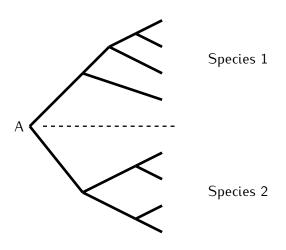
# Tests of Positive Selection based on the Comparison of Polymorphism and Divergence

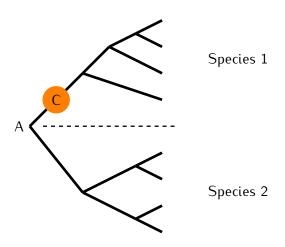
Julien Dutheil

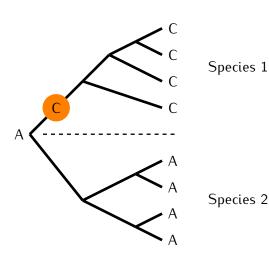
dutheil@evolbio.mpg.de

Max Planck Institute for Evolutionary Biology

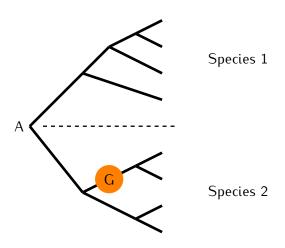
June 22nd 2015

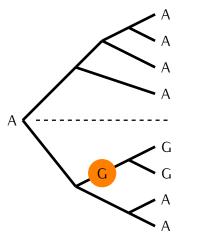






 Mutations on interspecies branches lead to fixed differences between species





Species 1

Species 2

- Mutations on interspecies branches lead to fixed differences between species
- Mutations on intraspecies branches lead to polymorphism in one species

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The ratio of polymorphic sites vs. fixed differences sites is constant along the genome!

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If mutation rate varies between sites but is constant over time in the two species, two predictions:

- 1 the ratio of polymorphism vs. divergence is constant between genes
- the ratio of non-synonymous to synonymous polymorphism equals the ratio of non-synonymous to synonymous divergence

Polymorphism and divergence are two facets of the same process

#### The HKA test Hudson, Kreitman and Agua<u>dé (1987)</u>

■ Compare at least 2 loci in 2 species, with polymorphism data in at least 1 species

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- Assumes free recombination between regions and no recombination within regions

#### The MK test McDonald and Kreitman (1991)

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		D. melanopaster	D. simulans	D. vakuba	
	Con.	abodefghijkl	abodef	abodefghijkl	
781	G	TTTTTTTTTTT		R	epl.
789	T				yn.
808 816	A G	7 7 7 7 7	TTTTTT		epl.
834	ř		000		yn. Vn.
859	c				epl.
867	C				yn.
870	C G	7 7 7 7 7 7 7 7 7 7 7 7 7 7	- 4	S	yn. yn.
960 974	G		T-TTTT		yn. Vn.
963	7				yn.
1019	c			A S	yn.
1031	C				yn.
1034	č				yn.
1063	č	7 T			yn. yn.
1089	c	11	AAAAAA	B	epl.
1101	G				epl.
1127	7			ccccccccccc s	yn.
1131	C				yn. yn.
1175	ż				yn.
1178	C			A- S	yn.
1184	C				yn.
1190	c			A S	yn.
1196 1199	G C	5 <del>7</del> 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5			yn. yn.
1202	7	-1			yn.
1203	C		T		yn.
1229	7	00000000000		S	yn.
1232	T C				yn.
1235 1244	c				yn.
1265	č			accacacacaca s	yn.
1271	A		- T - T	S	yn.
1277	T	A I			yn.
1283 1298	c	A A			yn.
1304	č		T-		yn.
1316	C		T T		yn.
1425	c	A A		S	yn.
1431	T	00	111111		yn.
1443	c				310 . 310 .
1490	Ä				epl.
1504	C	TTTTTTTTTTTT		S	yn.
1518	C				yn.
1524	T C	T 7 T T 7 T			373 . 373 .
1530	ğ	111111			yn.
1545	Ť			ccccccccccc s	ND.
1548	C				yn.
1551	C		7		yn.
1555	C	T T			epl.
1560	Ğ		4	8	Vii.
1573	G			ccccccccccc R	epl.
1581	¢				yn.
1584 1590	c	7777777777777	7 7 7		yn. Yn.
1596	G	A A - A A	7 7 7		yn. Vn.
1611	A			TTTTTTTTTTTT S	Vn.
1614	C		- G		yn.
1635	C				ym:
1657	A C				epl.
1669	C			S	ym.

- One coding gene in at least 2 species, with polymorphism data for at least 1 species
- Count synonymous and non-synonymous polymorphisms and fixed differences
- Build a contingency table and perform a G-test

	Fixed	Polym.
Non-syn.	7	2
Synon.	17	42

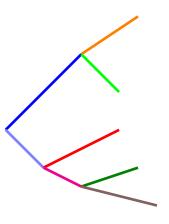
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	Com.	abodefghijkl	abodef	abodefghijkl	
781	G	**********			Repl.
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1504	C	TTTTTTTTTTTT			Syn.
1518 1524	Ť			99999999999	Syn . Syn .
1527	c	T 7 T T 7 T			Syn.
1530	G			A	Syn.
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1611	A	A A - A A		TTTTTTTTTTT	Syn.
1614	C		- 0	7	Syn.
1635	c				Sym.
1657	A			TTTTTTTTTTT	Repl.
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Consider at least 2 species, with one sequence per species

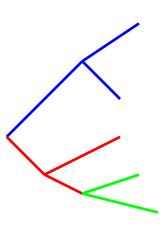
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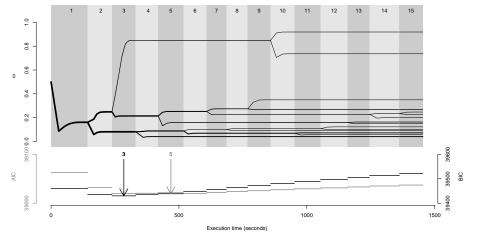
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  - Several clades  $\Rightarrow$  clade model
- Other parameters are constant throughout the tree

# Finding the best model Dutheil et al. (2012)

- The branch model suffers from overparametrization issues
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Yang and Nielsen (2002), Zhang, Nielsen and Yang (2005)

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- Likelihood ratio test to compare with a homogeneous M1a model.