OU: a top-down look

Stochastic motion rate

Ornstein-Uhlenbeck mean

Continuous state

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In what ways can a continuous trait change in an instant of time?

Randomly: increase or decrease slightly by chance

and/or

Directionally: be pulled towards some value

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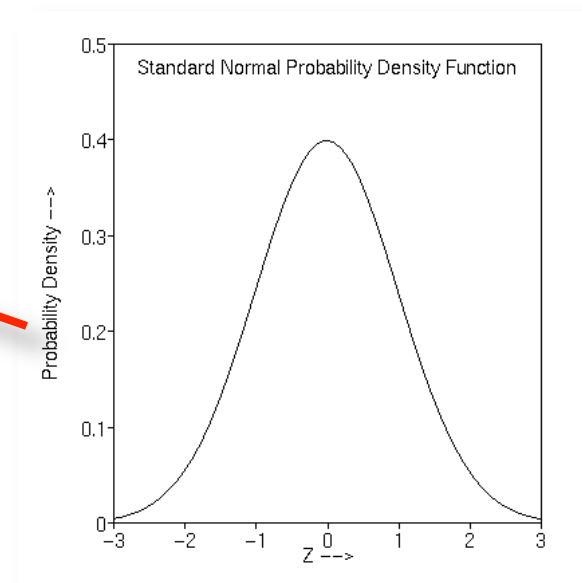
$$dX_T =$$

In what ways can a continuous trait change in an instant of time?

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$$dX_T = \quad dW_T$$

Standard Normal Probability Density Function

In what ways can a continuous
trait change in an instant of time?

Randomly: increase or decrease slightly by chance

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$$dX_T = \sigma \times dW_T$$

Rate of wiggle

In what ways can a continuous
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Directionally: be pulled towards **some value**

$$dX_T = \sigma \times dW_T \qquad \theta$$

In what ways can a continuous
trait change in an instant of time?

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$$dX_T = \sigma \times dW_T \boxed{+ \; (\theta - X_T)}$$

Adds the entire difference

In what ways can a continuous trait change in an instant of time?

Randomly: increase or decrease slightly by chance and/or

Directionally: be pulled towards some value

$$dX_T = \sigma \times dW_T + \alpha(\theta - X_T)$$

Allows directional change less than 100% (even zero)

In what ways can a continuous
trait change in an instant of time?

Randomly: increase or decrease slightly by chance

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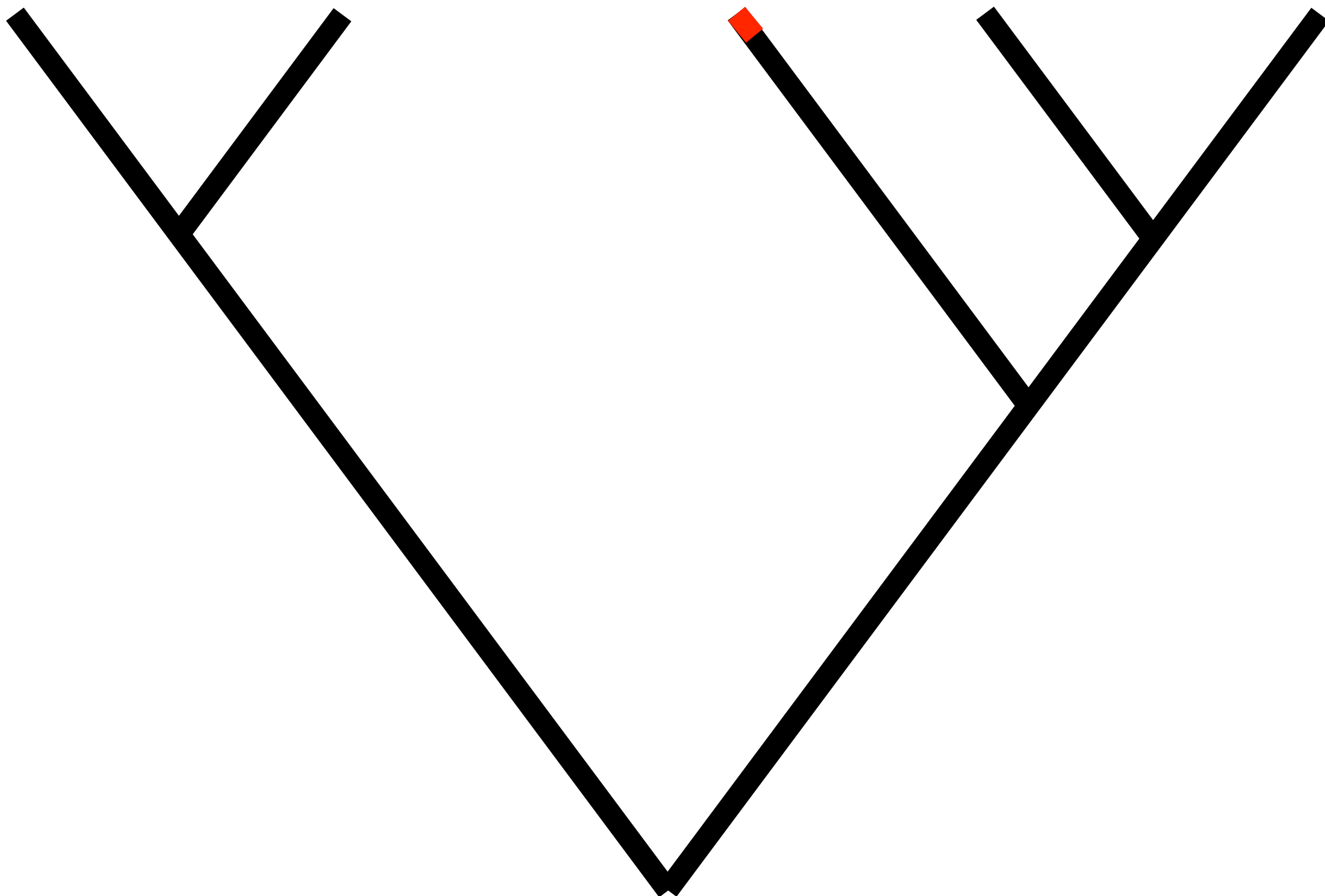Directionally: be pulled towards some value

$$dX_T = \sigma \times dW_T + \alpha(\theta - X_T)$$
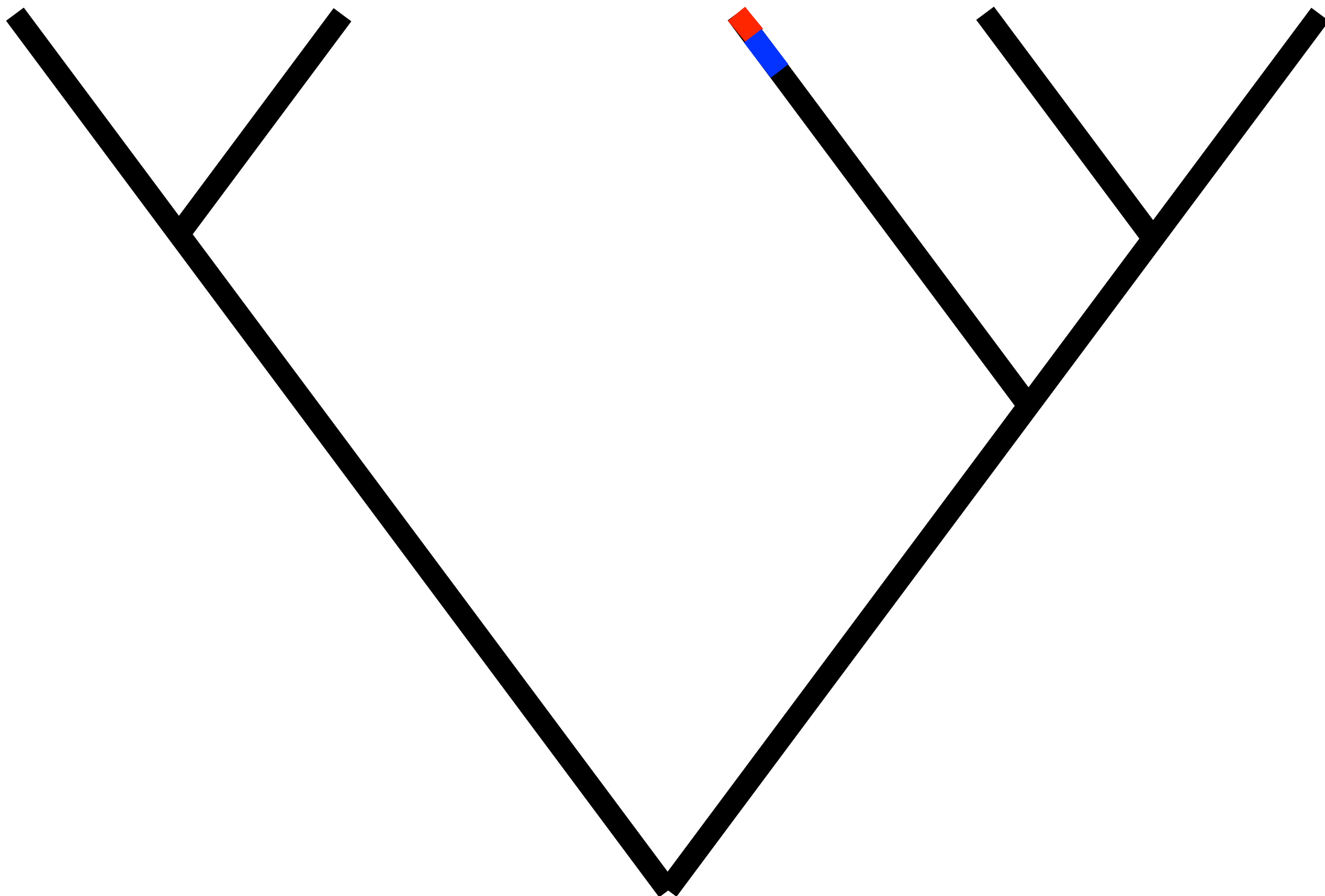
Ornstein-Uhlenbeck process

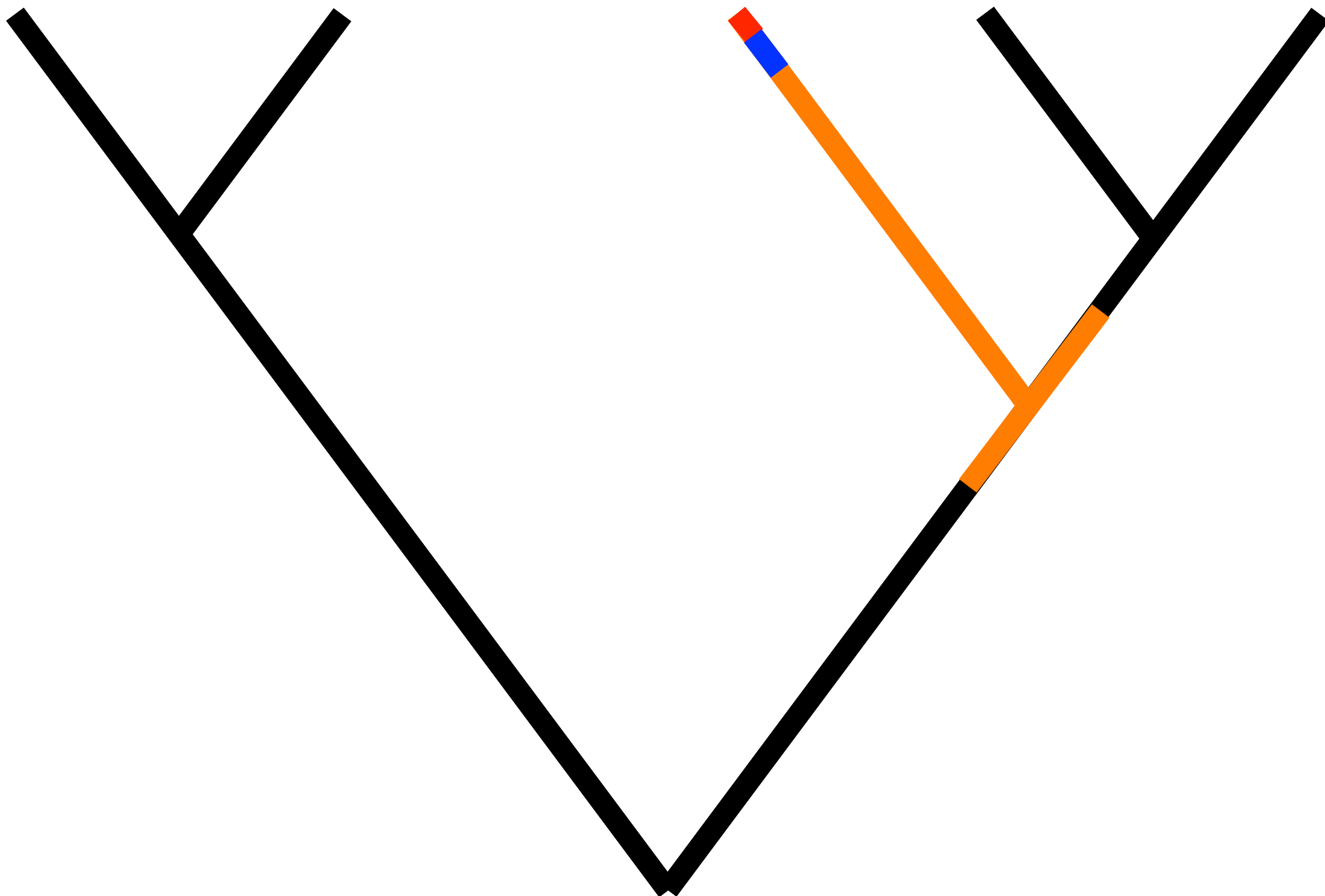$$dX_T = \sigma \times dW_T + \alpha(\theta - X_T)$$

Ornstein-Uhlenbeck process

$$dX_{T_1} = \sigma_1 \times dW_T + \alpha_1(\theta_1 - X_{T_1})$$

$$dX_{T_2} = \sigma_2 \times dW_T + \alpha_2(\theta_2 - X_{T_2})$$

$$dX_{T_3} = \sigma_3 \times dW_T + \alpha_3 (\theta_3 - X_{T_3})$$

And so forth...

$$dX_{T_3} = \sigma_3 \times dW_T + \alpha_3 (\theta_3 - X_{T_3})$$

$$\frac{\sigma_i}{\alpha_i \atop \theta_i}$$

$$dX_{T_i} = \sigma_i \times dW_T + \alpha_i(\theta_i - X_{T_i})$$

Brownian rate   OU attraction   OU mean

	Single rate Brownian motion	Multiple mean Ornstein-Uhlenbeck	Multiple rate Brownian motion	Multiple everything
σ_i	all equal	all equal	some vary	some vary
α_i	0	all equal	0	some vary
θ_i	NA	some vary	NA	some vary
	Independent contrasts (Felsenstein, 1985), ANCML (Schluter et. al, 1998)	Hansen, 1997; OUCH (Butler & King, 2004), SURFACE (Ingram & Mahler, 2012)	Brownie (O'Meara et al., 2006, Thomas et al., 2006), AUTEUR (Eastman et al. 2011)	OUwie (Beaulieu et al. 2012), bayou (Uyeda et al. 2014)

$$dX_{T_i} = \sigma \times dW_T + \alpha(\theta_i - X_{T_i})$$

Brownian rate   OU attraction   OU mean

Model	Optima (mean = M)	Sigma (variance = V)	Attraction (A)
BM_1		1	
BM_S		≥ 2	
OU_1	1	1	1
OU_M	≥ 2	1	1
OU_{MA}	≥ 2	1	≥ 2
OU_{MV}	≥ 2	≥ 2	1
OU_{MVA}	≥ 2	≥ 2	≥ 2

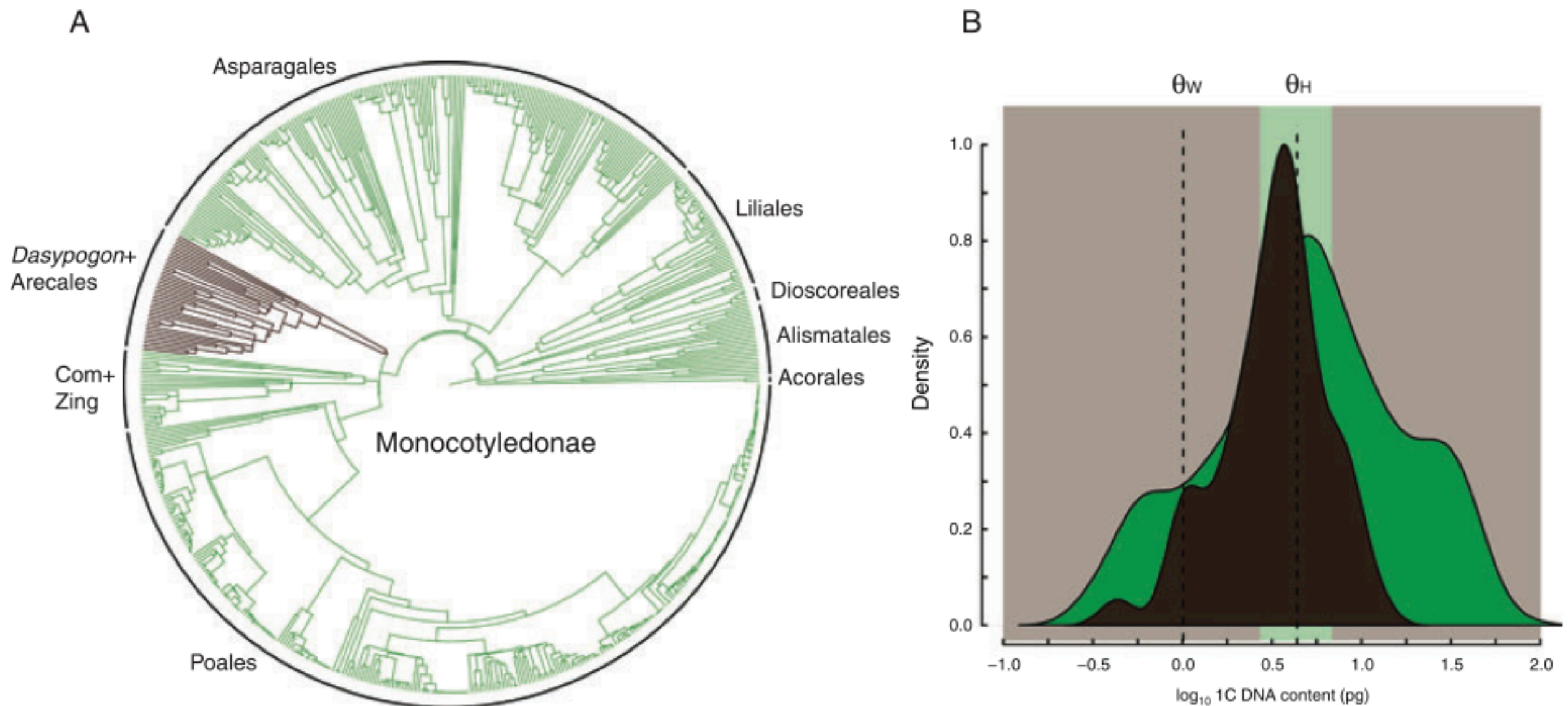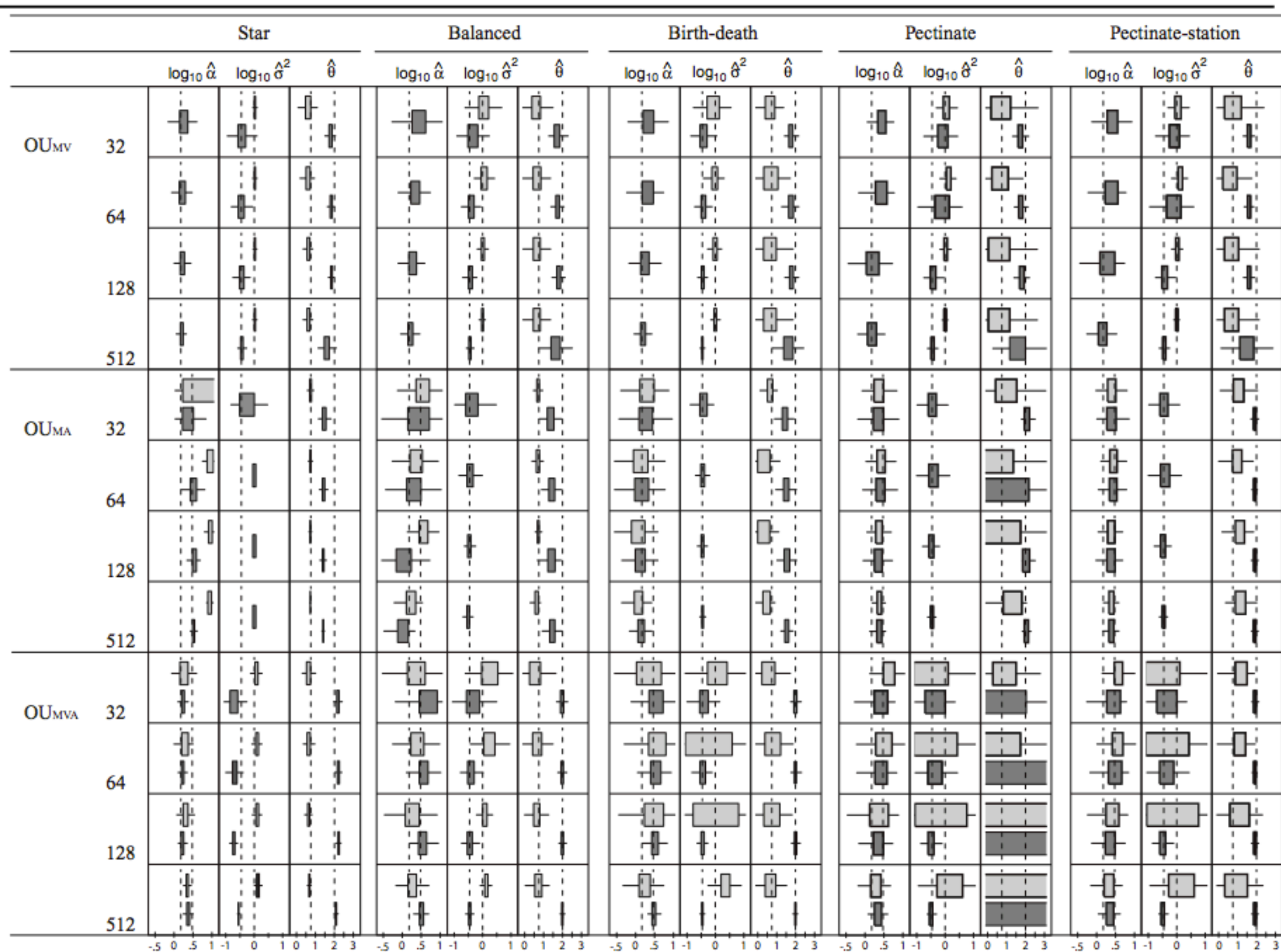Beaulieu, Jhwueng, Boettiger, O'Meara 2012

Figure 2. (A) Time-calibrated phylogeny of Monocotyledonae (monocots). The phylogeny is taken from a maximum likelihood analysis of 590 species based on combined analysis *atp*B, *mat*K, *ndh*F, *rbc*L, and *trn*L-F. The major clades of monocots are labeled, and estimates of the likeliest growth form state (woody = brown; herbaceous = green) across all branches in the tree. Com + Zing represents the combined clade of Commelinales and Zingiberales. (B) The distributions of 1C DNA content among growth form, with the optimum value for woody plants (θ_W) estimated to be larger than the optimum inferred for herbaceous lineages (θ_H). However, the optimum value for woody lineages was not identifiable, which may be explained by very weak selection ($\alpha < 0.001$) operating within this regime.

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Table 2. The fit of alternative models of genome size evolution in monocots. The best model, based on ΔAIC and Akaike weights, was the OU$_{MVA}$, which estimated a separate θ, α, and σ^2 for woody and herbaceous monocot lineages.

Model	-lnL	AIC	ΔAIC	w_i
BM1	−227.6	459.1	156.2	<0.01
BMS	−203.0	412.0	109.1	<0.01
OU1	−160.0	326.1	23.2	<0.01
OU$_M$	−159.2	326.5	23.6	<0.01
OU$_{MV}$	−147.3	304.6	1.7	0.290
OU$_{MA}$	−159.2	328.5	25.6	<0.01
OU$_{MVA}$	−145.3	302.9	0.0	0.678

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Table 3. Parameter estimates and their associated 95% confidence interval (CI) for the OU_{MVA} model, the model that best fit the genome size data. Each CI was obtained by multiplying each approximate standard error by the critical value in the t-distribution where the cumulative probability is equal to 0.975 (i.e., t (0.975, ∞) = 1.96).

	Herb Estimate	95% CI	Woody Estimate	95% CI
α	3.85	$\pm$ 0.955	<0.001	$\pm$ <0.01
σ^2	2.51	$\pm$ 0.376	0.531	$\pm$ 0.281
θ	0.618	$\pm$ 0.143	<0.001	$\pm$ ∞

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How do we figure out painting?
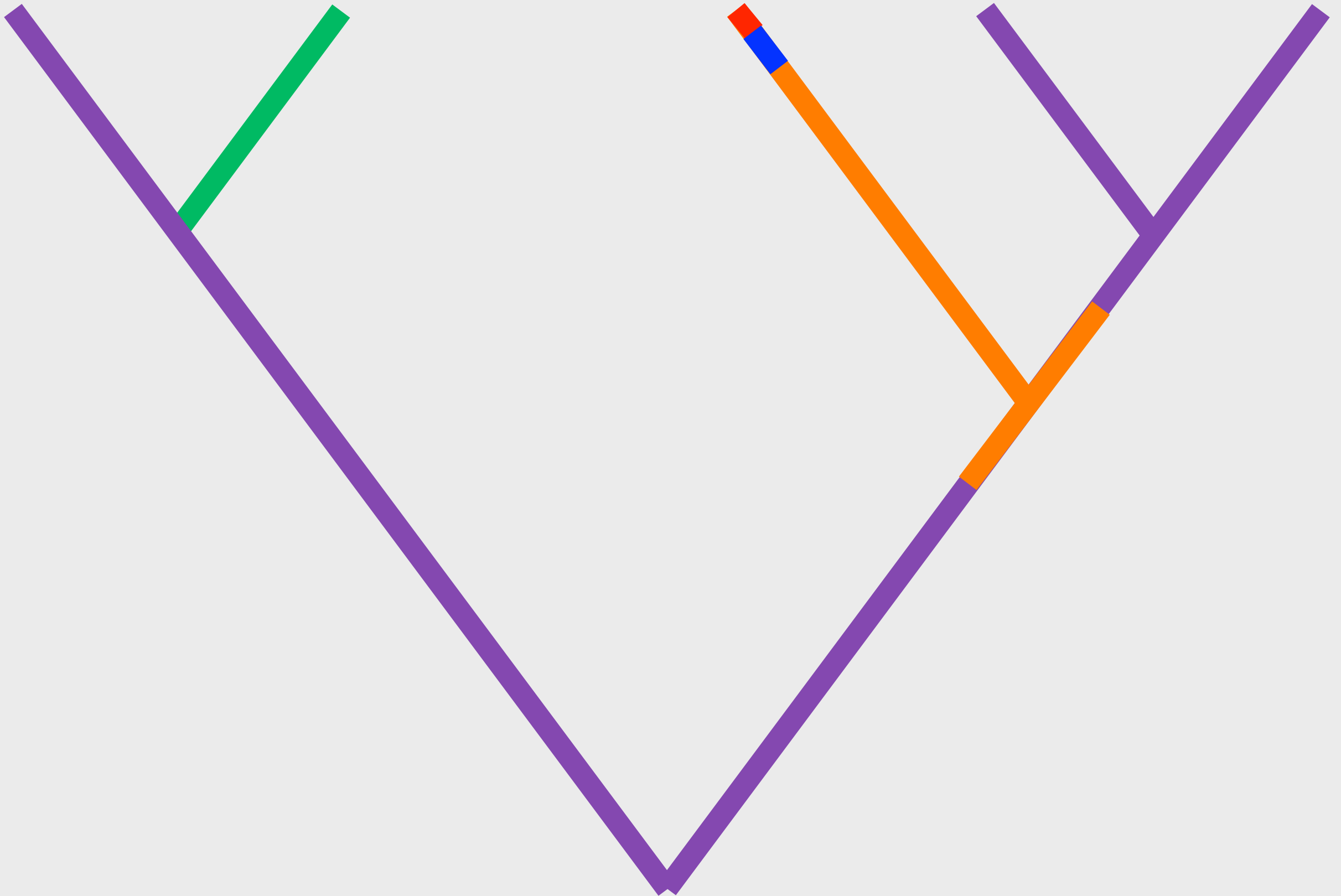
How do we figure out painting?

- a priori biological hypotheses
- Reconstruct a discrete trait, use that to paint continuous regimes
- Slice by taxonomy (monocots vs other plants)
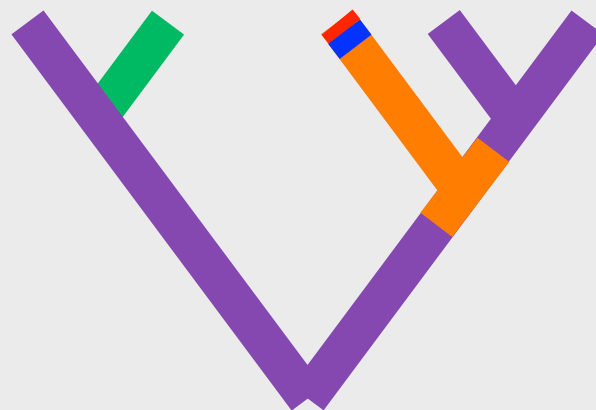- Slice by time (pre and post KT)

Table 2: Parameters estimated for the five models comparing character displacement with alternative hypotheses

	BM	OU(1)	OU(3)	OU(4)	OU(LP)
α		0	.32	14.67	2.49
σ	.21	.21	.20	.47	.22
θ_0	2.95	2.95	3.99	…[a]	.86
θ_{small}		…[a]	-1.40	2.58	2.75
θ_{medium}			.18	3.11	3.24
θ_{large}			2.71	3.30	3.56
$\theta_{ancestral}$				2.83	

Phylogenetic half life
= Tree height scaling × ln(2) / α
= 30 MY × ln(2) / 2.49
= 8.4 MY
to go halfway from log(25 mm) to log(35 mm) head lengths: 0.6 mm/MY, or 0.24% of the starting value/MY
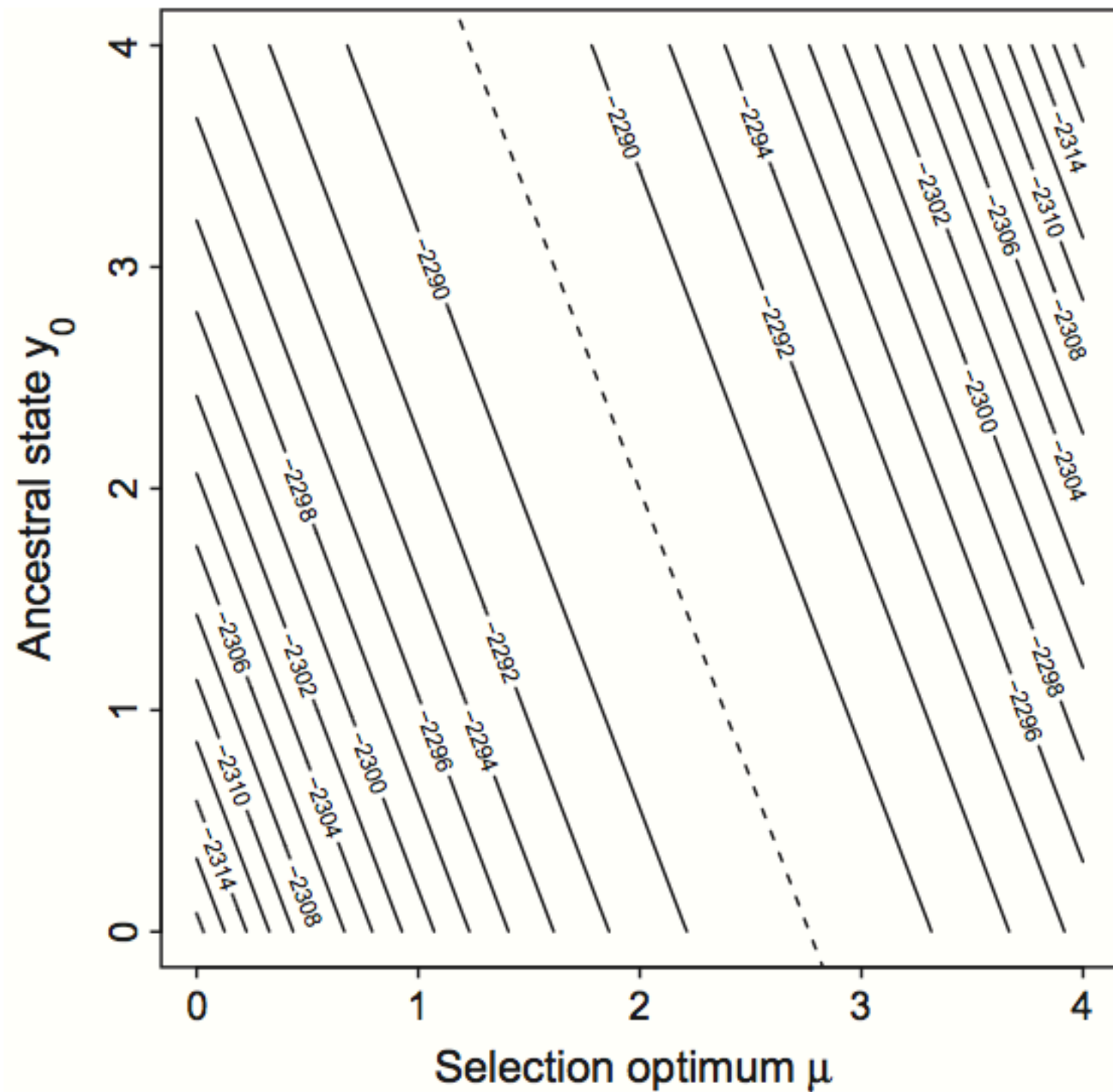
Fig. 1. Log likelihood surface with respect to (y_0, μ) from data simulated on a 4507-taxon tree, with other parameters fixed to their ML values. The dash line $y_0 e^{-\hat{\alpha}T} + \mu(1 - e^{-\hat{\alpha}T}) = 1\cdot998$ is where the likelihood achieves its maximum.
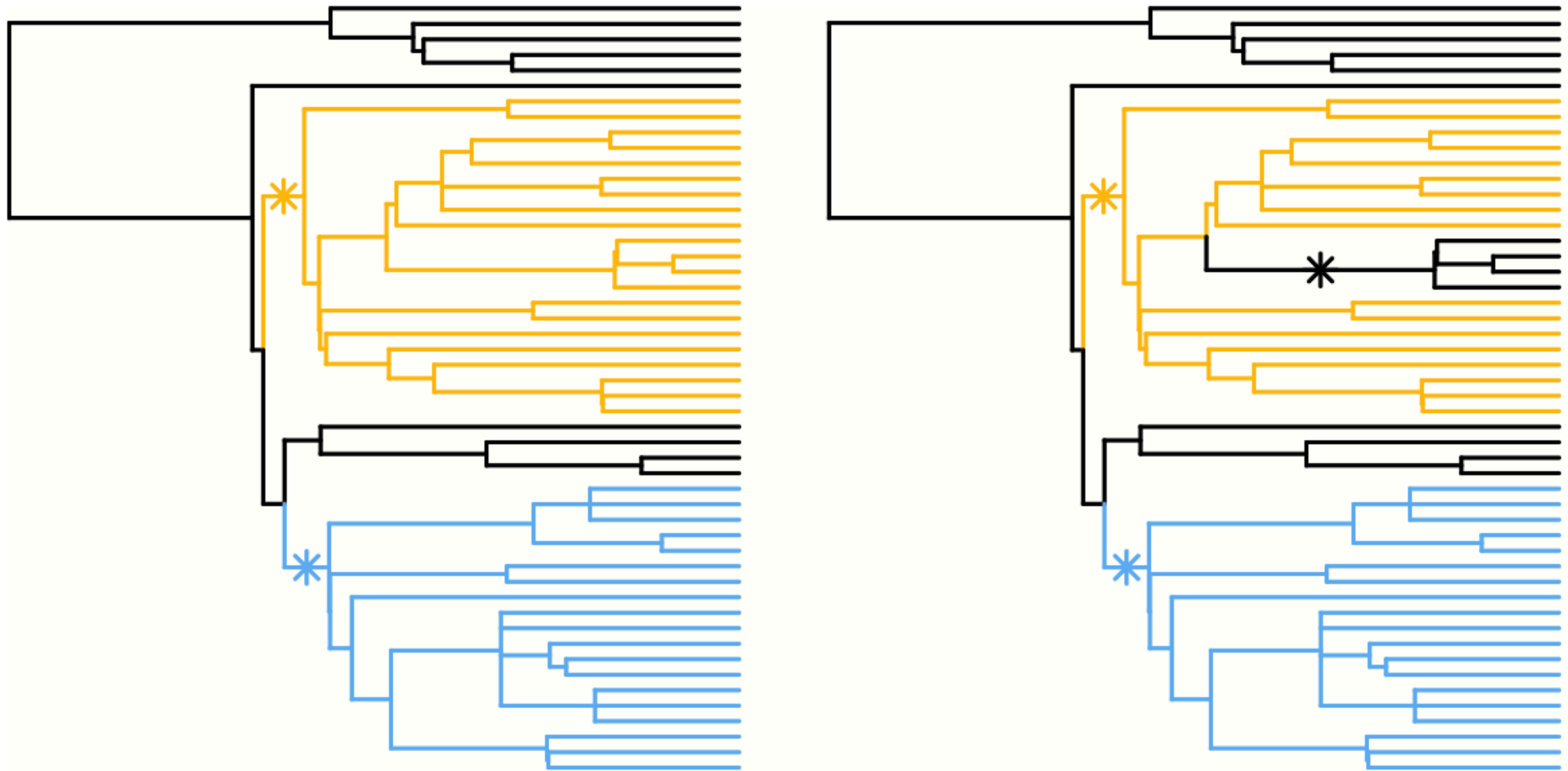
Fig. 2. Edges are 'painted' according to their selection regime, with one optimum μ_ℓ for each colour. Unidentifiability case (left): every selection regime forms a connected component. Identifiability case (right): one regime (black) covers two disconnected parts in the tree.

Ho & Ané 2014