

Speciation and hybridisation

Part 1: The quest for Isla de Muerta

Simon Martin

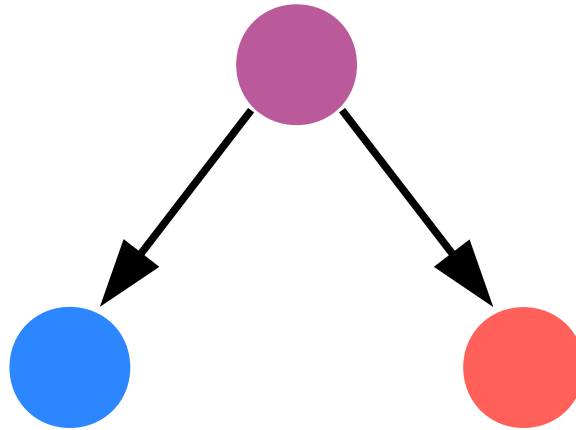
Institute of Evolutionary Biology
University of Edinburgh

January 2020

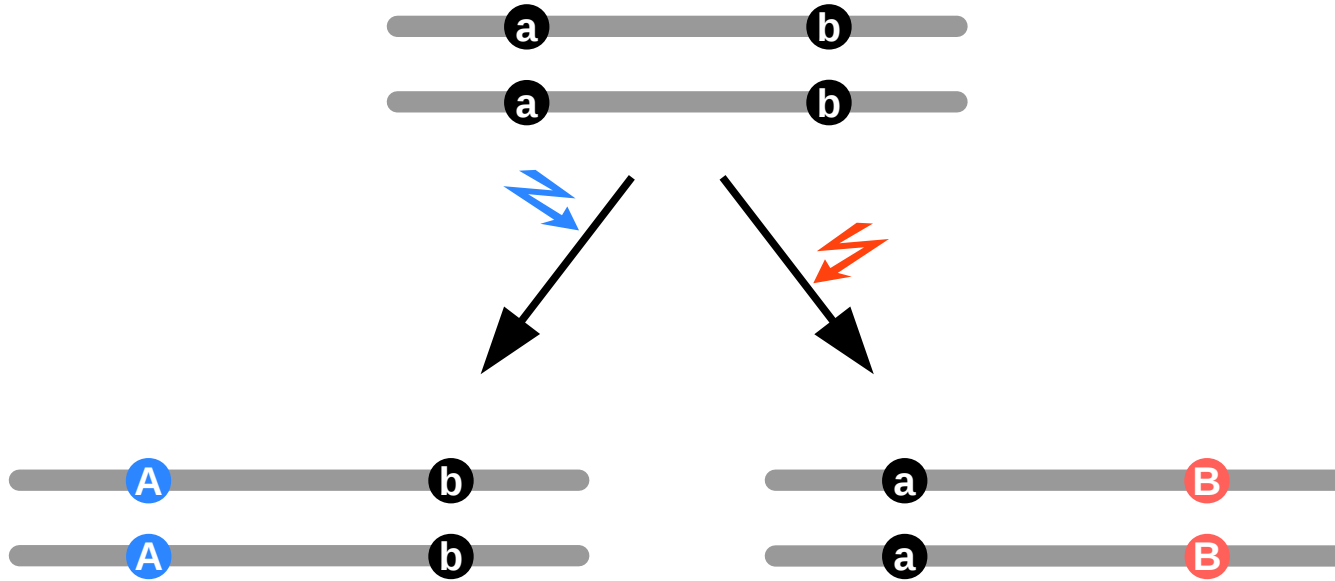
Using genomics to study reproductive isolation

pattern vs **process**

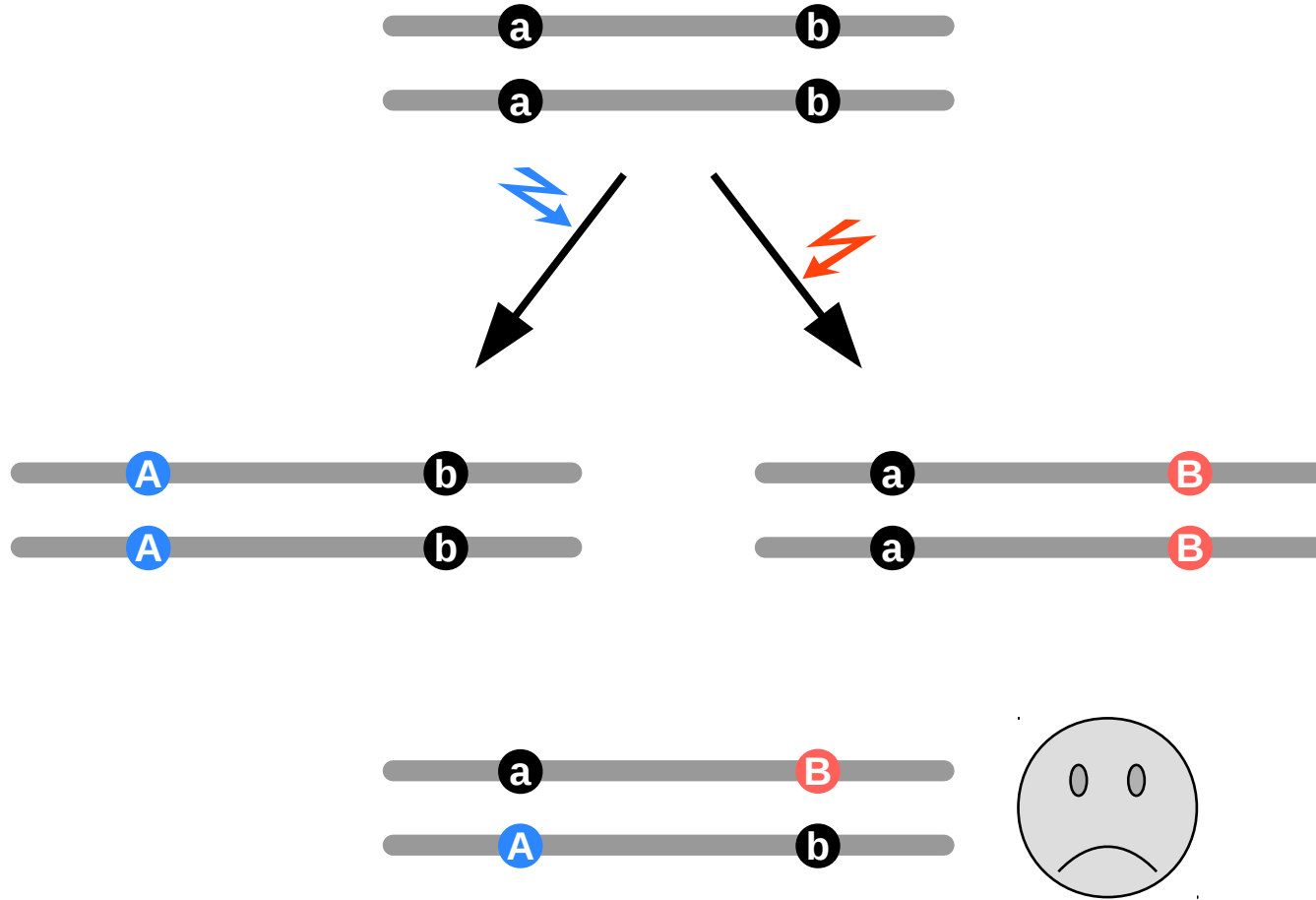
Some models of speciation
through the evolution of reproductive isolation



“BDMIs”



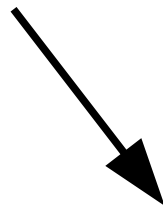
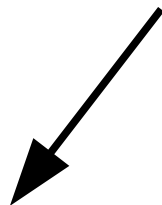
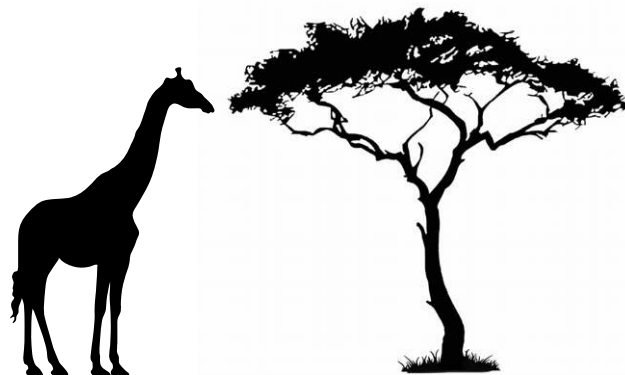
“BDMIs”



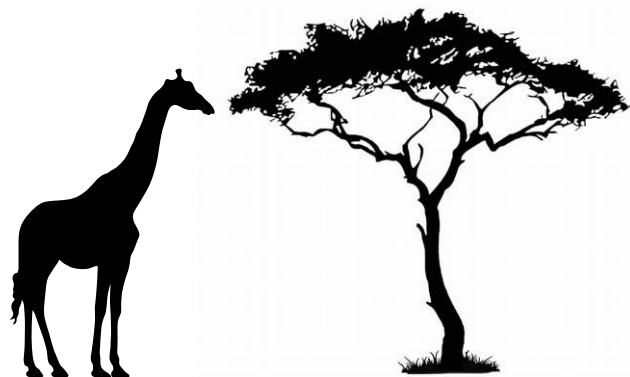
Bateson 1909, Dobzhansky 1937, Muller 1939, Orr 1996

Indirect interaction models

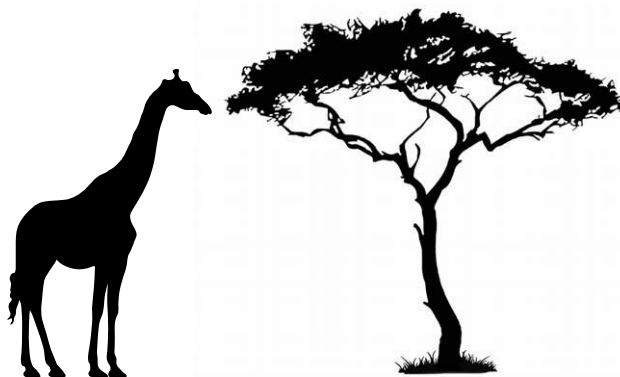
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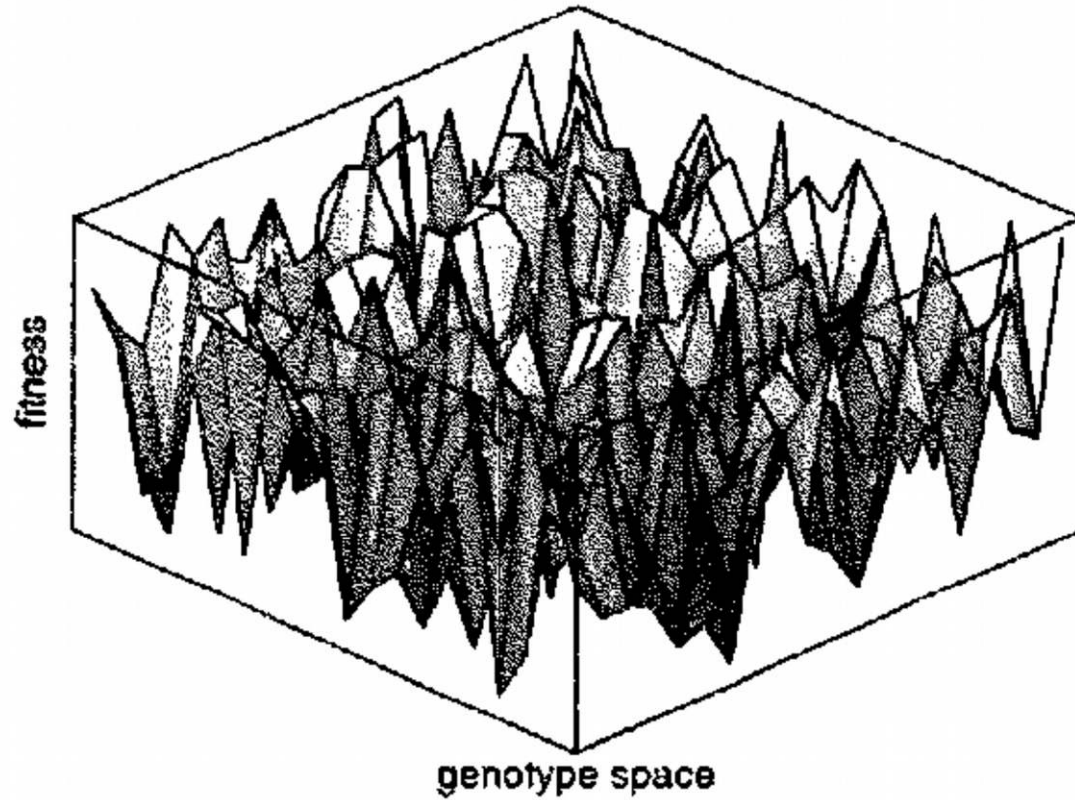
+5 +15 -30 +10
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-20 +5 +15
a b C d e F g h I j ...

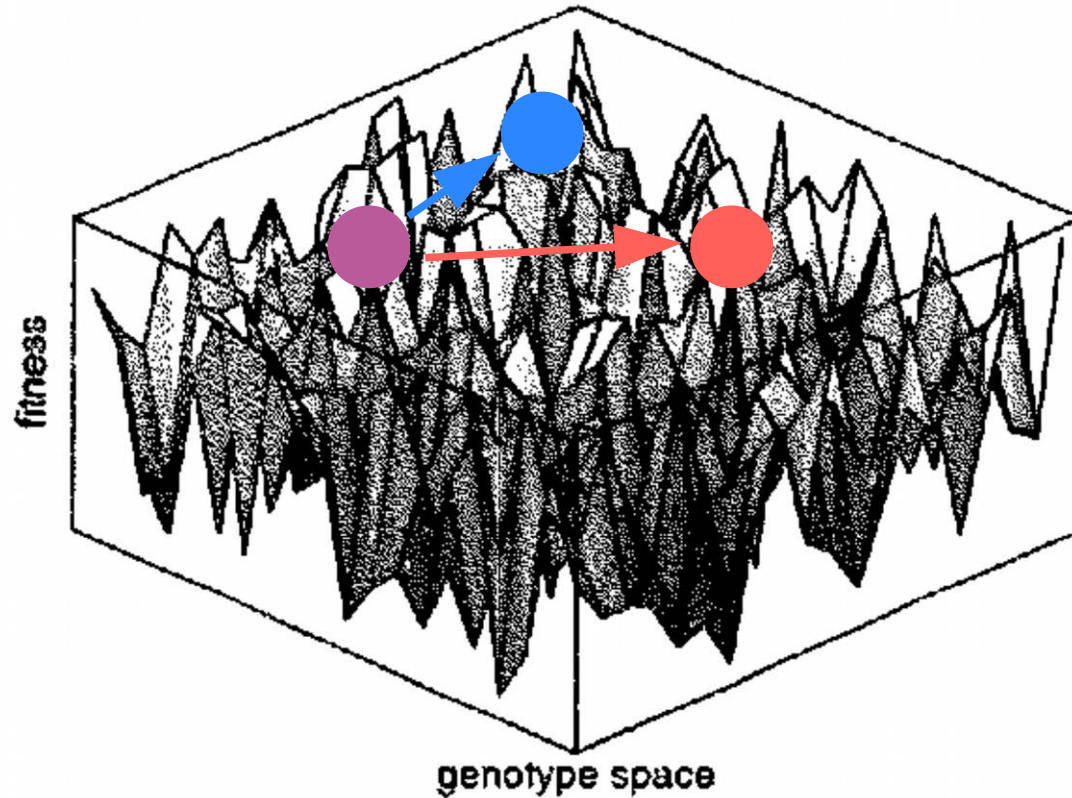


The fitness landscape



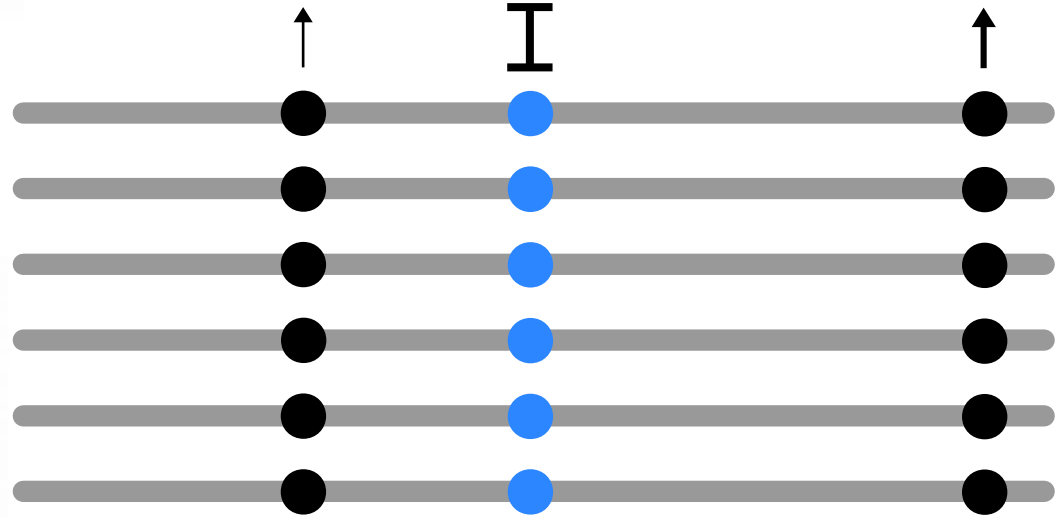
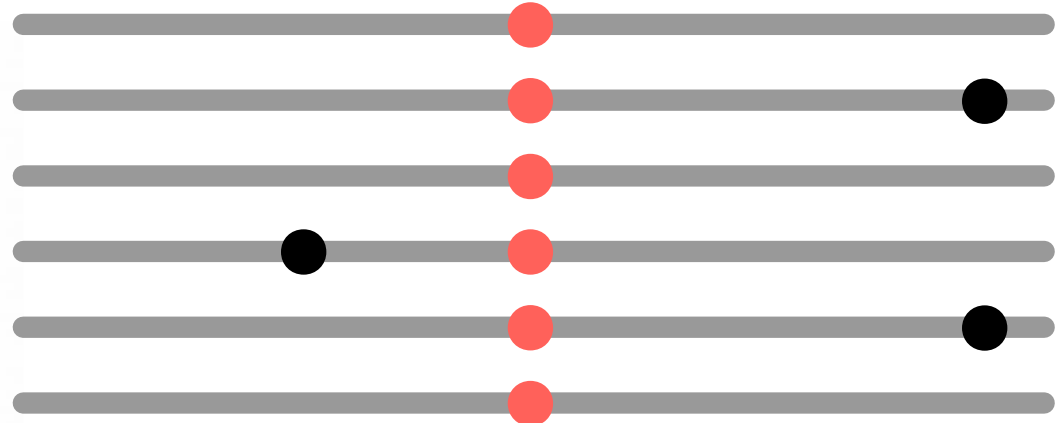
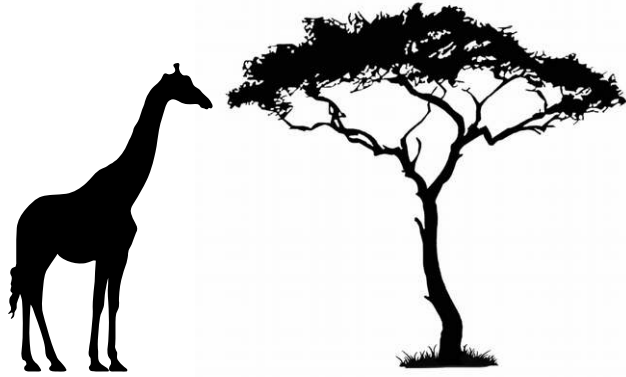
Gavrilets 1997, Wright 1935, Barton 1989, Fierst and Hansen 2010

Drift on the fitness landscape can lead to reproductive incompatibility

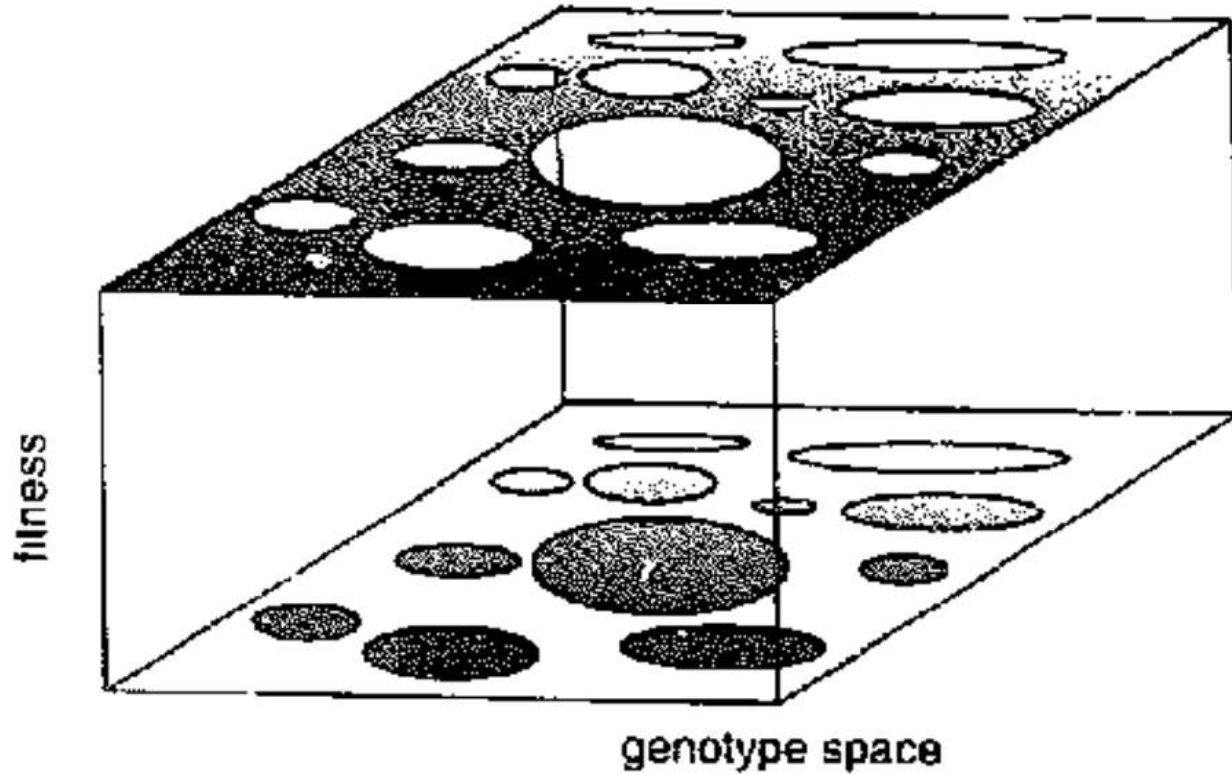


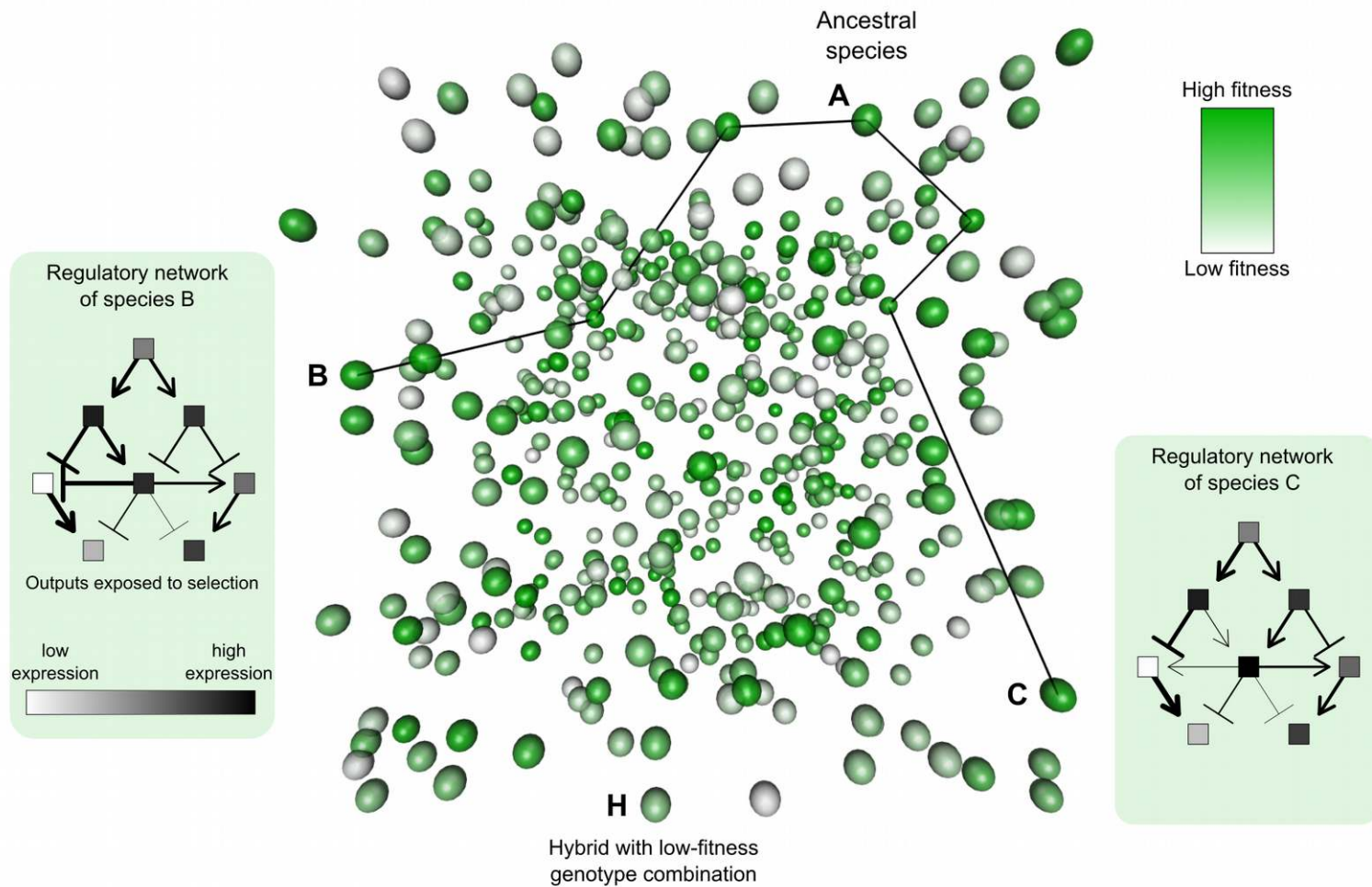
Gavrilets 1997, Wright 1935, Barton 1989, Fierst and Hansen 2010

Local adaptation creates “barrier loci”

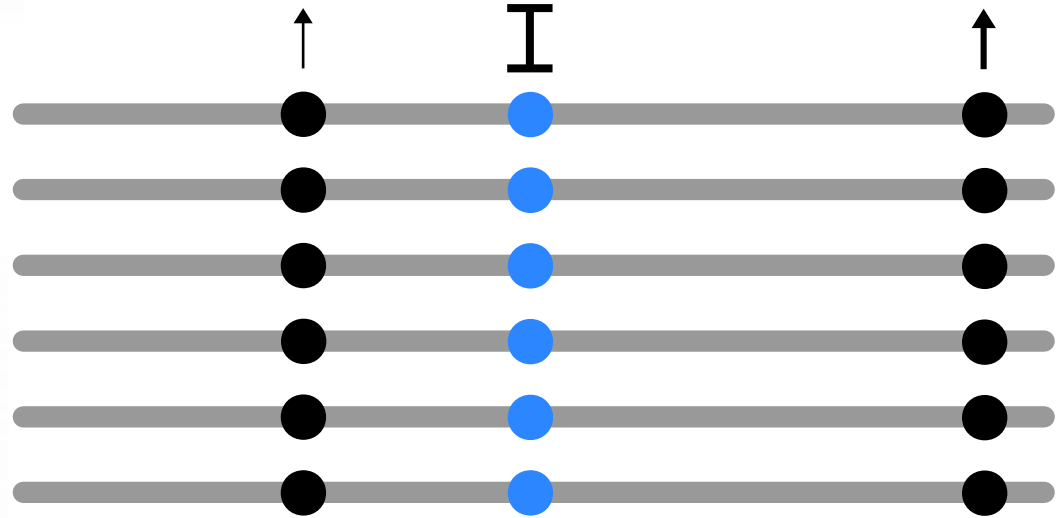
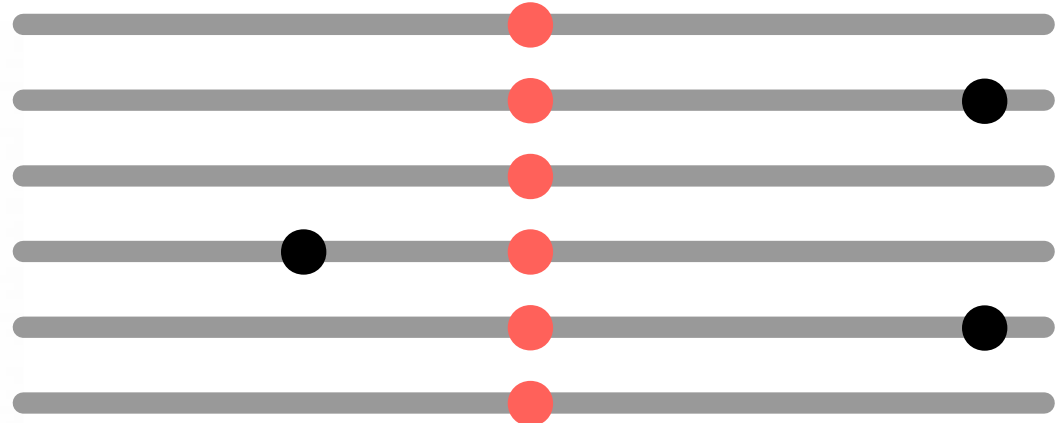
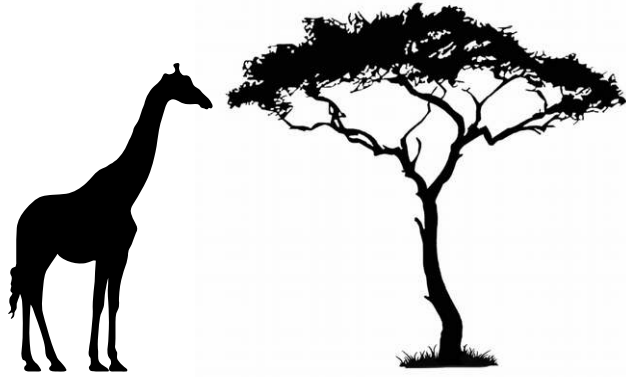


...and polygenic fitness landscapes could make drift very easy

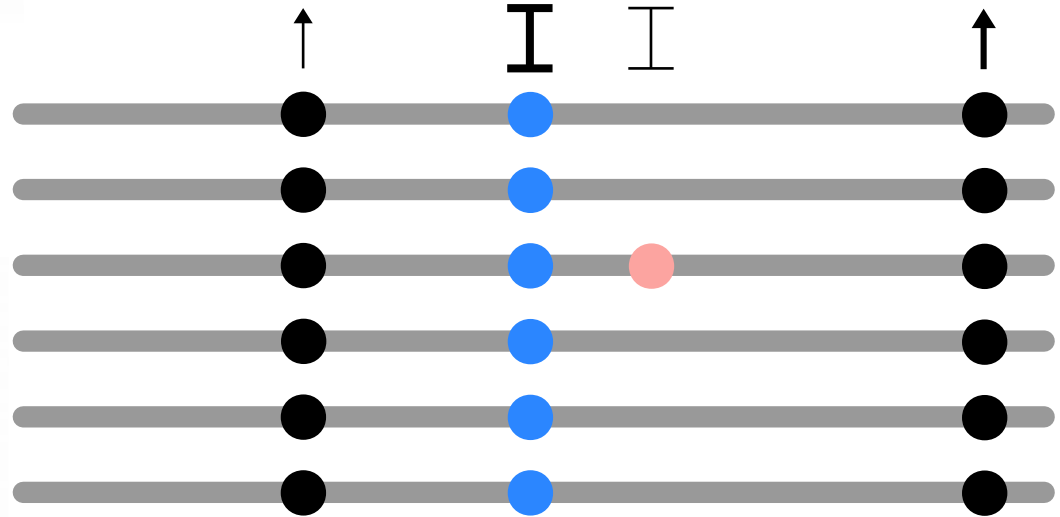
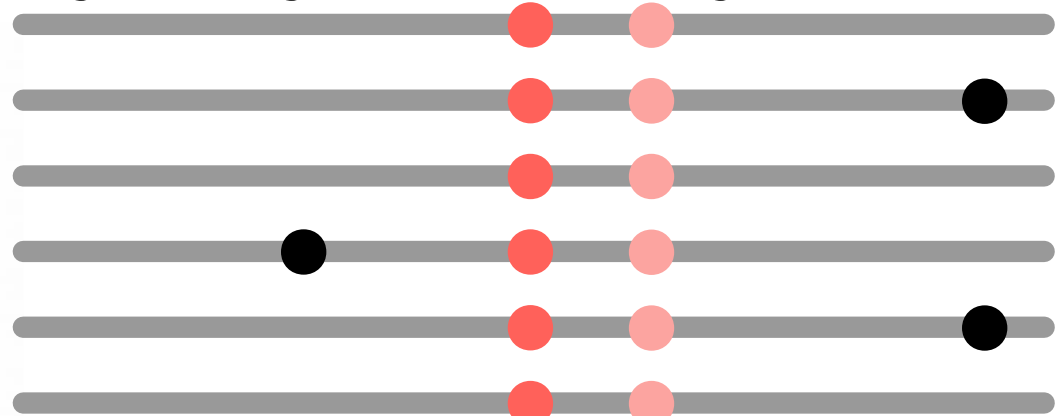
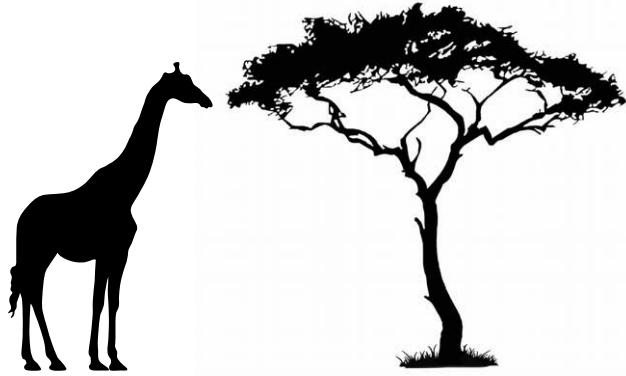




Local adaptation creates “barrier loci”

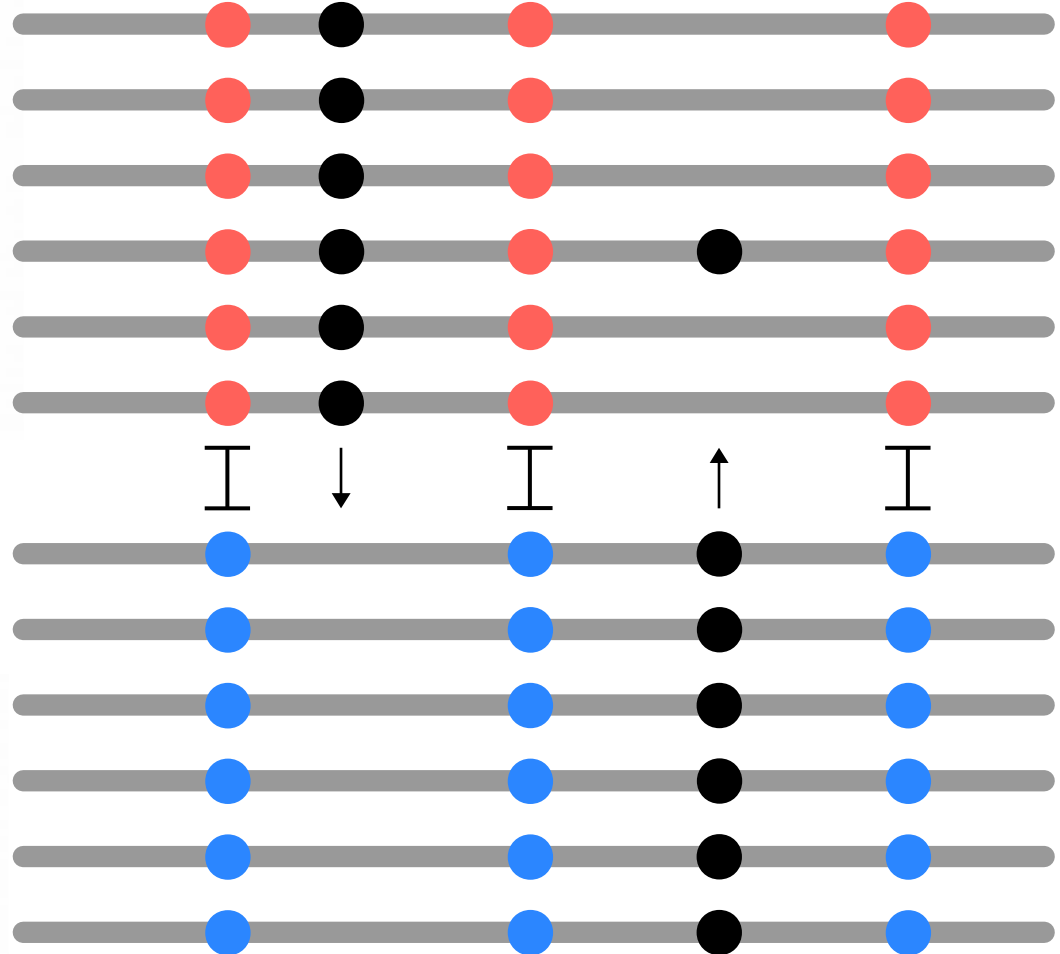
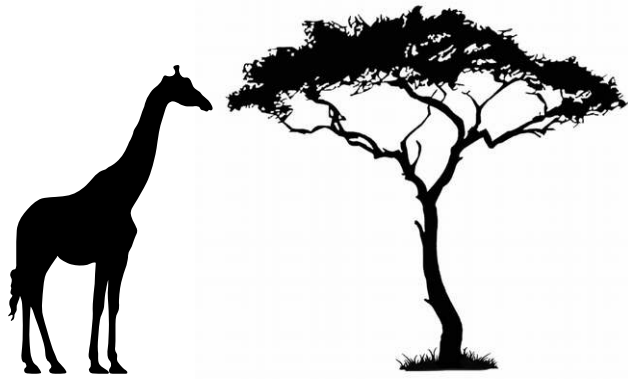


Barrier loci could grow through divergence hitchhiking

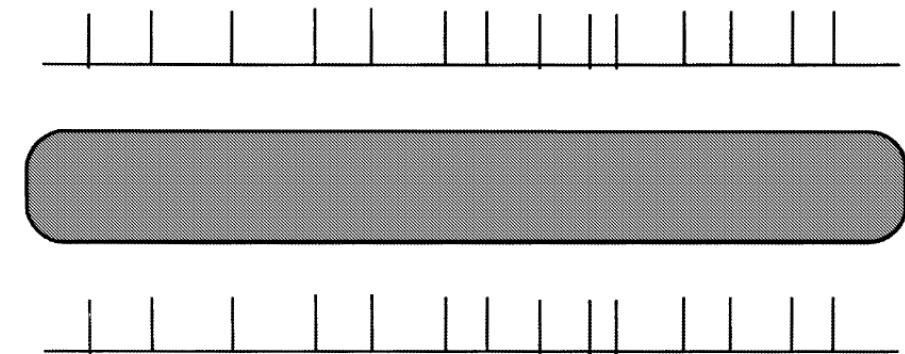
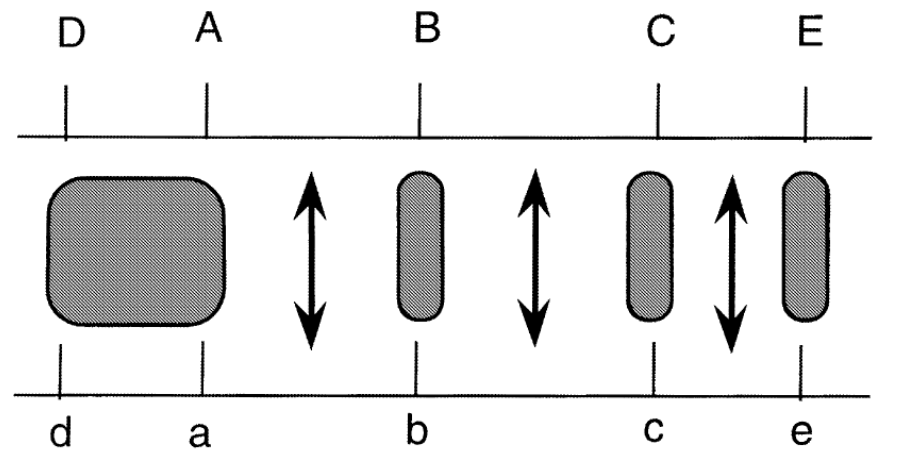
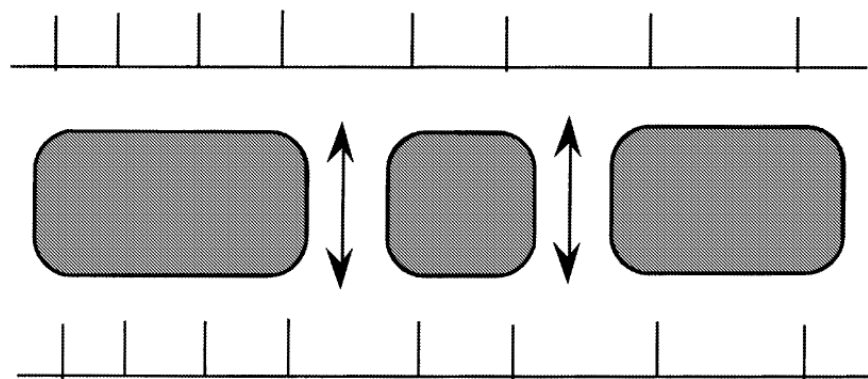
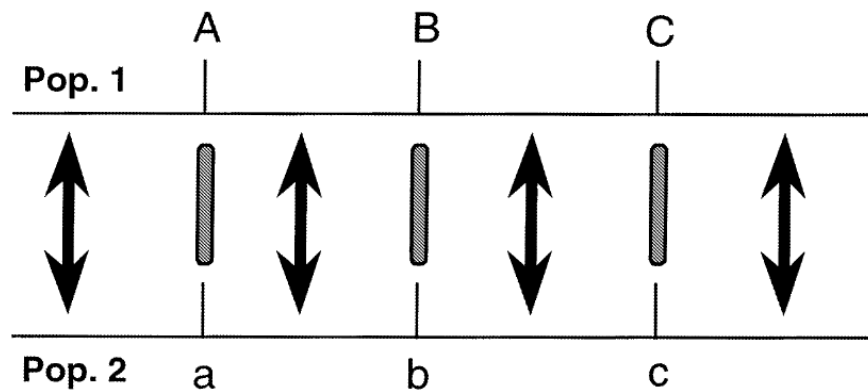


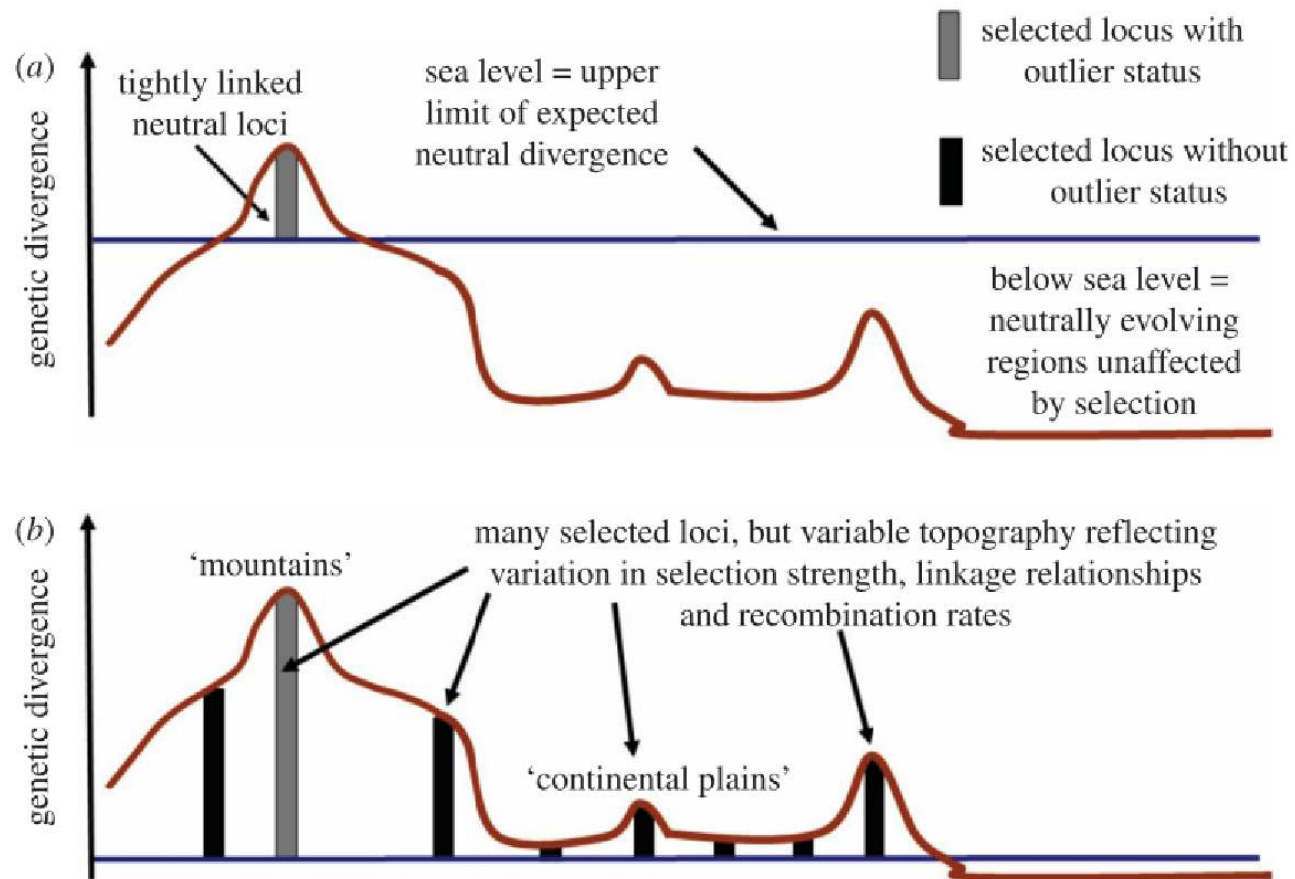
Navarro and Barton 2003, Yeaman & Whitlock 2011, Via et al. 2012, Feder et al. 2012
Flaxman et al. 2013, Aeschbacher and Bürger 2014, Yeaman et al. 2016, Rafajlović et al. 2016

Many barrier loci create a genome-wide barrier



Barton 1983, Barton & Bengtsson 1985, Baird 1995, Flaxman et al. 2014
Tittes & Kane 2014, Nosil et al. 2017, Aeschbacher et al. 2018







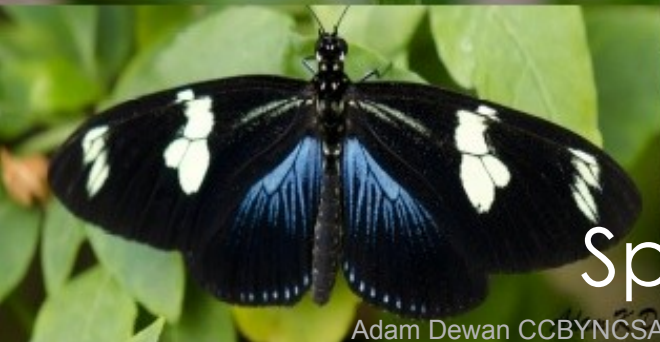
Roberto Monroy CCNC



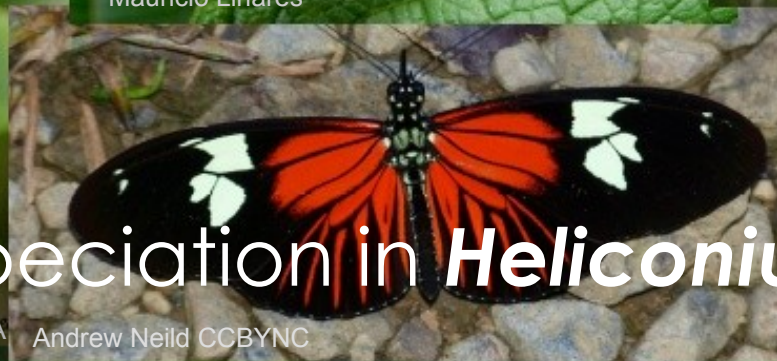
Mauricio Linares



Mauricio Linares



Adam Dewan CCBYNCSA



Andrew Neild CCBYNC



Juan Guillermo Montañés
and Mauricio Linares



Pavel Kirillov CCBY



Carol Hunt CCBYNCSA



That Bee (Flickr) CCBYNCND

Speciation in *Heliconius*



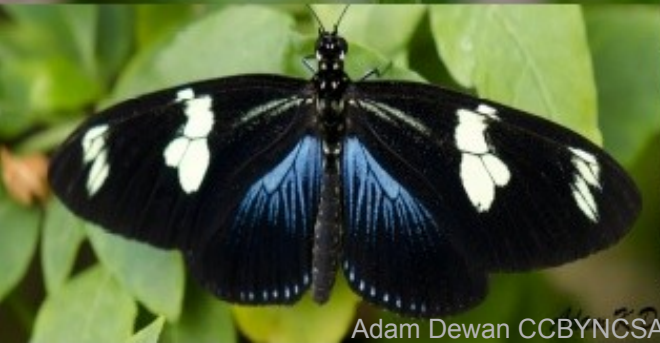
Roberto Monroy CCNC



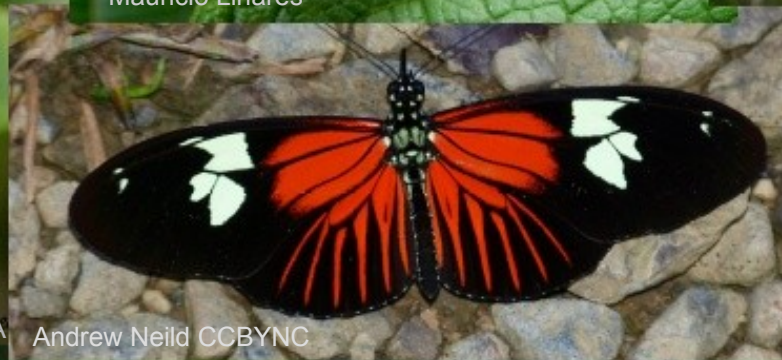
Mauricio Linares



Mauricio Linares



Adam Dewan CCBYNCSA



Andrew Neild CCBYNC



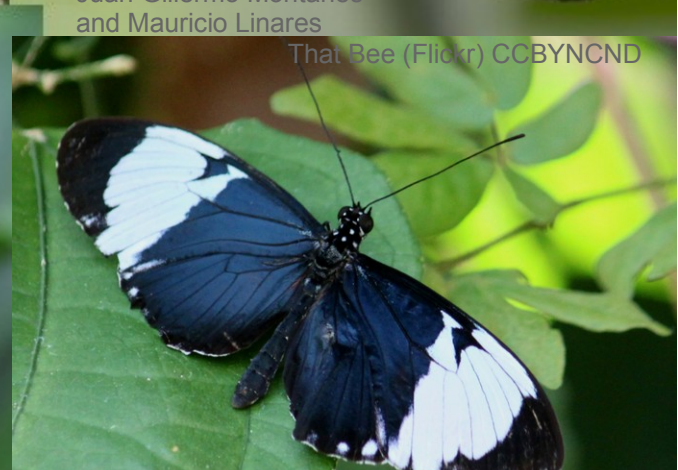
Juan Guillermo Montañés
and Mauricio Linares



Pavel Kirillov CCBY



Carol Hunt CCBYNCSA



That Bee (Flickr) CCBYNCND

Heliconius **Races**



Carol Hunt CCBYNCSA

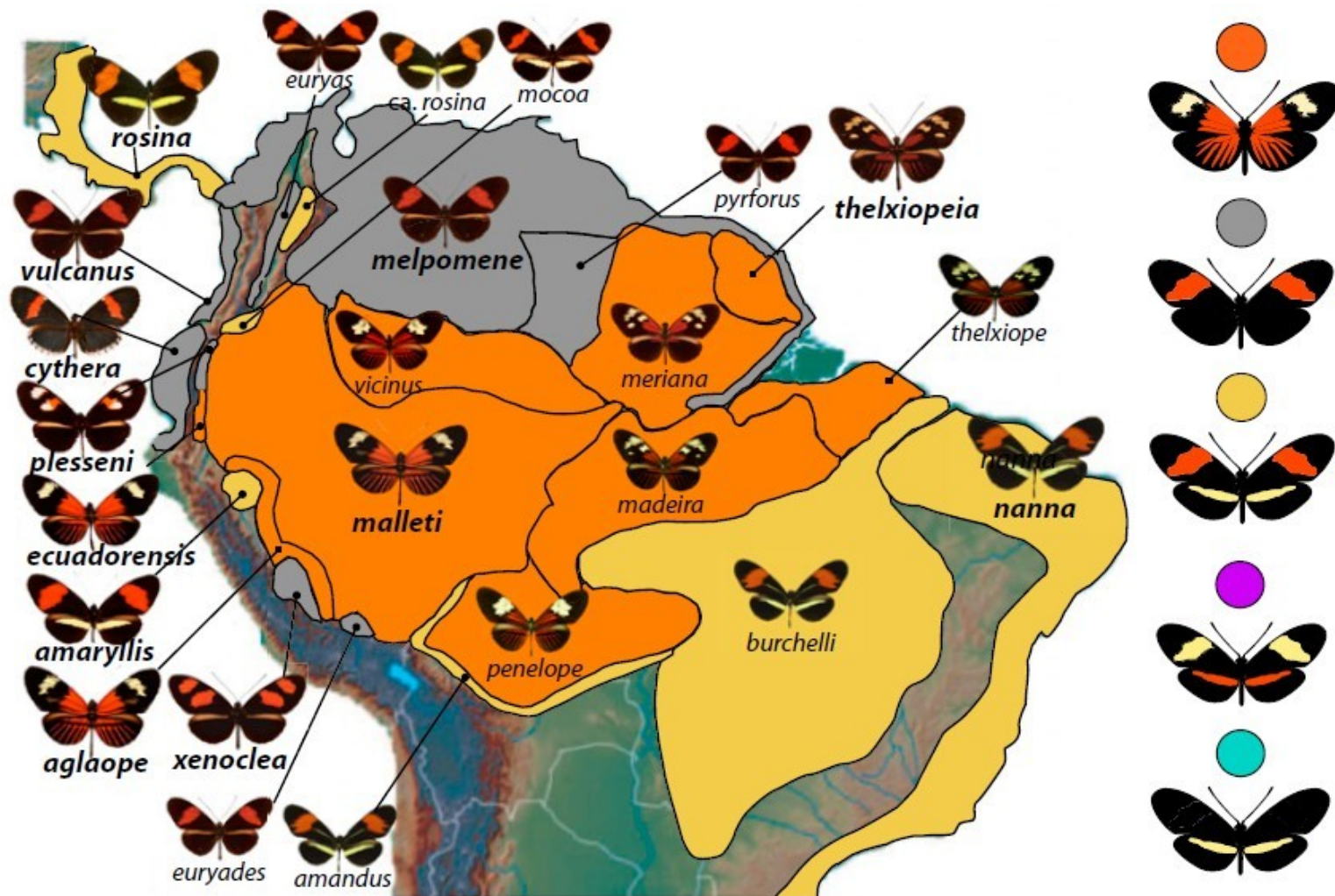
H. melpomene rosina

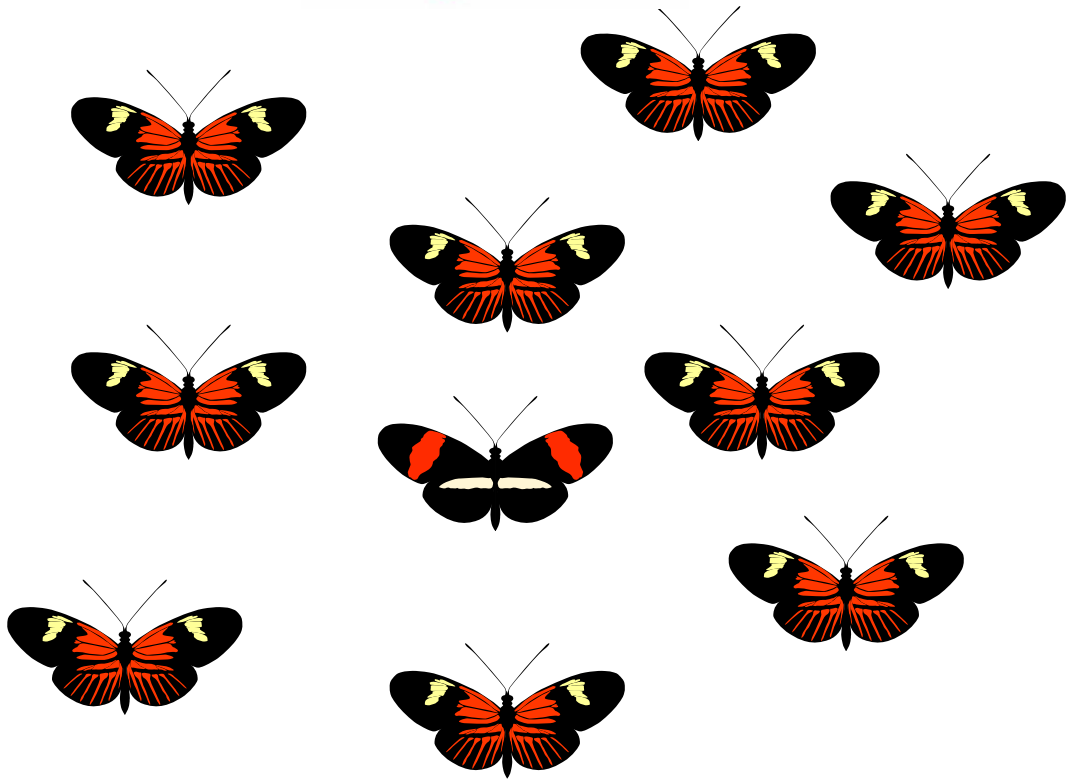
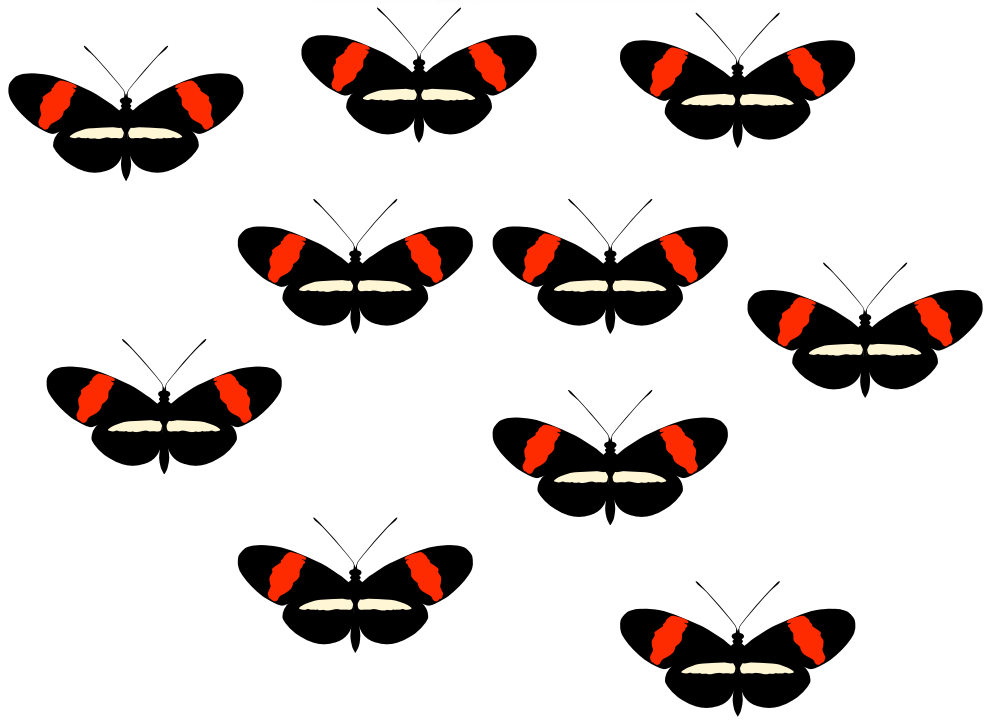


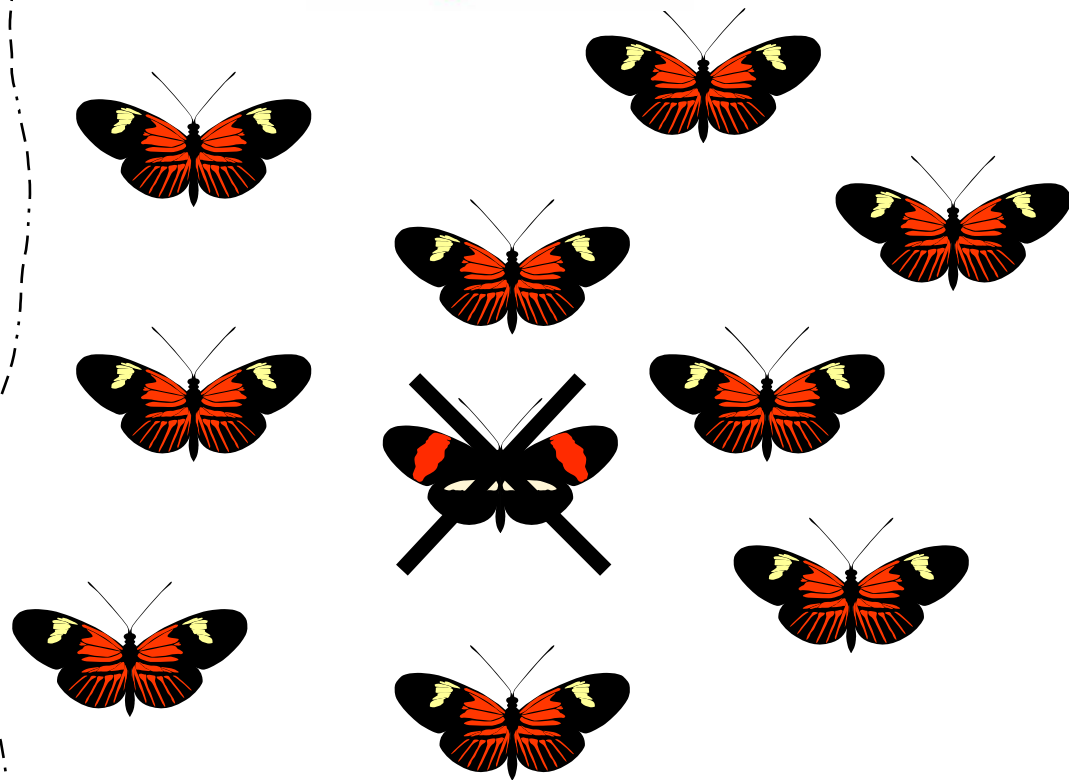
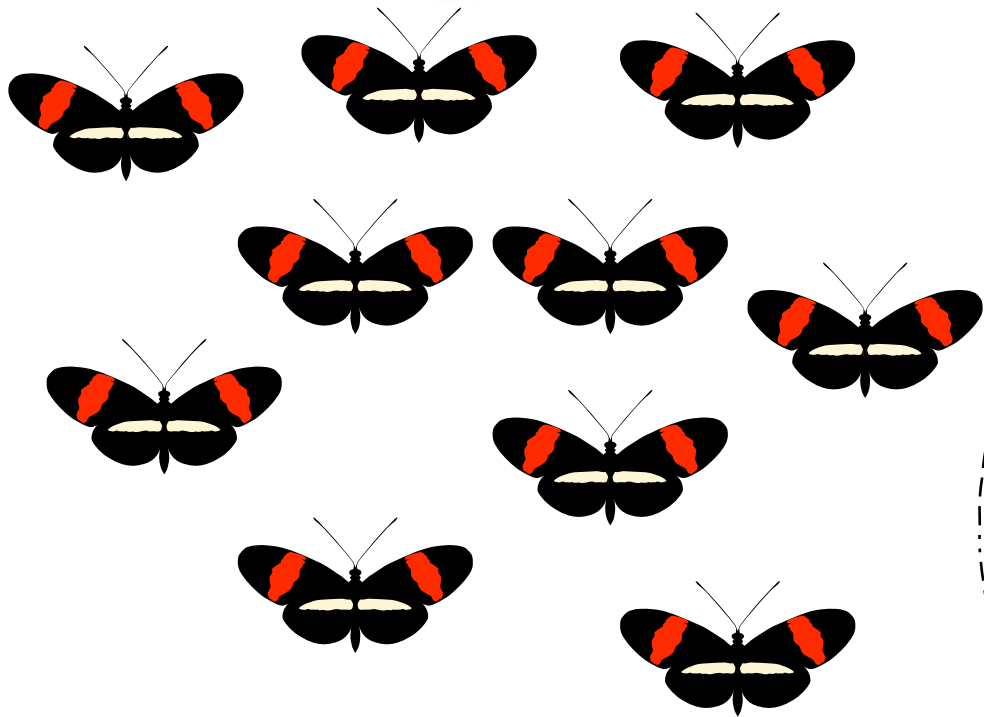
Mauricio Linares

H. melpomene malleti

Races of *H. melpomene*







chromosome 18

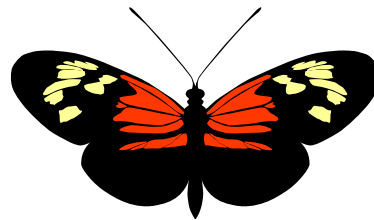
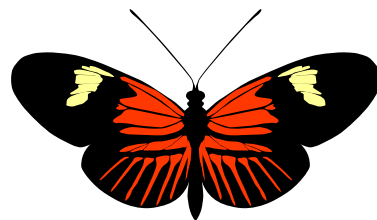
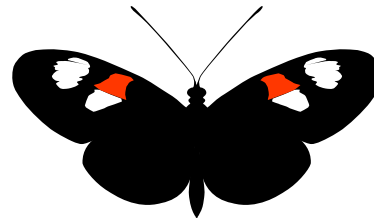
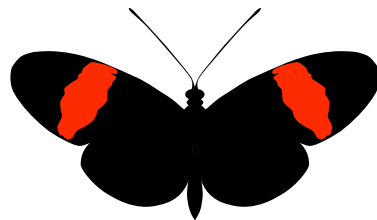
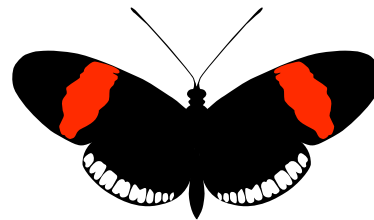
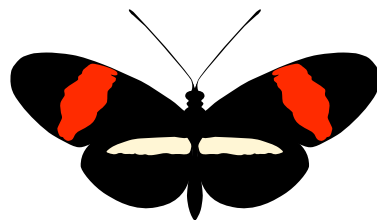
optix

chromosome 10

wnt-A

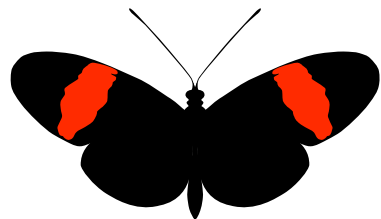
chromosome 15

cortex



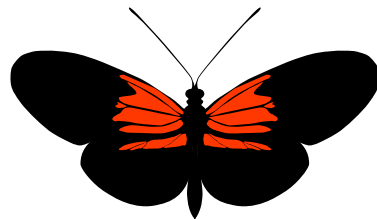
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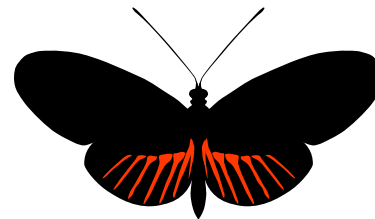
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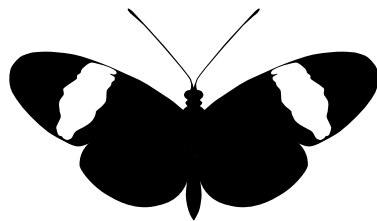
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cortex



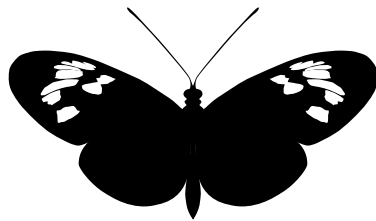
chromosome 18

optix



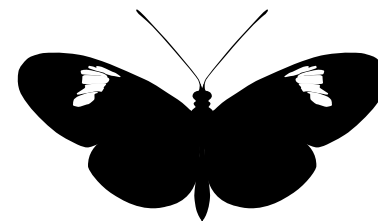
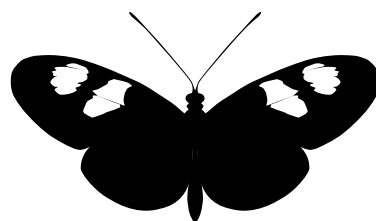
chromosome 10

wnt-A



chromosome 15

cortex



chromosome 18

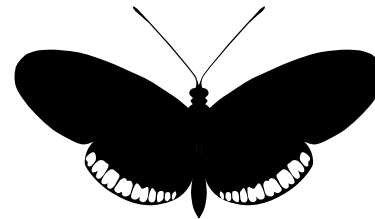
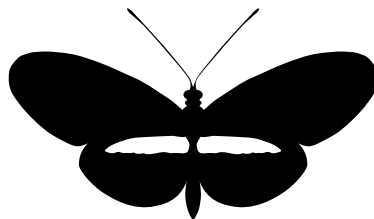
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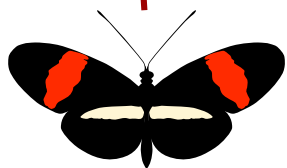
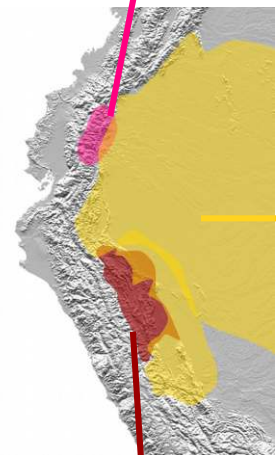
chromosome 10

wnt-A

chromosome 15

cortex





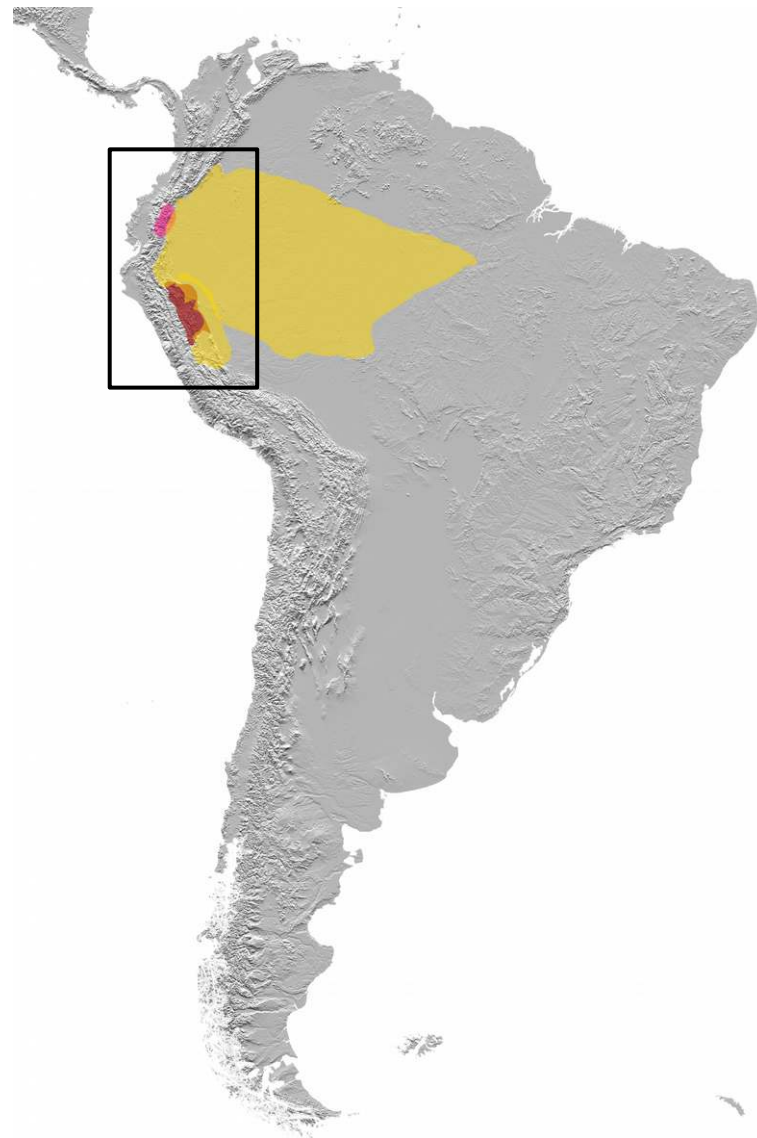
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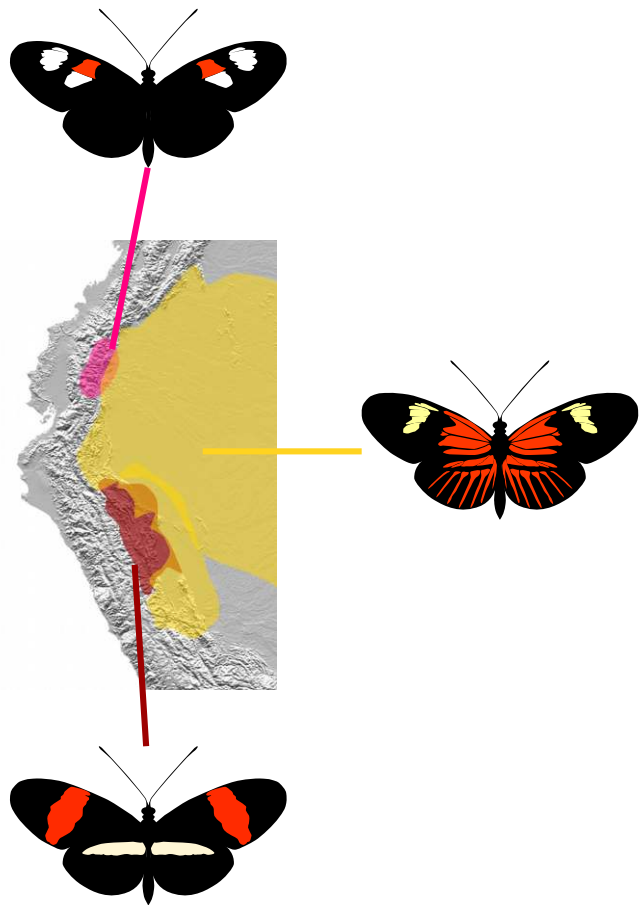


cortex

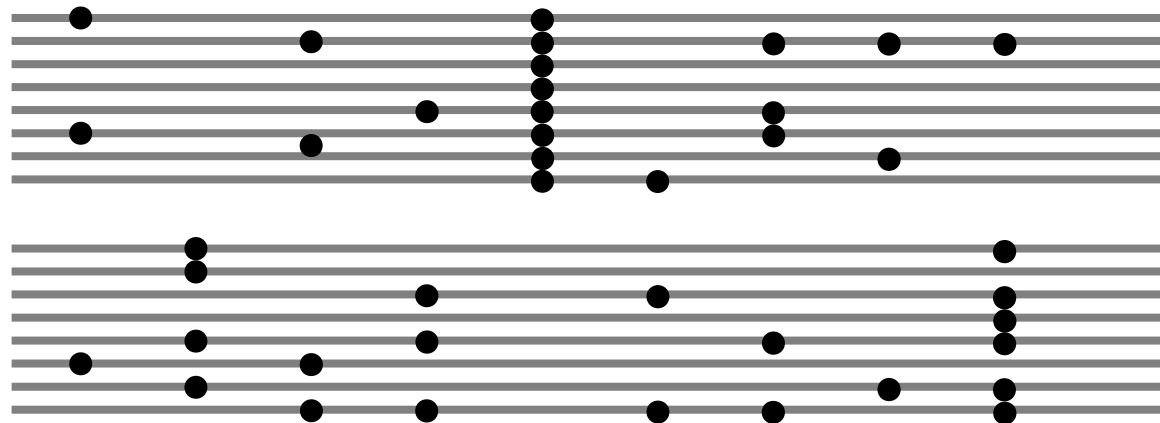


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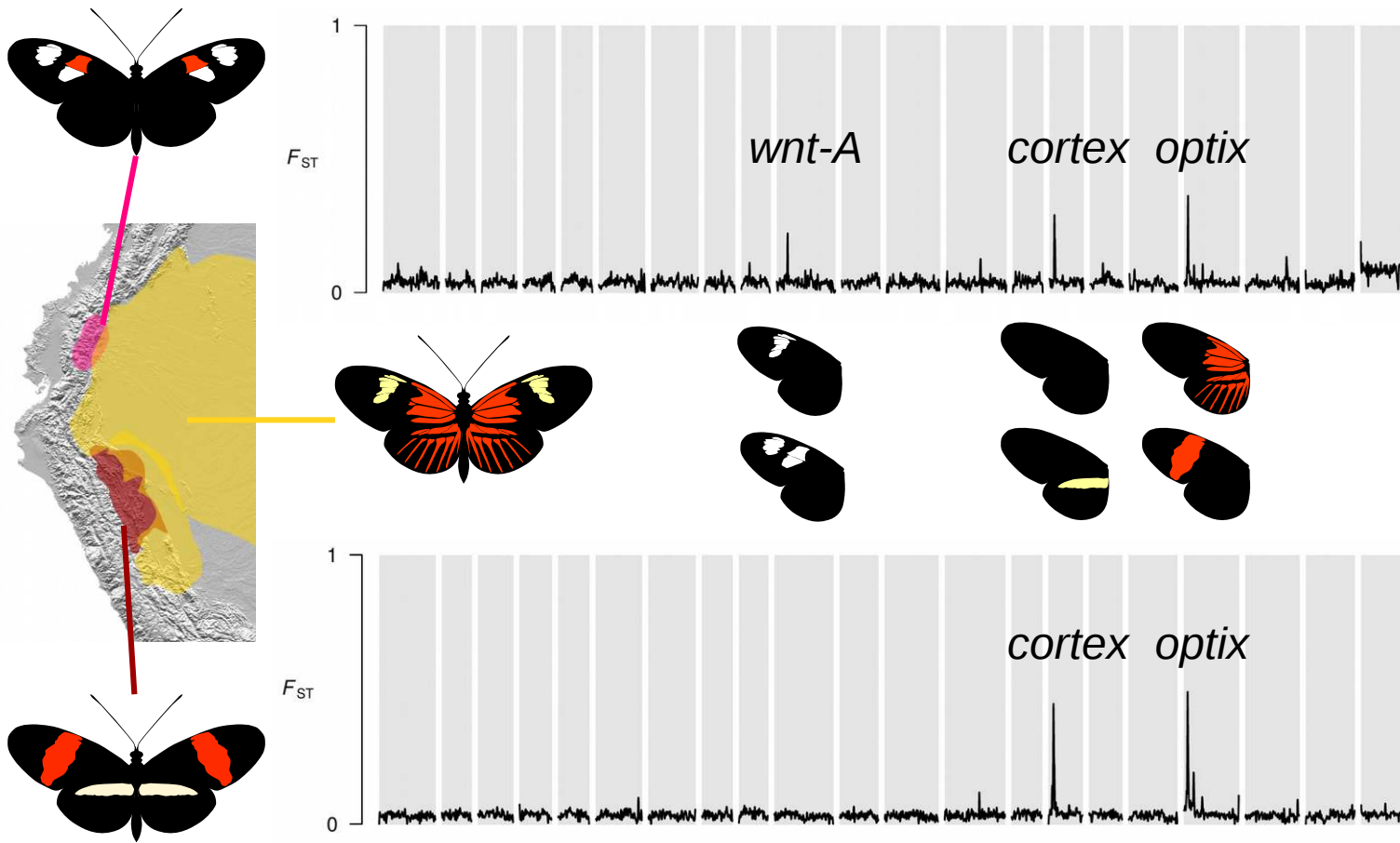




$$F_{ST} = \frac{\pi_{total} - \pi_{subpop}}{\pi_{total}} = 1 - \frac{\pi_{subpop}}{\pi_{total}}$$







Heliconius **Species**



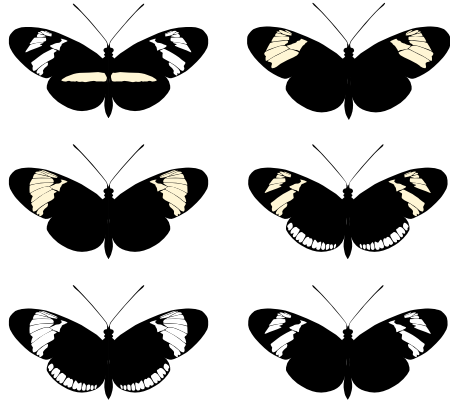
Henry T. McLin CCBYNCND

H. cydno

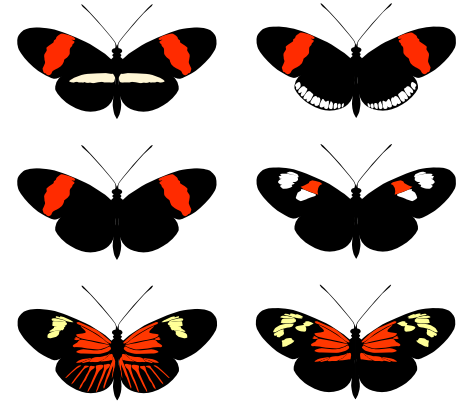
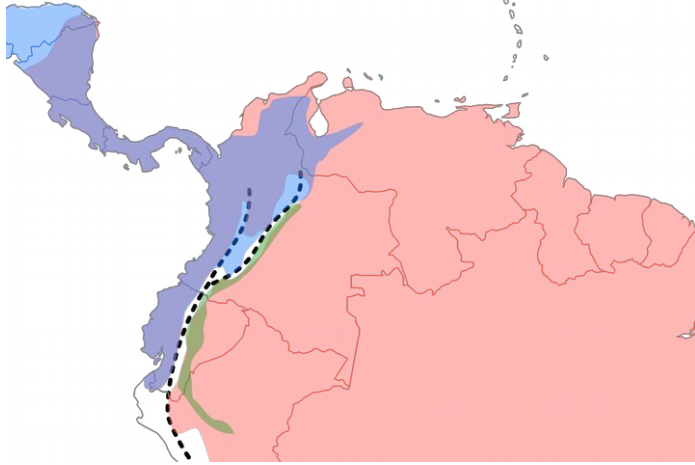


Carol Hunt CCBYNCNSA

H. melpomene



H. cydno



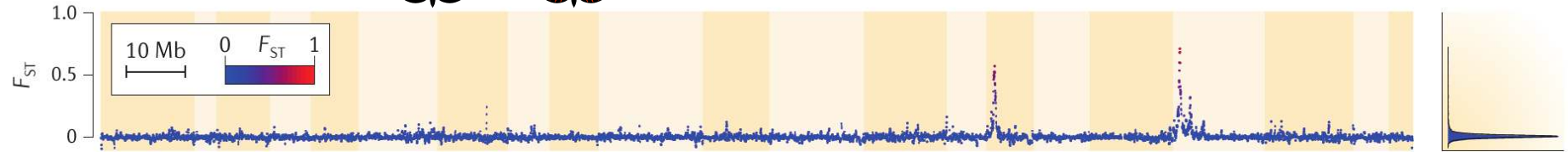
H. melpomene



- Habitat preference
- Host plant choice
- Assortative mating
- Hybrid female sterility (Haldane's Rule)



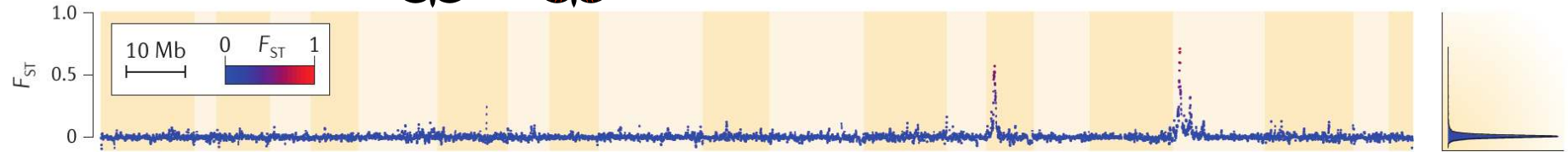
Parapatric Races



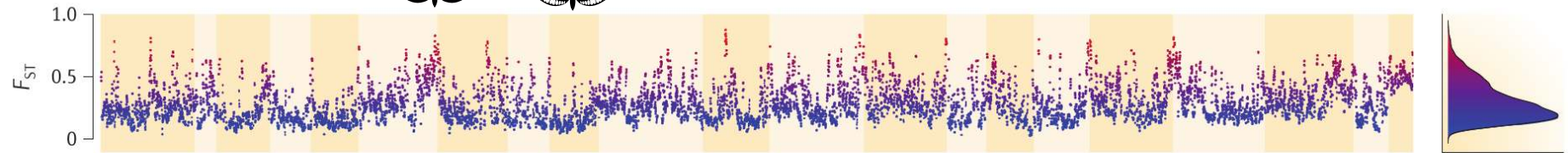
Sympatric species

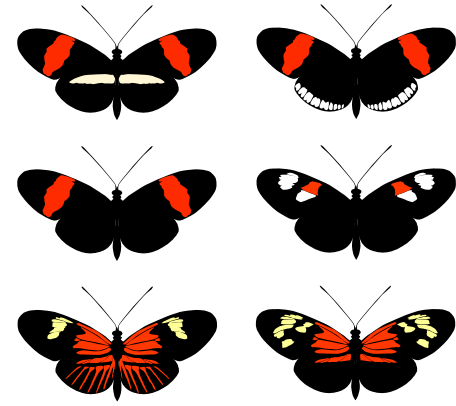


Parapatric Races



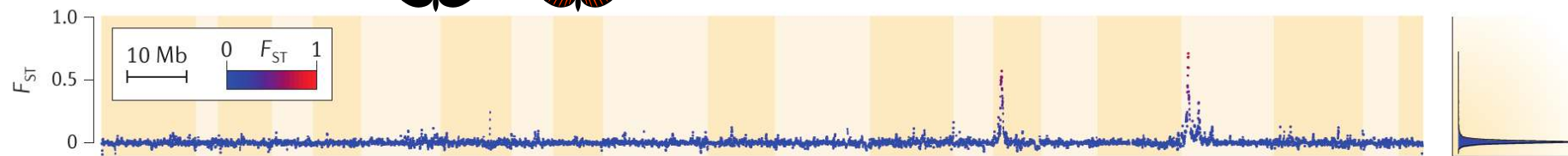
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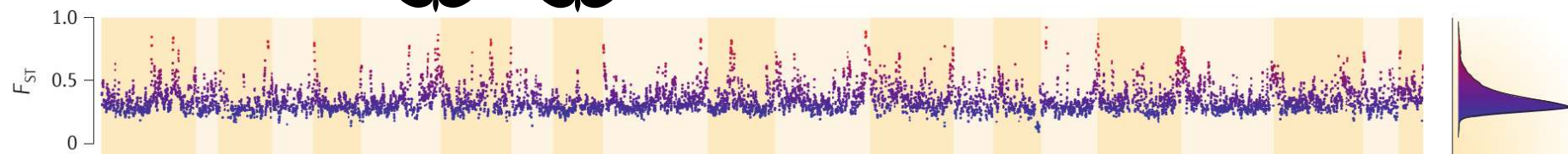


H. melpomene

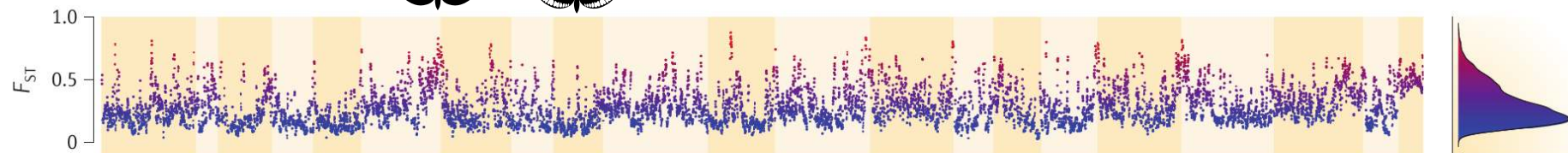
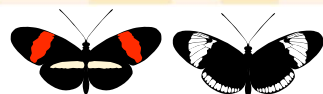
Parapatric Races



Allopatric Races

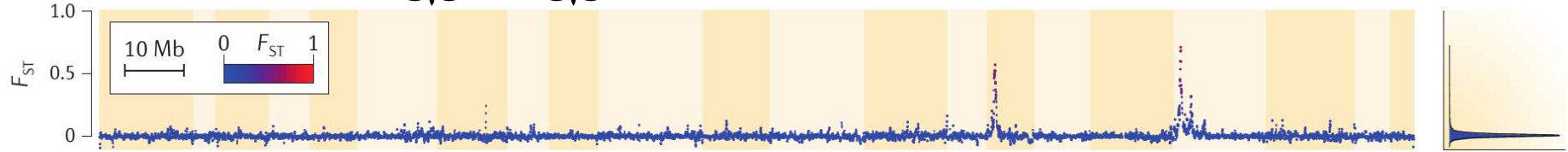


Sympatric species

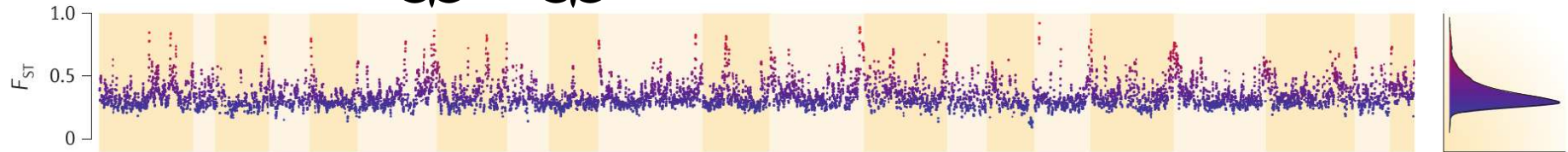


The problem is not FST, the problem is how we interpret it

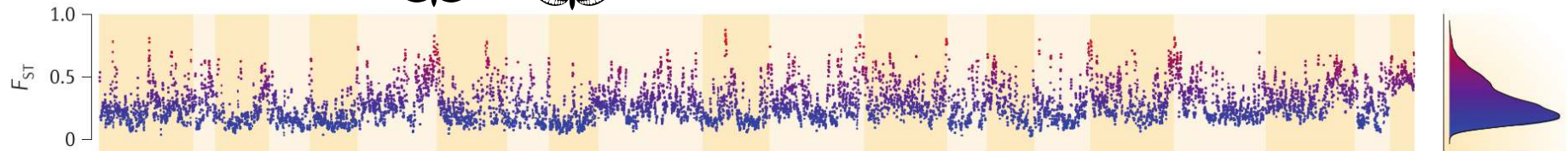
Parapatric Races

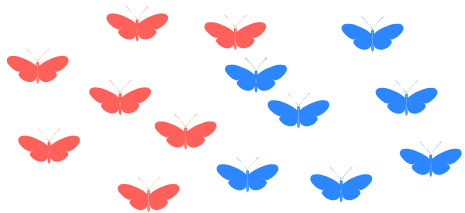


Allopatric Races



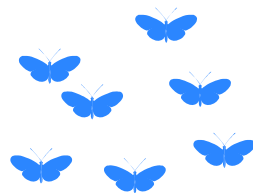
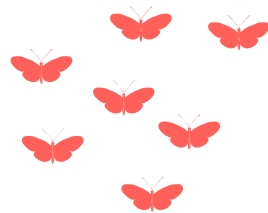
Sympatric species

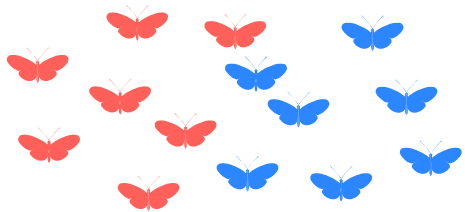




$$F_{ST} = 1 - \frac{\pi_{subpop}}{\pi_{total}}$$

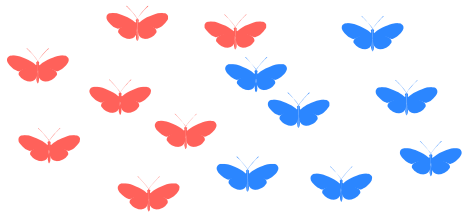
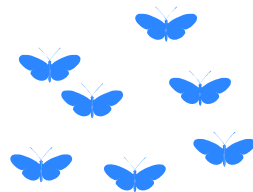
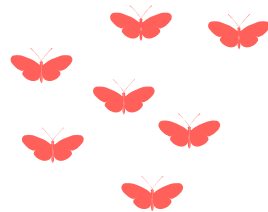
A red arrow points upwards from the π_{total} term in the denominator of the fraction.





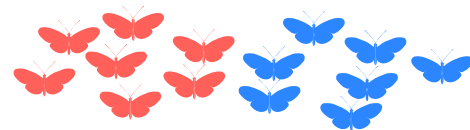
$$F_{ST} = 1 - \frac{\pi_{subpop}}{\pi_{total}}$$

↑



$$F_{ST} = 1 - \frac{\pi_{subpop}}{\pi_{total}}$$

↓



INVITED REVIEWS AND SYNTHESSES

Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow

TAMI E. CRUICKSHANK* and MATTHEW W. HAHN*†

**Department of Biology, Indiana University, Bloomington, IN 47405, USA, †School of Informatics and Computing, Indiana University, Bloomington, IN 47405, USA*

INVITED REVIEWS AND SYNTHESSES

Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow

TAMI E. CRUICKSHANK* and MATTHEW W. HAHN*†

**Department of Biology, Indiana University, Bloomington, IN 47405, USA, †School of Informatics and Computing, Indiana University, Bloomington, IN 47405, USA*

Islands of Speciation or Mirages in the Desert? Examining the Role of Restricted Recombination in Maintaining Species*

Mohamed A. F. Noor¹ and Sarah M. Bennett¹

¹ Biology Department, Duke University, Durham, NC USA

Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow

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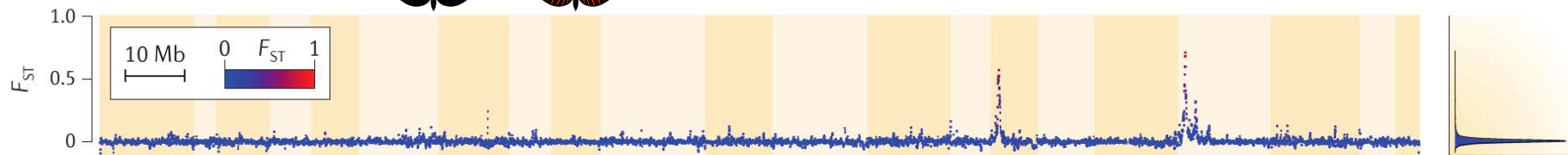
¹ Biology Department, Duke University, Durham, NC USA

The effects of local selection, balanced polymorphism and background selection on equilibrium patterns of genetic diversity in subdivided populations

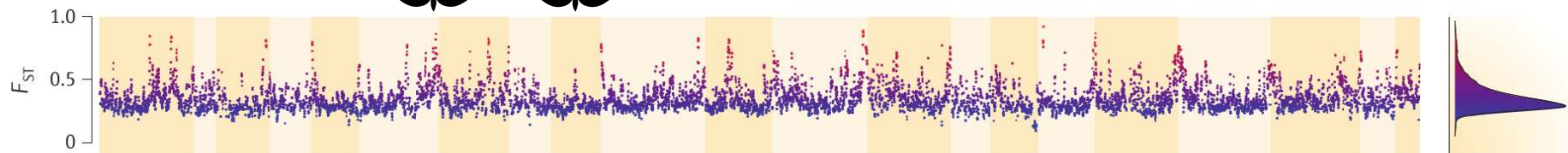
BRIAN CHARLESWORTH*†, MAGNUS NORDBORG‡
AND DEBORAH CHARLESWORTH†

Department of Ecology and Evolution, University of Chicago, 1101 E 57th Street, Chicago, IL 60637, USA

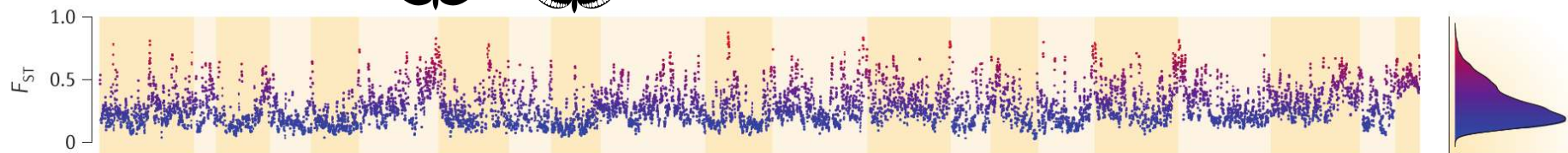
Parapatric Races



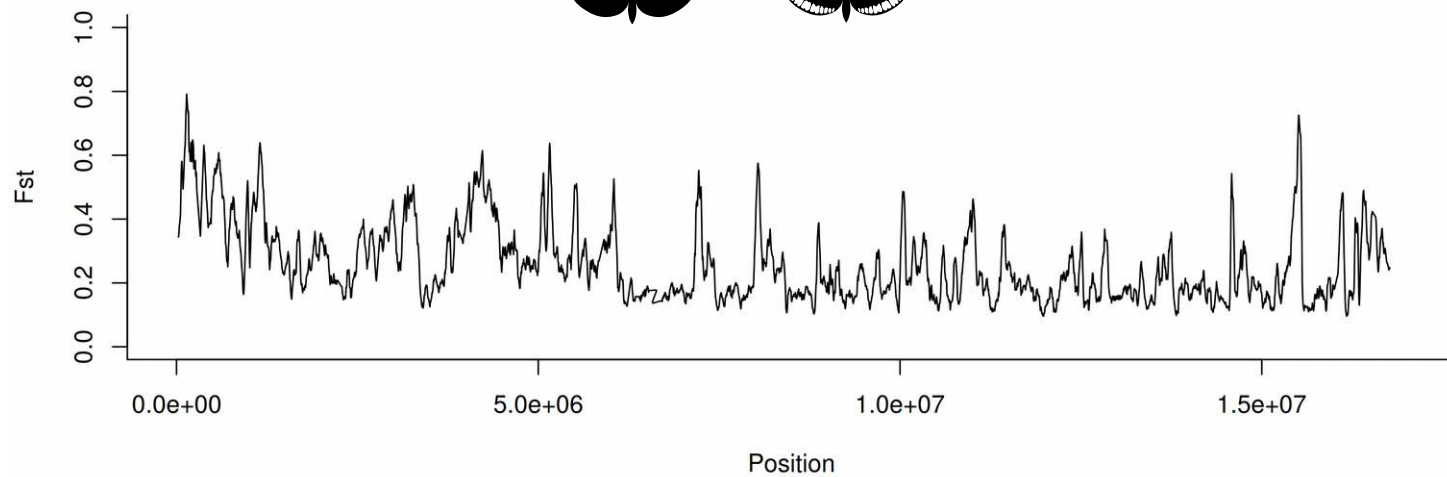
Allopatric Races



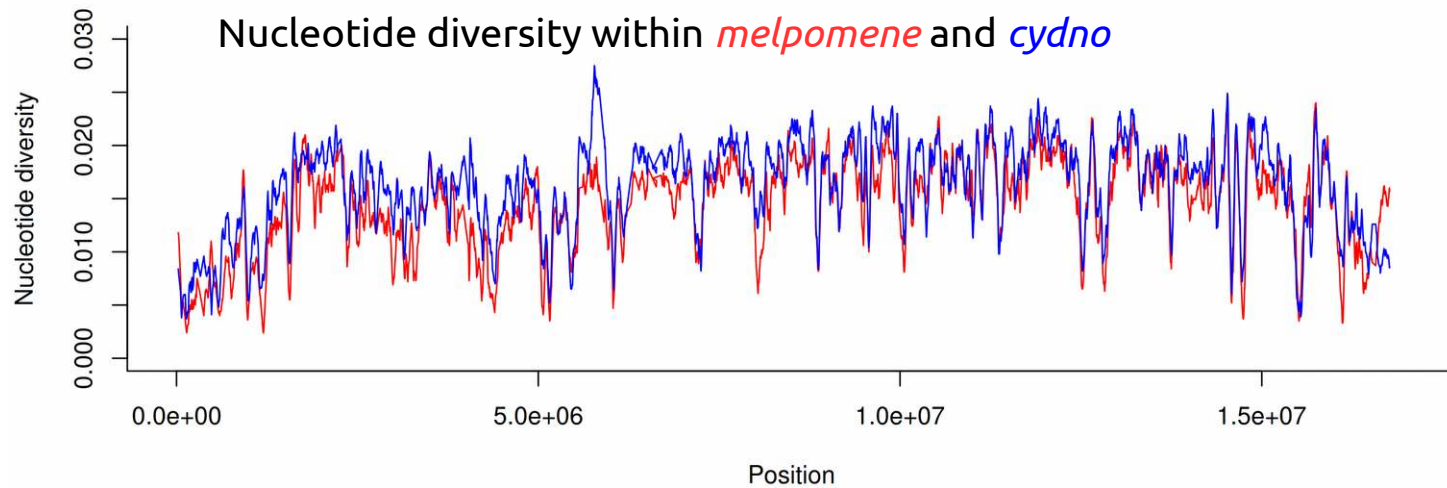
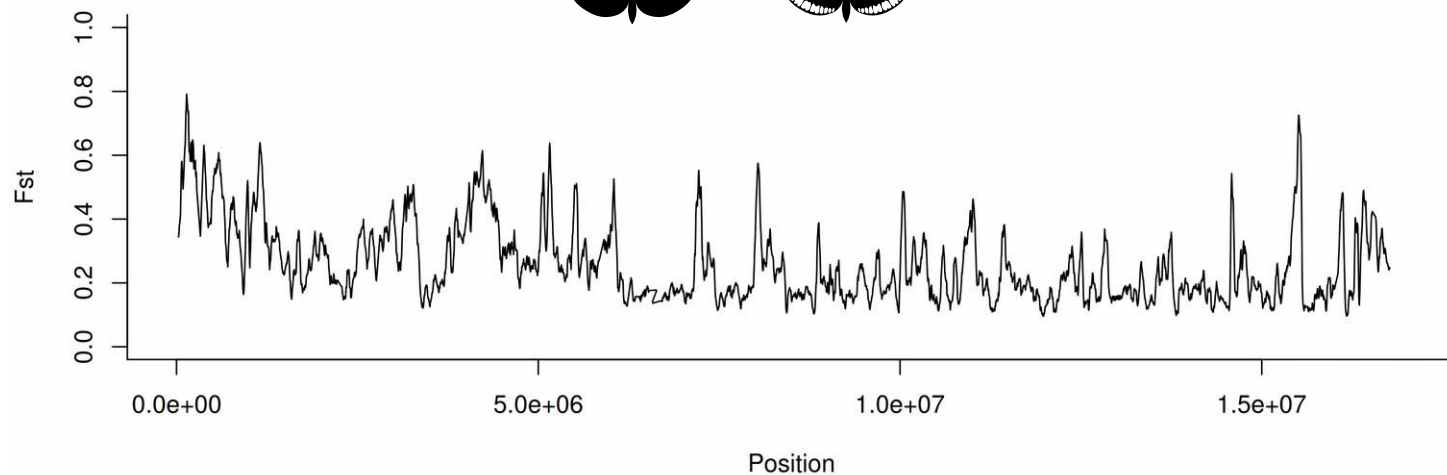
Sympatric species



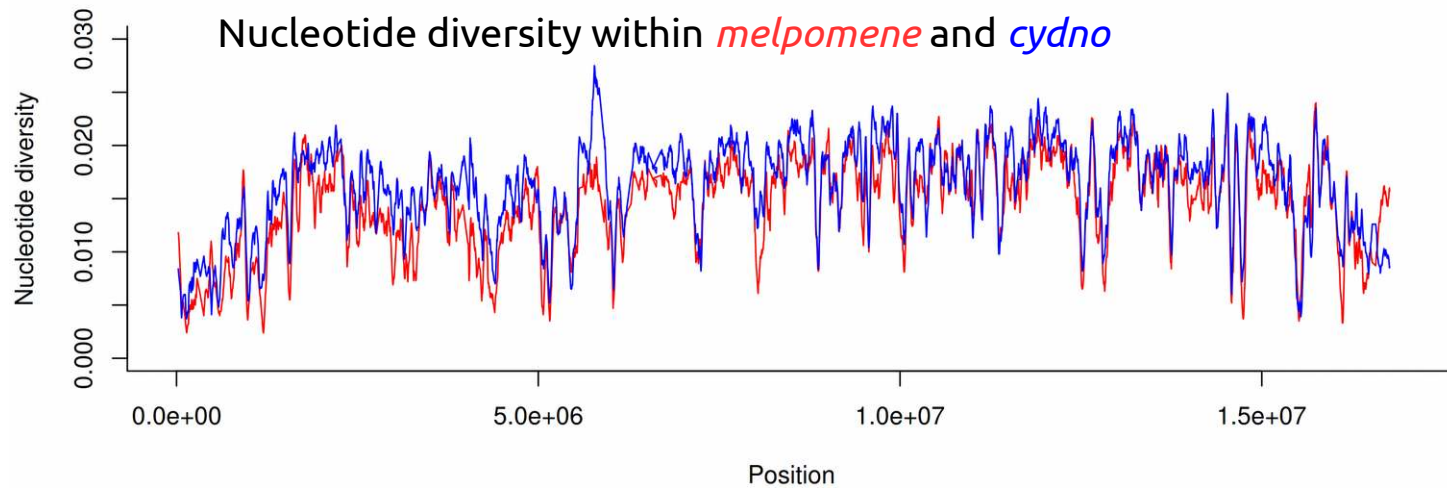
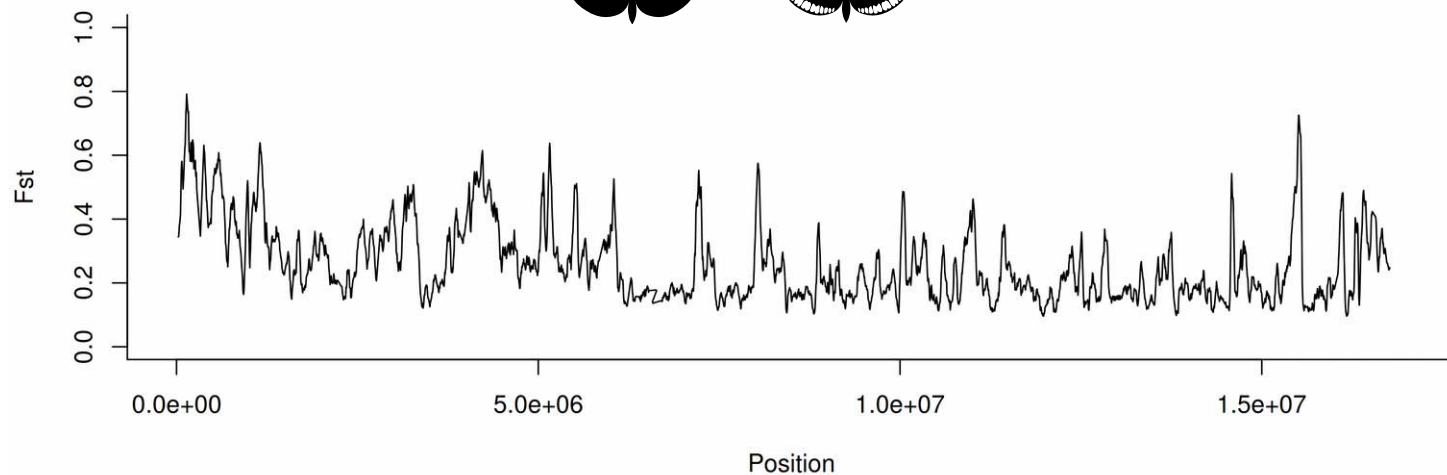
F_{ST} between *melpomene* and *cydno*



F_{ST} between *melpomene* and *cydno*



F_{ST} between *melpomene* and *cydno*



"Surely you've heard the stories?"

The Black Pearl sails from the dreaded Isla de Mureta...

An island that cannot be found -- except by those who already know where it is."

Pirates of the Caribbean, The curse of the Black Pearl, 2003

Interpreting differentiation landscapes in the light of long-term linked selection

Reto Burri^{1,2}

NEWS AND VIEWS

Perspective

Linked selection, demography and the evolution of correlated genomic landscapes in birds and beyond

Reto Burri 

TARGET REVIEW

Interpreting the genomic landscape of speciation: a road map for finding barriers to gene flow

M. RAVINET^{*†} , R. FARIA^{‡§¶}, R. K. BUTLIN^{¶**}, J. GALINDO^{††}, N. BIERNE^{‡‡}, M. RAFAJLOVIĆ^{§§} , M. A. F. NOOR^{¶¶} , B. MEHLIG^{§§} & A. M. WESTRAM[¶]

WILEY **MOLECULAR ECOLOGY**

COMMENTARY

Dissecting differentiation landscapes: a linked selection's perspective

R. BURRI 

Department of Population Ecology, Institute of Ecology, Friedrich Schiller University Jena, Jena, Germany

COMMENTARY

Parallelism in genomic landscapes of differentiation, conserved genomic features and the role of linked selection

H. ELLEGREN^{*}  & J. B. W. WOLF^{*†}

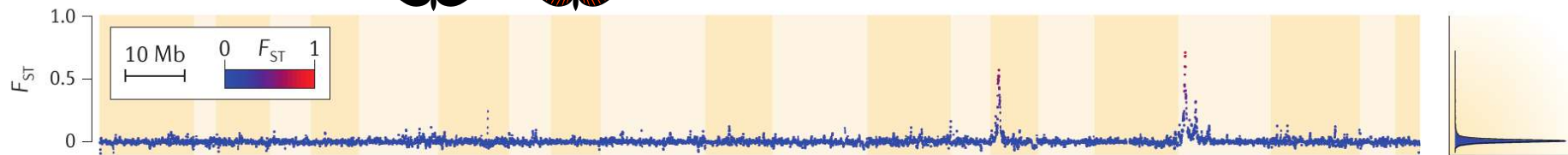
**Department of Evolutionary Biology, Uppsala University, Uppsala, Sweden*

†Division of Evolutionary Biology, Faculty of Biology, Ludwig-Maximilians-Universität München, Planegg-Martinsried, Germany

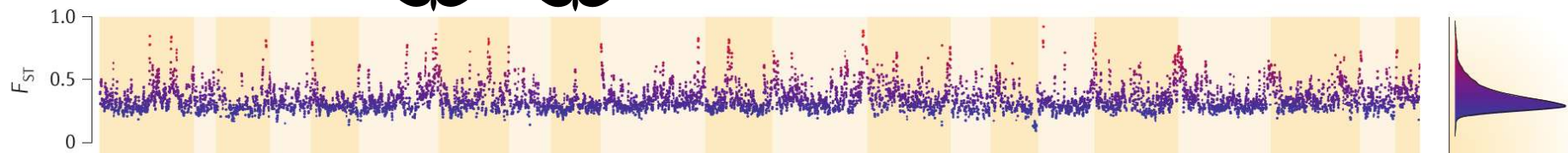
Making sense of genomic islands of differentiation in light of speciation

Jochen B. W. Wolf^{1,2} and Hans Ellegren¹

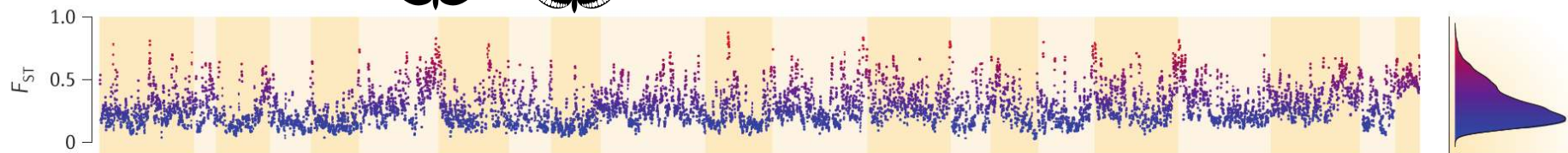
Parapatric Races



Allopatric Races

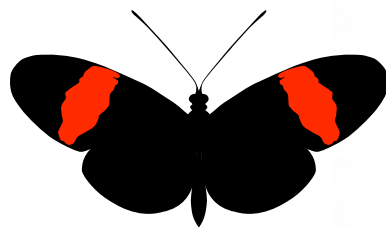
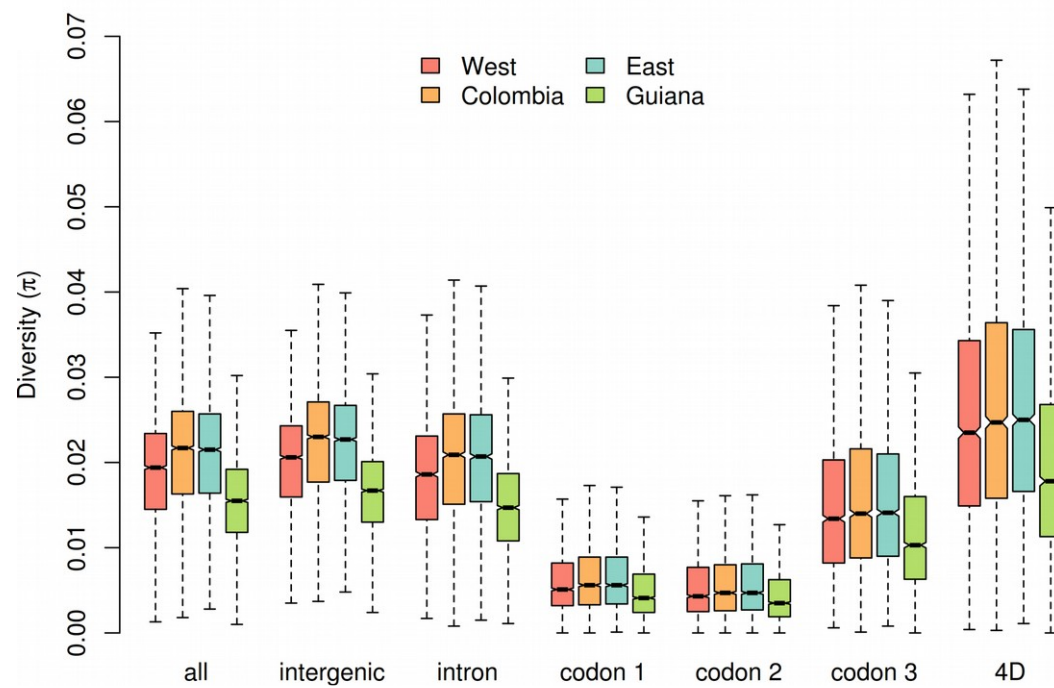


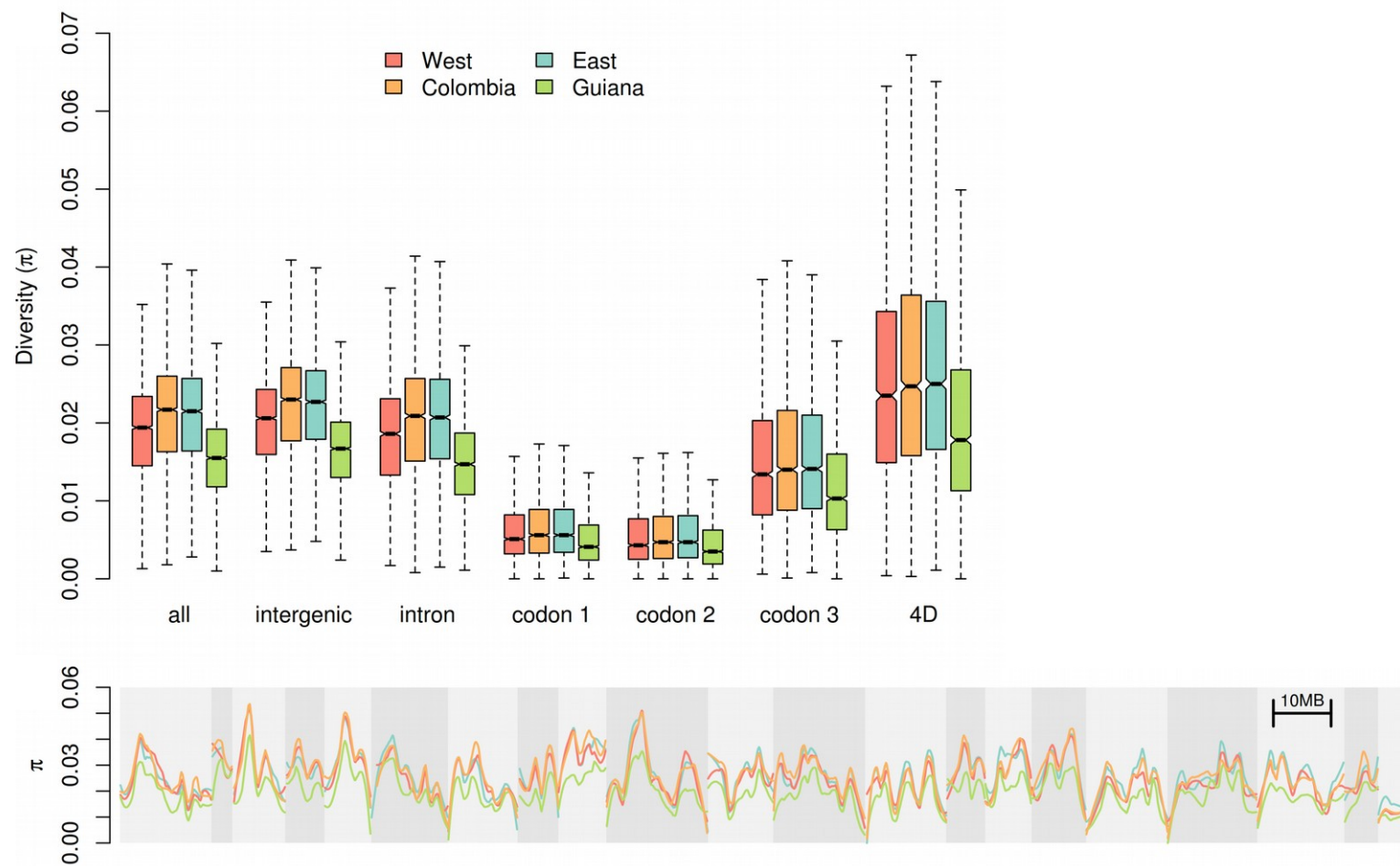
Sympatric species



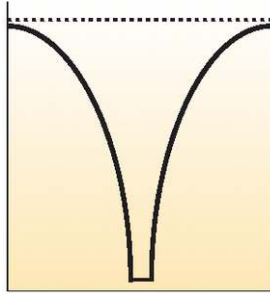
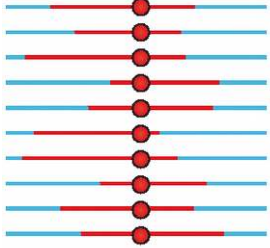
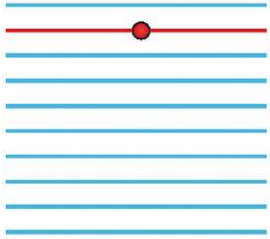
Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of *Ficedula* flycatchers

Reto Burri,¹ Alexander Nater,¹ Takeshi Kawakami,¹ Carina F. Mugal,¹ Pall I. Olason,² Linnea Smeds,¹ Alexander Suh,¹ Ludovic Dutoit,¹ Stanislav Bureš,³ Laszlo Z. Garamszegi,⁴ Silje Hogner,^{5,6} Juan Moreno,⁷ Anna Qvarnström,⁸ Milan Ružić,⁹ Stein-Are Sæther,^{5,10} Glenn-Peter Sætre,⁵ Janos Török,¹¹ and Hans Ellegren¹

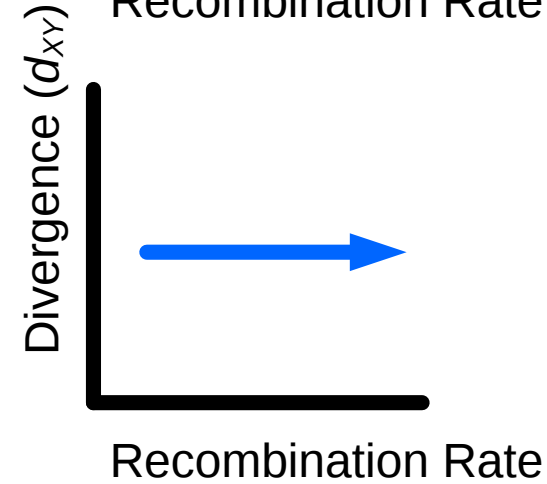
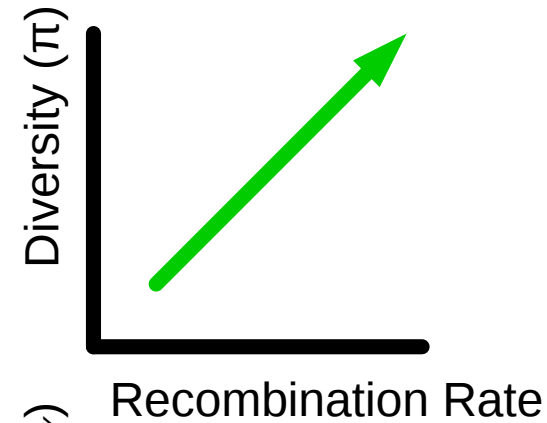
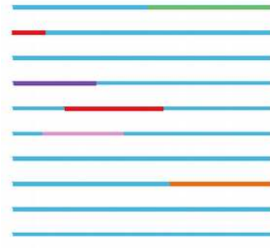




Genetic Hitchhiking (Sweeps)



Background Selection



What explains variation in neutral diversity?

Synonymous
substitution rate



Gene density



Recombination rate

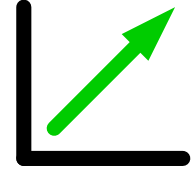


Non-synonymous
substitutions

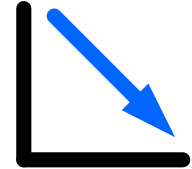


What explains variation in neutral diversity?

Synonymous substitution rate



Gene density



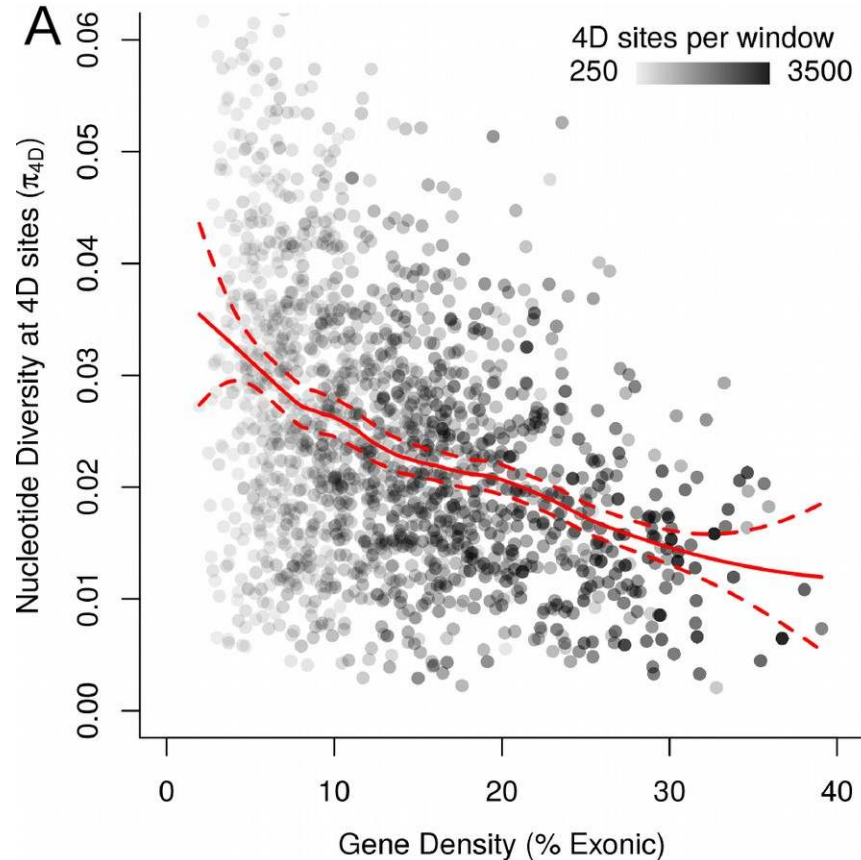
Recombination rate



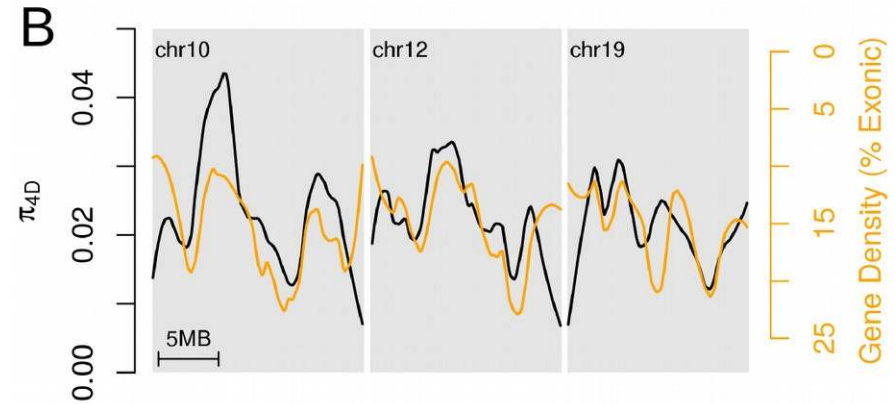
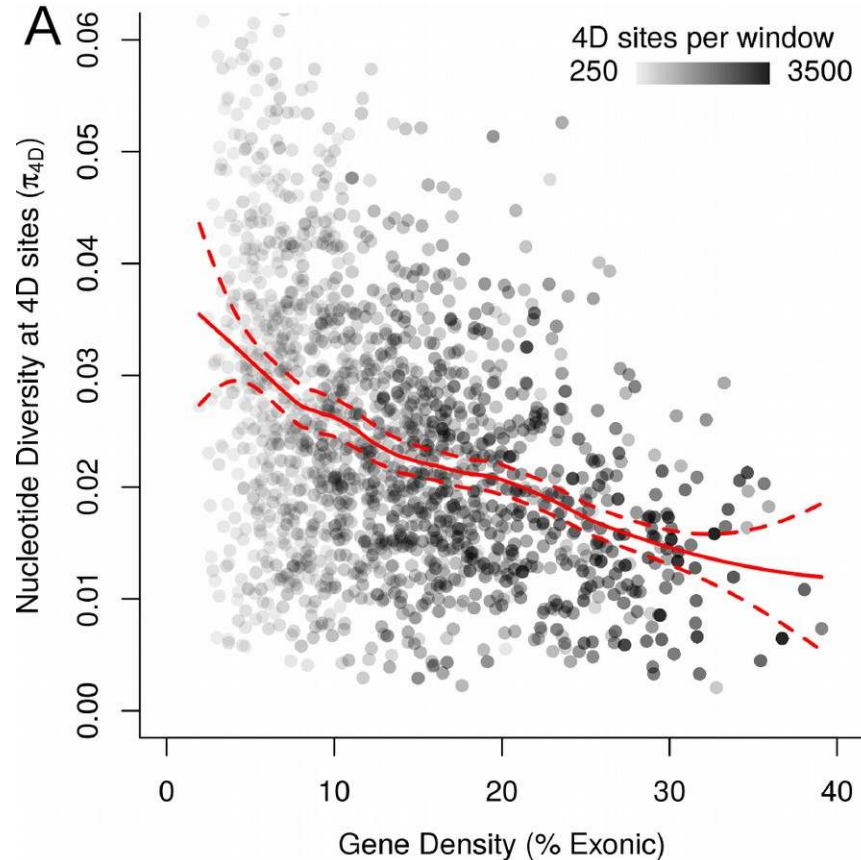
Non-synonymous substitutions



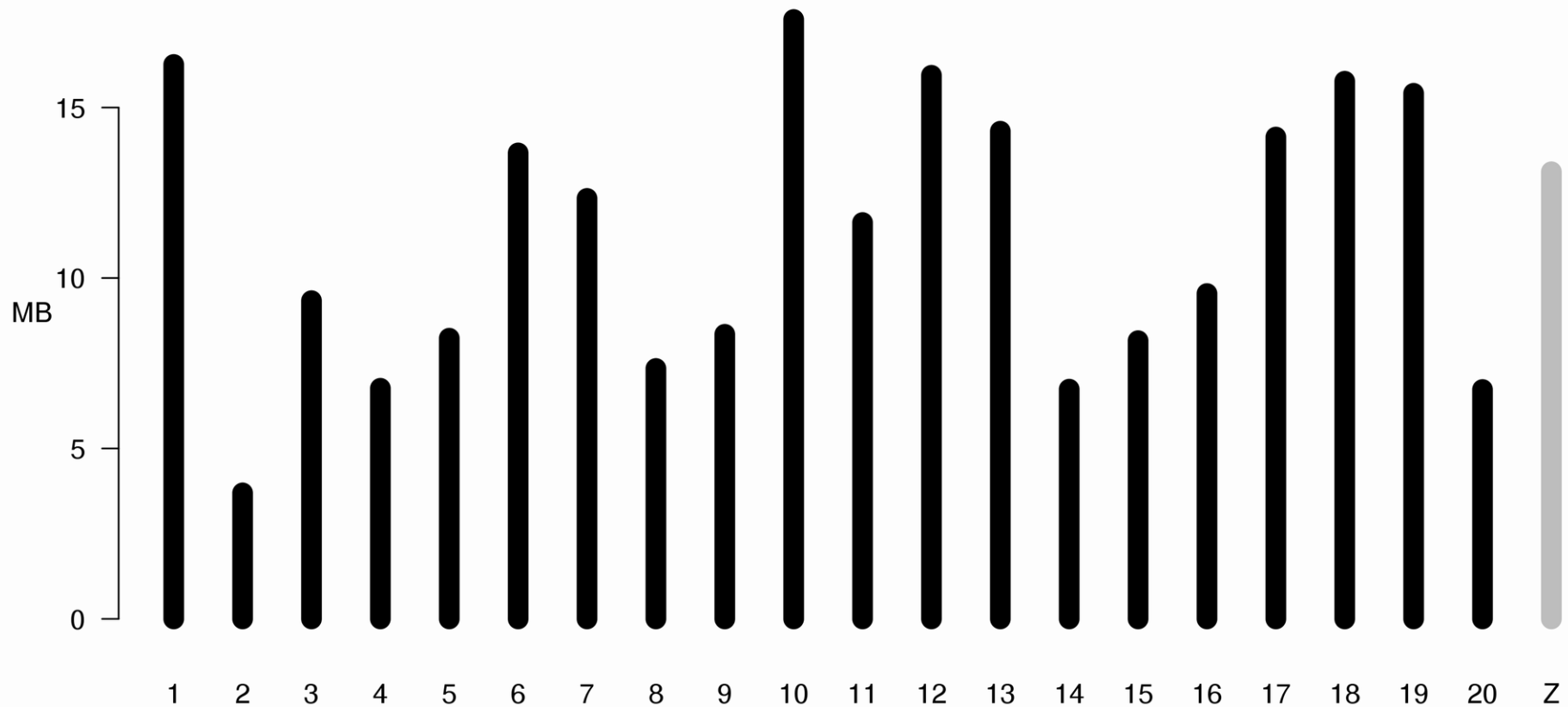
Gene density is highly predictive of neutral diversity



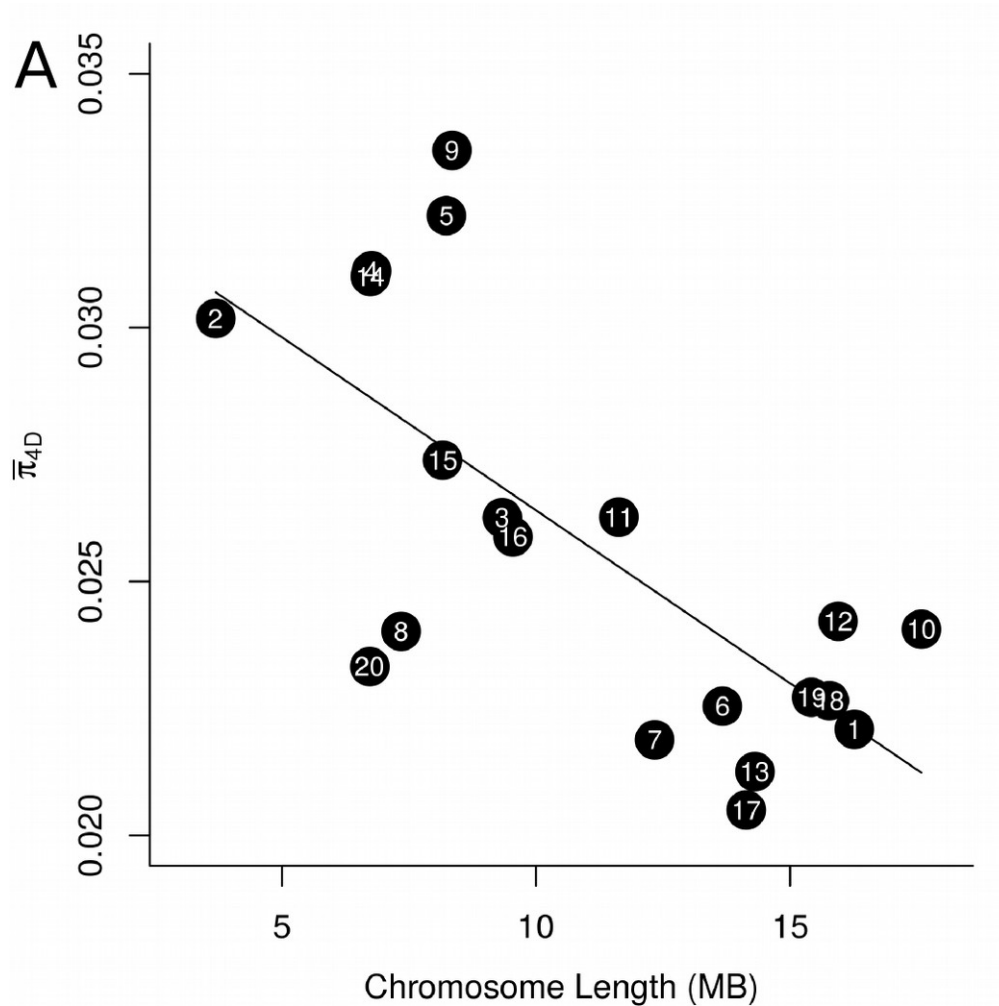
Gene density is highly predictive of neutral diversity



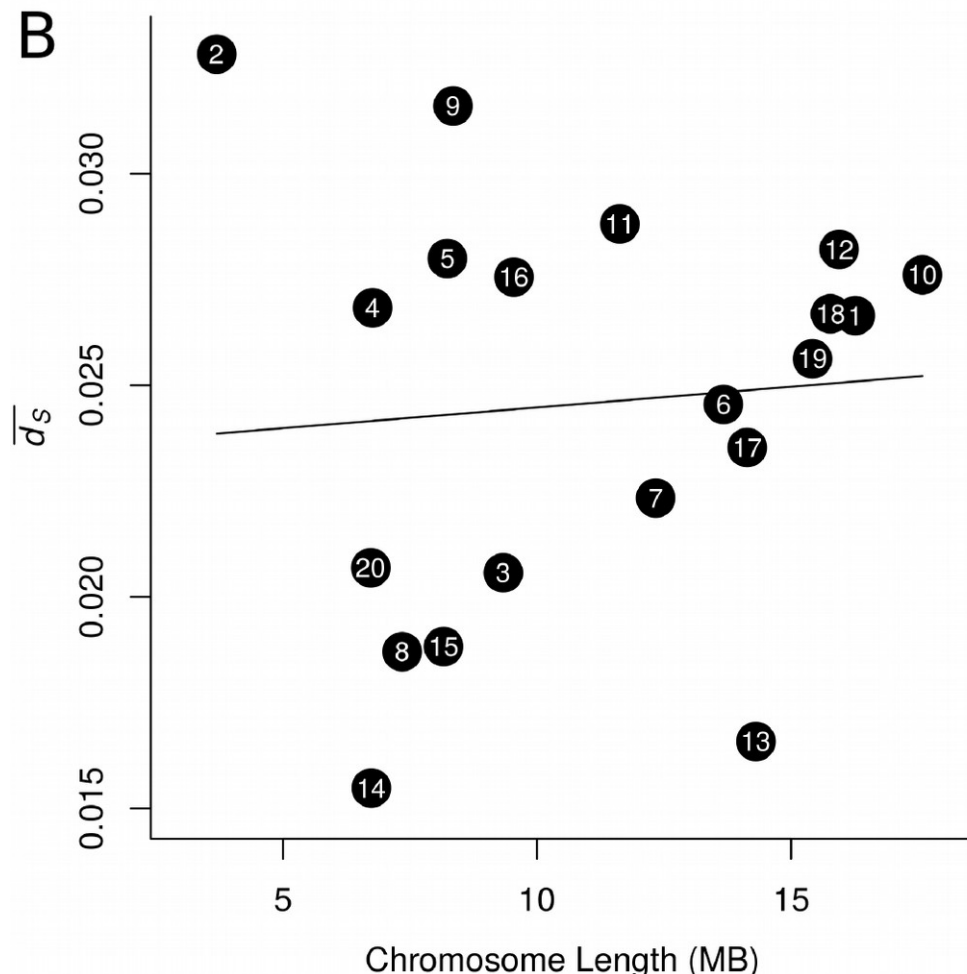
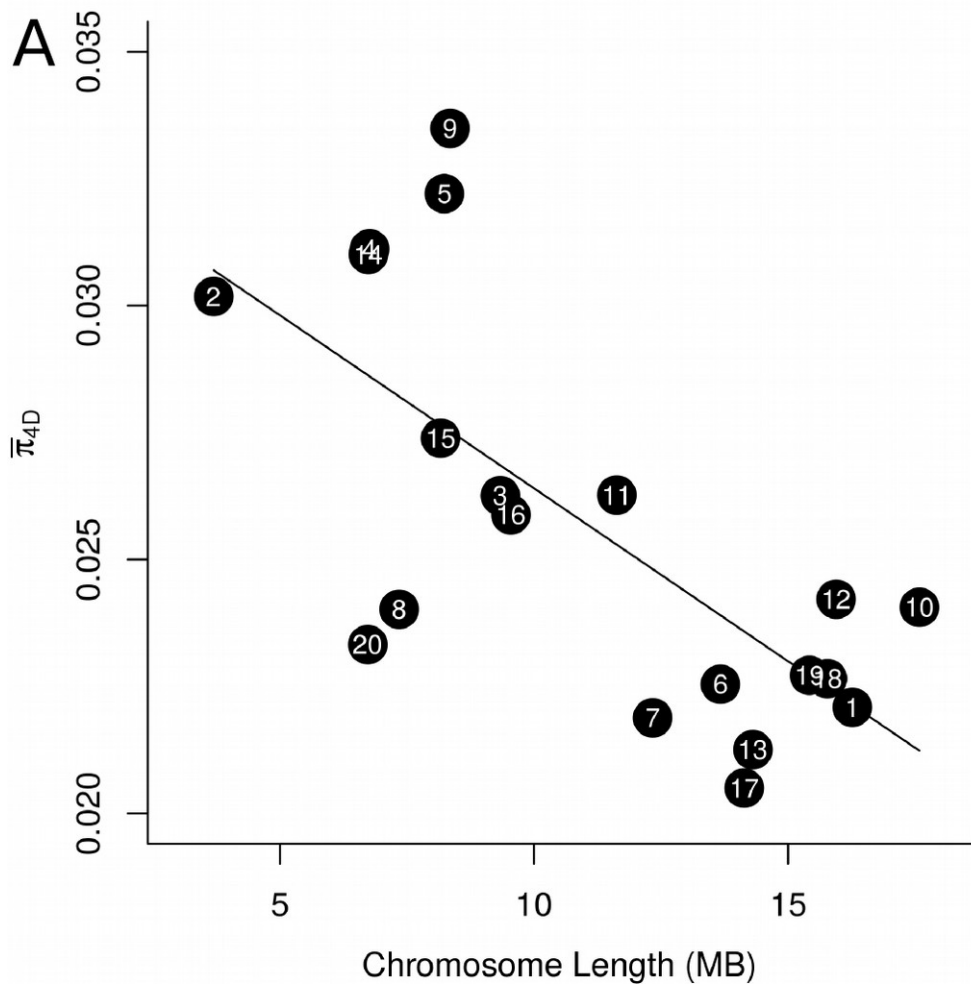
Chromosome length is also predictive of diversity



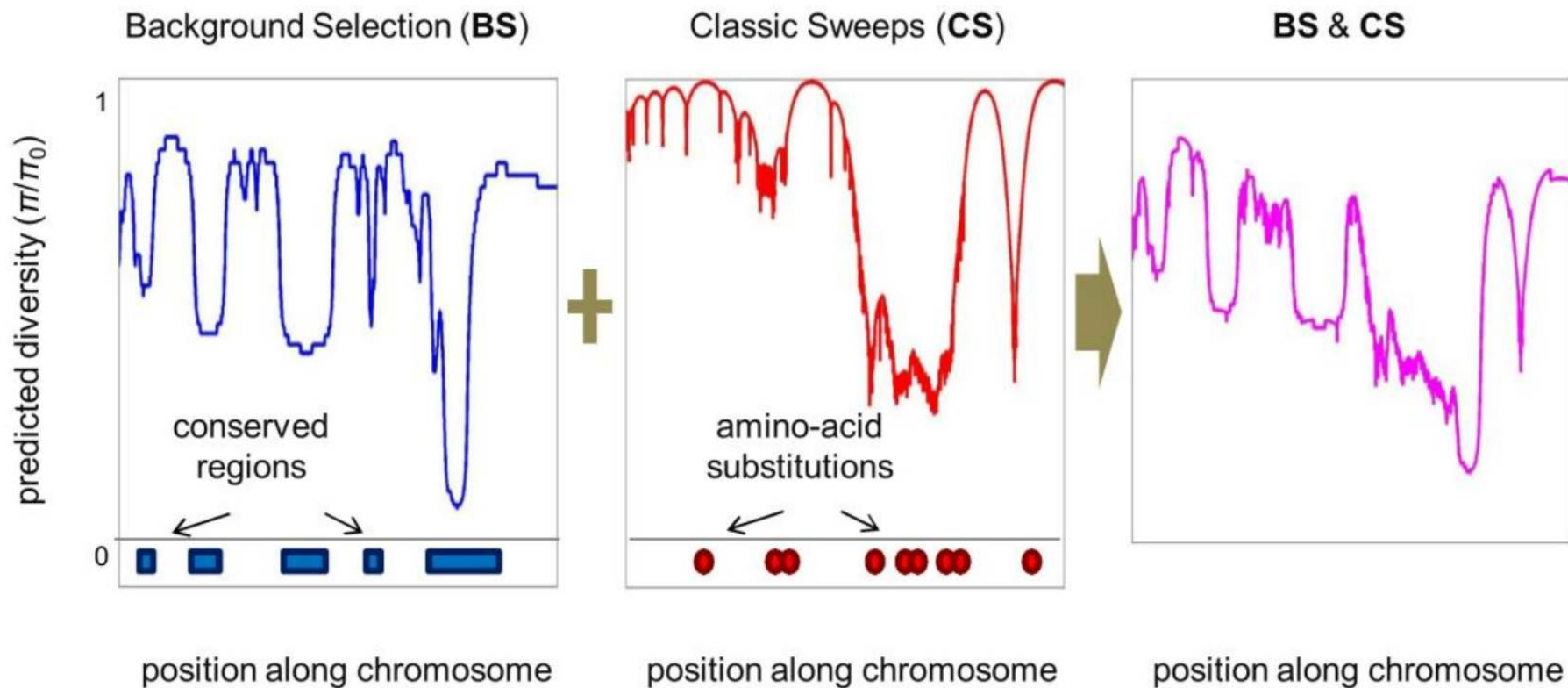
Chromosome length is also predictive of diversity



Chromosome length is also predictive of diversity



Explicit models can predict genomic diversity



But how's this going to help us find speciation genes?

But how's this going to help us find speciation genes?

It isn't

But there ARE ways to better study species barriers using
genomics