Evolution*. 2010 Dec; 27(12):2864-78

McDonald WP*, **Martin A***, Reed RD. Butterfly wings shaped by a molecular cookie cutter: Evolutionary radiation of lepidopteran wing shapes associated with a derived Cut / *wingless* wing margin boundary system. *Evolution and Development*. 2010 May; 12:296-304

McGowan L, Kuo E, **Martin A**, Monuki ES, Striedter G. Species differences in early patterning of the avian brain. *Evolution*. 2010 Mar ; 65(3):907-11

Pantalacci S, Sémon M, **Martin A**, Chevret P, Laudet V. Heterochronic shifts explain variations in a sequentially developing repeated pattern: palatal ridges of muroid rodents. *Evolution and Development*. 2009 Jul-Aug; 11(4):422-33

Pantalacci S, Prochazka J*, **Martin A***, Rothova M, Lambert A, Bernard L, Charles C, Viriot L, Peterkova R and Laudet V. Patterning of palatal rugae through sequential addition reveals an anterior-posterior boundary in palatal development. *BMC Developmental Biology*. 2008 Dec ; 8(1):116

Papa R*, **Martin A***, Reed RD. Genomic hotspots of adaptation in butterfly wing pattern evolution. *Current Opinion in Genetics and Development*. 2008 Dec; 18(6):559-64. Review

Chevalier S, **Martin A**, Leclère L, Amiel A, Houliston E. Polarised expression of FoxB and FoxQ2 genes during development of the hydrozoan *Clytia hemisphaerica*. *Development Genes and Evolution*. 2006 Nov; 216(11):709

KNOWLEDGE TRANSFER

Teaching Assistant (2007-2008): Physiology Laboratory (Upper Division – taught two Quarters) ; From Organisms to Ecosystems (Core Biology Curriculum – taught one Quarter) – University of California, Irvine

Undergraduate research: Supervised the projects of eight undergraduate students at UC Irvine, including six female students and one male student in the framework of a Minority

Program. Two of these students are now attending Medical Schools and two others are pursuing research careers and attending Graduate School programs at Cornell University and UC Riverside. At UC Berkeley, I am supervising the projects of three undergraduate students. Two of them are working on CRISPR genome editing in crustaceans and will be co-authors on my next publication.

Scientific outreach:

2007 Poster about butterfly evolution for the exhibition “Evolution... Révolution ! De Darwin à nos jours” hosted by the Botanical Garden of Lyon (France).

2010 Dispatch article: **Martin A**, Kapan DD, Gilbert LE. Wing patterns in the mist. *PLoS Genetics*. 2010 Feb; 6(2):e1000822.

2011 Contributed figures for public outreach articles:

- Carroll SB. How great wings can look alike. *Science*. 2011 Aug ; 26;333(6046):1100-1
- Chin A. Disguise genes. *Scientific American Magazine*. 2011 Oct.

2012 Contributed figures for two popular evolutionary biology textbooks:

- Freeman and Herron, *Evolutionary Analysis*, 5th Edition (Prentice Hall)
- Zimmer and Emlen, *Evolution: Making Sense of Life* (Roberts & Company)

Counseled the pre-production of a TV segment about butterfly evolution (*Secrets of our Living Planet*, BBC Production) while stationed at STRI Panama.

2014 Live demonstrations for children on the theme of butterfly biology at the Lawrence Berkeley Hall of Science.

Contributed images for science-inspired art exhibit (BAASIC/Aggregate Space, Oakland, CA)

Referee for the journals *Evolution*, *PLoS One* and *Nature Communications*. Approved co-referee for the journals *Trends in Plant Science*, *Nature* and *Science*.

Invited seminars and workshops:

UC Irvine, Ecology and Evolutionary Biology Department seminar series (2008, 2010)

6th International Conference on the Biology of Butterflies, Edmonton (2010)

Smithsonian Tropical Research Institute seminar series, Panama (2011)

4th Conference of the Eur. Soc. for Evolutionary Developmental Biology, Lisbon (2012)

Indiana University, Bloomington – EvoDevo Faculty Search Seminar (2014)

University of Arizona, Tucson – Evolutionary Genetics Faculty Search Seminar (2014)

San Diego State University – Evolutionary Genetics Faculty Search Seminar (2014)

University of Hawaii, Manoa – EvoDevo Faculty Search Seminar (2014)

International Heliconius Symposium, Puerto Rico (2014)

Fondation des Treilles – “Mechanisms of Evolutionary Change” (invited, 2015)

COLLABORATORS

Recent Collaborators: Nipam Patel (UC Berkeley), Lawrence Gilbert (UT Austin), Thomas Schilling (UC Irvine), Owen McMillan (Smithsonian Tropical Research Institute), Tony Long (UC Irvine), International Heliconius Genome Consortium, Virginie Orgogozo (Institut Jacques Monod, Paris), Marcus Kronforst (University of Chicago), Sean Mullen (Boston University), Adriana Briscoe (UC Irvine). **Undergraduate and Graduate Advisors:** Evelyn Houlston (Observatoire de Villefranche-sur-Mer and Université Pierre et Marie Curie), Patricia Beldade and Paul Brakefield (Leiden University), Sophie Pantalacci and Vincent Laudet (Institut de Genomique Fonctionnelle de Lyon), Robert Reed (UC Irvine)

LANGUAGES

French (native), **English** (fluent), **Spanish** (basic knowledge)

SIDE INTERESTS

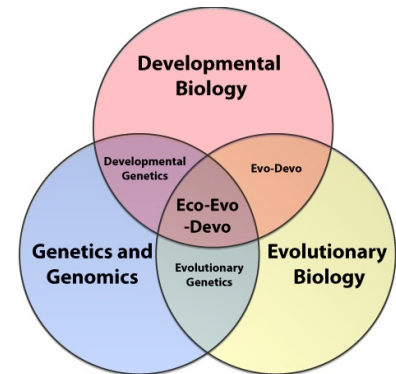
Hiking, Field Entomology, Saxophone, Literature.

Research Statement

What are the mutations and mechanisms that underlie phenotypic evolution?

Eco-Evo-Devo – linking genetics, developmental and evolutionary biology to better explore the genotype-phenotype map and understand how it generates diversity.

A comprehensive understanding of biodiversity requires the identification of **the genes and mutations that underlie differences** between individuals, populations and species in the wild. **Butterflies and moths** form a pinnacle of morphological variation and are a model of choice for this research agenda. My work with these organisms **aims at bridging the gap between developmental biology and population genetics**, as well as developing community-oriented tools for **functional genomics and meta-analysis**.



I have been perfecting the methods allowing gene expression profiling in butterfly wings for nine years, and my developmental expertise is continuously solicited by various research groups (past and ongoing collaborations with Marcus Kronforst and Sean Mullen in the US; Chris Jiggins, Ilik Saccheri and Mathieu Joron in Europe; Krushnameg Kunte in India). This testifies for a vacant niche in the world of butterfly biology that I am keen to occupy and enrich. Currently, I am working hard on the next logical step (from gene *expression* to gene *function*), by taking advantage of the **CRISPR/Cas9 genome editing technique** to induce targeted mutations in lepidopteran genomes.

Main Theme: Evo-Devo of Butterfly and Moth Wing Patterns



1- The developmental toolkit of wing patterning in butterflies and moths. Color patterns form diverse and relatively simple phenotypes that can be used as a proxy of morphological evolution. I have been accumulating a large comparative dataset demonstrating that two **genes of the Wnt pathway (*Wnt1* and *WntA*) drive the development and evolution of a conserved set of wing patterns in both butterflies and moths**. While

this work sheds light on the modes of evolutionary tinkering behind the tremendous diversity of wing patterns at various phylogenetic levels, I have only started to scratch the surface of a fascinating developmental system. First, I will screen the wing expression of classical developmental gene candidate pathways and pigment synthesis genes in order to expand the patterning toolkit known to date. Second, I will functionally test the developmental function of the genes showing an association with color patterns by

CRISPR/Cas9 mutagenesis. In parallel, I will functionally test the effects of known *cis*-regulatory mutations that have repeatedly triggered spatial shifts of *WntA* expression in butterflies. This later part aims at deciphering the first-steps of morphological evolution at a sequence-level by taking advantage of the power of butterfly hybrid zones to detect smoking guns of selection (eg. for *WntA* in various species: Nat. Comm. 2014 ; Nadeau et al. Genome Res. 2014 ; and work in progress)



2- A new model organism for routine transgenesis in Lepidoptera.

The use of butterflies and moths (Lepidoptera) as model systems in biology has been limited by the lack of a laboratory model suitable for genome editing and the long-term maintenance of many lines. Here I propose to make this breakthrough by using the moth *Ephestia kuhniella*

as a laboratory model. Much like the flour beetle *Tribolium castaneum*, this flour moth is resistant to drought and inbreeding, each female lays hundreds of injectable eggs, and mature adults develop in less than 3 weeks. *Ephestia*'s low-maintenance needs make it ideal for establishing mutant and transgenic lines and easily share them between labs for follow-up characterization. I will dedicate significant efforts to the development of this model organism by developing **CRISPR/Cas9 genome editing** (gene knock-out; GFP-fusion proteins ; insertion and reporter expression of regulatory sequences in a heterologous context). This technical work is synergistic with the more hypothesis-driven Projects 1, 3 and 5.



3- Genetic basis of industrial melanism in peppered moths. Industrial

melanism in peppered moths represents perhaps one of the most emblematic examples of natural selection in action. Recent work by the group of Ilik Saccheri (University of Liverpool, UK) has pinpointed a genomic region of about 30 genes bearing the mutation that was responsible for the melanic phenotype, which was advantaged by tree bark

darkening during the English industrial era. I will actively collaborate with this group to identify and characterize the exact genetic mechanism that underlies this polymorphism, using an *in situ hybridization* screen as well as functional testing in a heterologous context (*Ephestia* moths, see Projects 1-2). Finally, I will also test whether **melanism shares a similar genetic basis between European and American peppered moths** (collecting trips in Virginia, in collaboration with Bruce Grant). This work aims at completing our knowledge of a textbook example of evolution, and should also yield many insights into the genetics of adaptation and convergence.

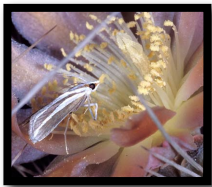
Other Projects

These “side” projects will go beyond the main focus of my lab on wing patterns. They combine a potential for high-profile discovery and reasonable time frames that could fit into a Senior or Master Thesis project.



4- Meta-analysis of the “Genes of Evolution” across Eukaryotes. We need important efforts of synthesis in biology, and taxon-specific observations are vain if they are not integrated into a broader picture. I curate a large dataset summarizing the published literature on the genetic basis of phenotypic evolution in Eukaryotes (article in *Evolution* 2013 and ongoing progress: more than a 1,000 entries so far). In collaboration with

Virginie Orgogozo (CNRS-Paris), I received funding to generate and maintain **an online database of genetic evolution** that will compile most of our knowledge about genotype-phenotype relationships in nature. Our goal is to provide geneticists with a rich template for pattern extraction and hypothesis testing (e.g. *Are there many genetic answers to the same selective pressure? Are there emerging principles that unify or distribute processes into defined categories, such as sensory, morphological, or behavioral evolution? To which extent natural evolution and domestication differ in their underlying genetic basis?*). I will encourage every student/post-doc in my lab to start a meta-analytical project based on the growing database, with the dual goal to publish an original review article and acquire a comprehensive knowledge of the literature relevant to their topic of interest.



5- Testing the parallel evolution of dependence to the senita cactus.

The genetic mechanism responsible for the dependence of *Drosophila pachea* to the Sonoran Desert senita cactus was recently revealed (Lang et al. *Science* 2012), and involves a loss of function in the cholesterol metabolism gene *Neverland*. Interestingly, the senita moth *Upiga virescens* is also dependent to the senita (this interaction often features in ecology

textbooks, as the moth is both a parasite and the main pollinator of the senita). In collaboration with Virginie Orgogozo (last author on the *D. pachea* study), I will test the hypothesis that evolutionary dependency to the senita cactus *independently evolved* by modifications of the cholesterol biosynthetic pathway in the fly and moth lineages, thus testing the relative predictability implied by the observation of *genetic hotspots of evolution* (*Evolution* 2013). While we can not easily envision a senita moth colony in the lab, **this project will benefit from the closely-related *Ephestia* laboratory model for functional testing using CRISPR (Project 2).**

Strategy for extra-mural funding

Projects 1 and 2 will start immediately using start-up funds in order to generate preliminary data and I plan to submit grant proposals about one year after the beginning of my appointment. Importantly, I am already working on important aspects of these projects, with the long-term goal to perform **CRISPR/Cas9 genome editing** in non-model organisms. The first step was to assess the suitability of CRISPR in generating informative morphological phenotypes.

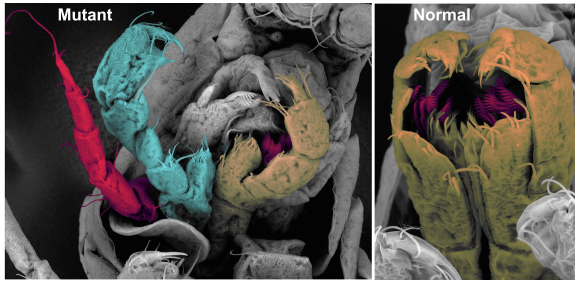


Figure (manuscript in preparation): Mosaic homeotic transformations of *Parhyale* mouthparts into thoracic appendages by induced CRISPR-mutagenesis of the Hox gene *Scr*. The mutant animal shows maxilla-to-leg (red) and maxilliped-to-claw transformations (blue) on its right side. *Scr* is specifically expressed in these segments during embryogenesis.

Shortly after I joined the Patel Lab (June 2014), I generated CRISPR G0 knock-outs of six Hox genes in *Parhyale hawaiiensis*, a crustacean model for arthropod evo-devo. The technique outperformed all my expectations in terms of efficiency (6 genes knocked-out in 2 months; phenotypes in up to 60% of individuals surviving the injection), showing great promise for my butterflies and moths.

My primary goal in the next months will be to adapt CRISPR to 1- *Junonia coenia*, a butterfly species entirely reared in the lab, with the perspective to generate mosaic wing knock-outs in the injected generation (*ie.* as in the *Parhyale* Hox mutants); **2- *Ephestia* moths**, with the goal to generate mutant lines for long-term maintenance, a prospect that would be unreasonable with butterflies themselves. I will visit in Winter 2015 the lab of Paul Shirk (USDA Gainesville), benefiting from his experience with *Ephestia* transgenics to learn the rearing and injection protocols specific to this species. I expect **Project 2** to yield diverse funding opportunities (**NSF-IOS and USDA**) once the first modified lines will have been generated.

Project 3 should create a certain enthusiasm and will be submitted as NSF-IOS and –DEB proposals, with preliminary data emerging from Projects 1 and 2. In addition, it would fit into **collaborative grant proposals** at the US or international levels (*eg.* NSF, Human Frontiers). The genetics of industrial melanism involve an important population genomics component, and I am in contact with the research groups that will be competent to collaborate on these aspects (Ilik Saccheri in the UK; or other US labs such as the Kronforst / Counterman / Mullen labs).

Project 4 is already funded (Templeton Foundation, Grant Competition “The Meanings of Convergence”: 270,000 USD), and I plan to submit a proposal for its renewal in 2017.

Project 5 requires little funding and will be ideal for applications to small awards (travel grants, graduate student fellowships, EDEN network). I collected samples from Baja California in April 2014 that are immediately available for deep transcriptome sequencing by RNAseq.

Teaching Philosophy

Experience. I have been teaching Organismal Biology and Physiology classes as a Teaching Assistant at University of California Irvine for 3 quarters total. Across terms, my personal evaluation scores averaged **3.4 on a 4.0 scale**, which was quite strong for my first year living and teaching in an English-speaking country. Anonymous student evaluations included:

- *“Arnaud is very caring and tries to tend to his student's needs. I like that he is very helpful during lab as well as outside of class. I am not afraid to ask him questions or for help because he is always straightforward and makes things much clearer for me to understand. Also, he is easy to understand even with his accent.”*
- *“He does a great job on explaining hard concepts and he tries to think of examples other than the ones used in the books or in lecture.”*
- *“I loved going to discussion. Arnaud is a great teacher”*

General approach. My overarching goal during a class is to maintain the students focused, and biology can allow many side interventions (short videos, interactivity with the students, live demonstrations) that should **break the routine of colloquial teaching**, refreshing the attention of the audience towards sequences of more knowledge-dense materials. Whenever possible, I incorporate examples to which the students can relate (e.g. connections with human biology, technological analogies, references to pop-culture, animal or plant “fun facts”), short quizzes on reading material, or open topic homework based on online resources (GeneBank/Ensembl, PubMed, Tree of Life, FlyAtlas). In addition, I want to introduce the students to **contemporary research** so they are prepared to work with the tools of tomorrow (genomic sequencing, genome editing, imaging...), while also becoming more aware of **other career paths than med school** in conservation biology, academic research, and biotechnologies.

Finally I want to make sure my students become agents of reason and good thinkers. I often put emphasis on **basic scientific principles** of general importance (e.g. differences between cause and correlation; what is a scientific theory; *absence of evidence is not evidence of absence*; basic rules of logic).

In a few words, I would like each lecture **1-** to alternate information-heavy and entertaining content; **2-** to be interactive; **3-** to make a large use of examples, analogies, and recent research advances; **4-** to transfer elements of scientific concepts and methods that student can apply broadly.

Spectrum of topics. **Genetics, Genomics, Evolution, Zoology, and Developmental Biology at any level.** At advanced levels, I would like to craft an Evolutionary Genetics course with large section on applications such as **Personal Genomics**, where students would notably get to understand and analyze sequence data a la “*23andme*”, and understand the future ethical and scientific challenges of genetic sciences.

I will also put a strong emphasis on humans if I get the opportunity to teach **an Evolutionary Developmental Biology course**. This class would combine selected readings from two books: **1-** *Evolution: a Developmental Approach* by Wallace Arthur, which excels at explaining general concepts with a wealth of natural examples; and **2-** *Quirks of Human Anatomy: an Evo-Devo Look at the Human Body* by Lewis Held Jr, which focuses on how our own singularities make sense at the light of historicity and generative processes. In my experience, student performance is transcended when they can re-propagate themselves the class material to their family and friends.