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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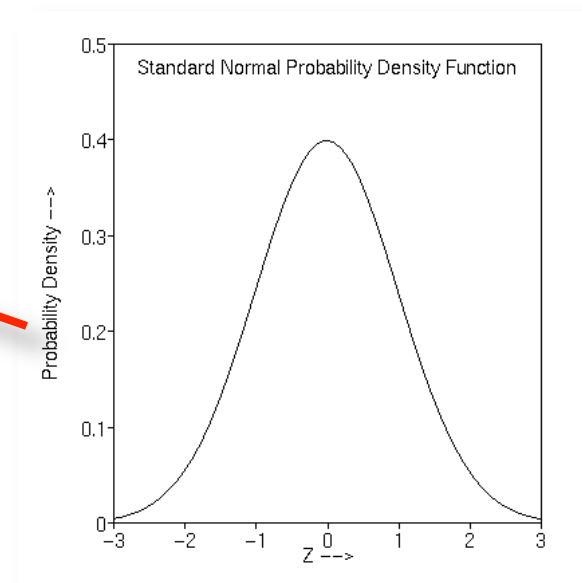
$$dX_T =$$

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

Randomly: increase or decrease slightly by chance

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$$dX_T = \qquad dW_T$$

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

and/or

Directionally: be pulled towards some value

$$dX_T = \sigma \times dW_T$$

Rate of wiggle

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**

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

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

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

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

and/or

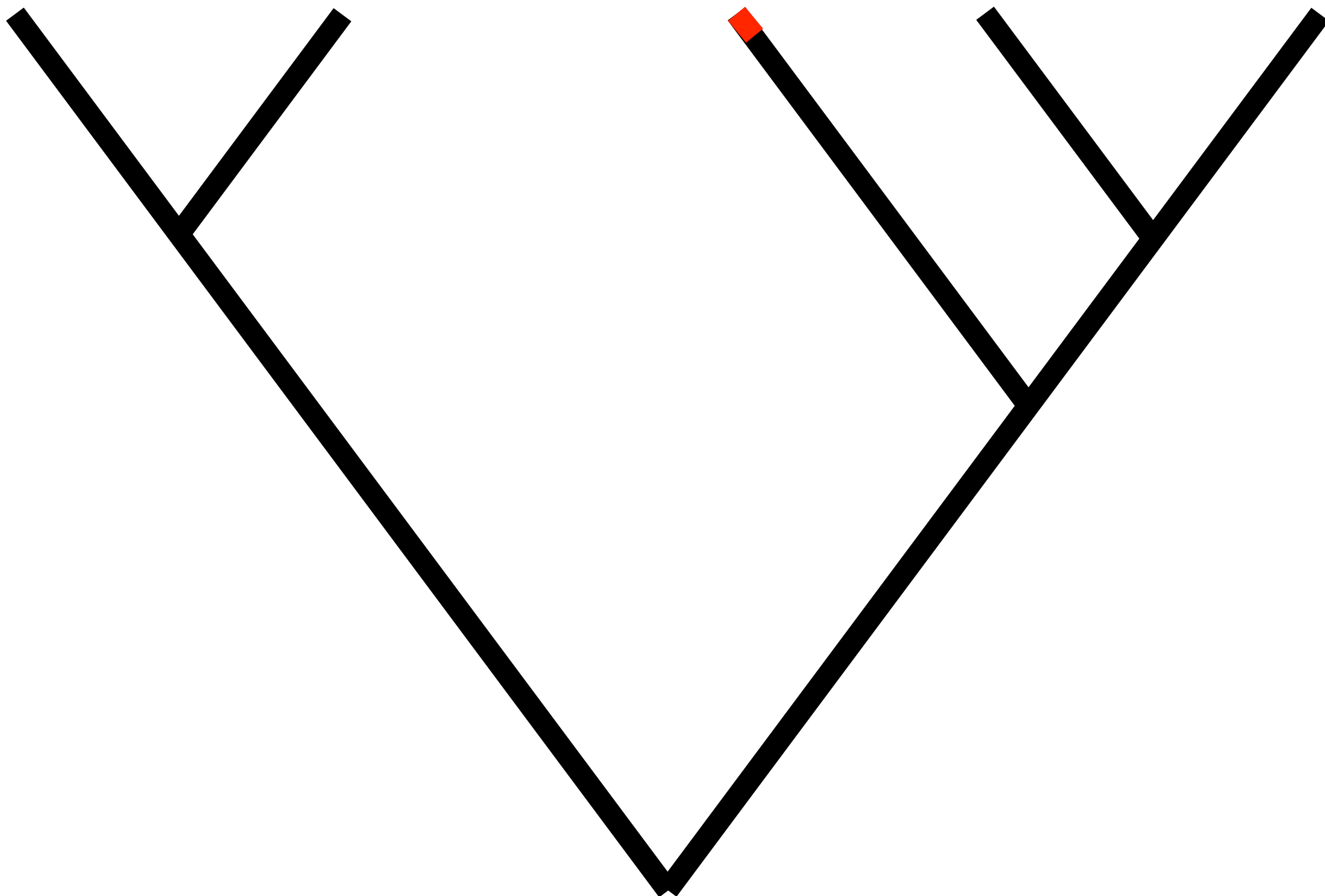Directionally: be pulled towards some value

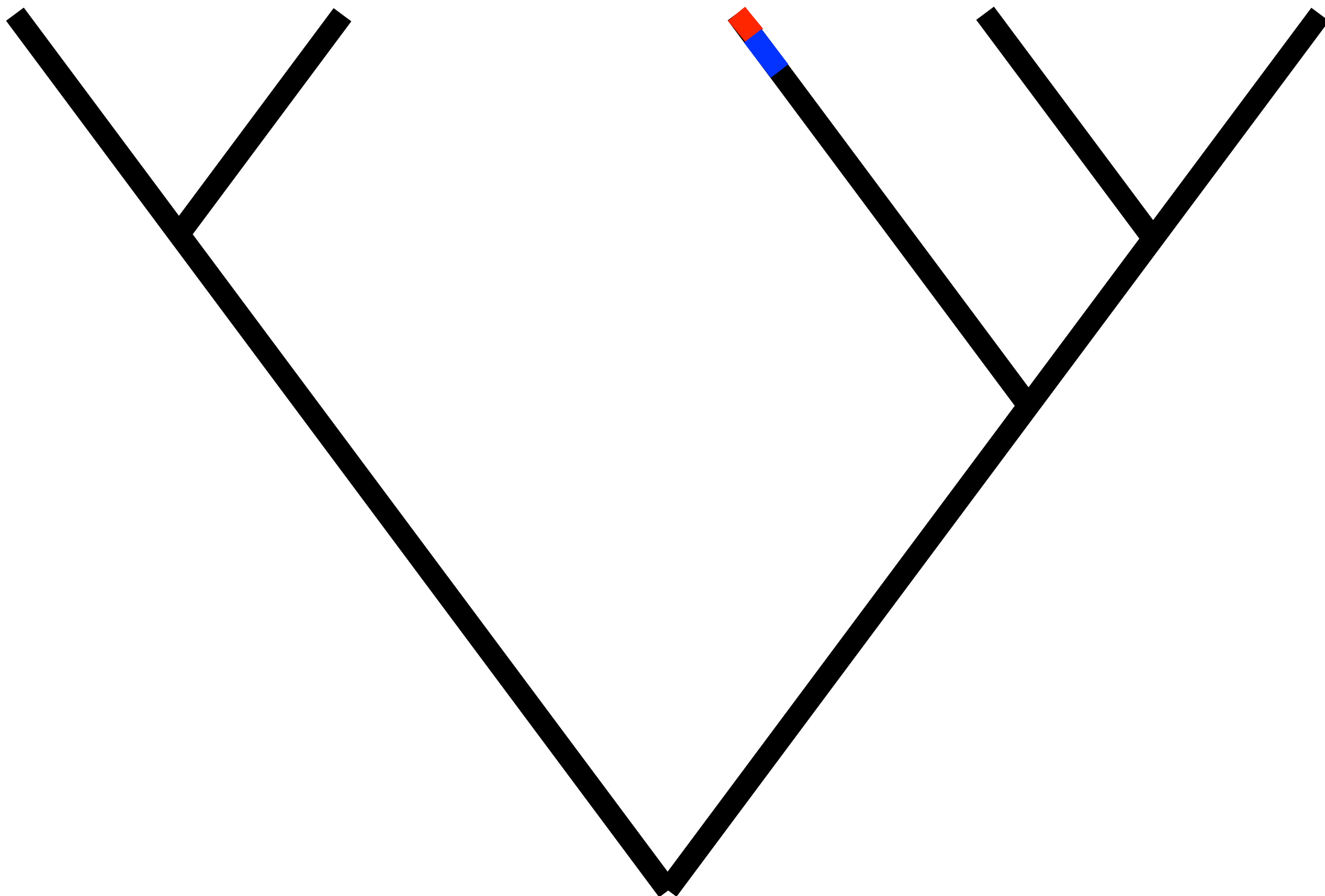$$dX_T = \sigma \times dW_T + \alpha(\theta - X_T)$$

Ornstein-Uhlenbeck process

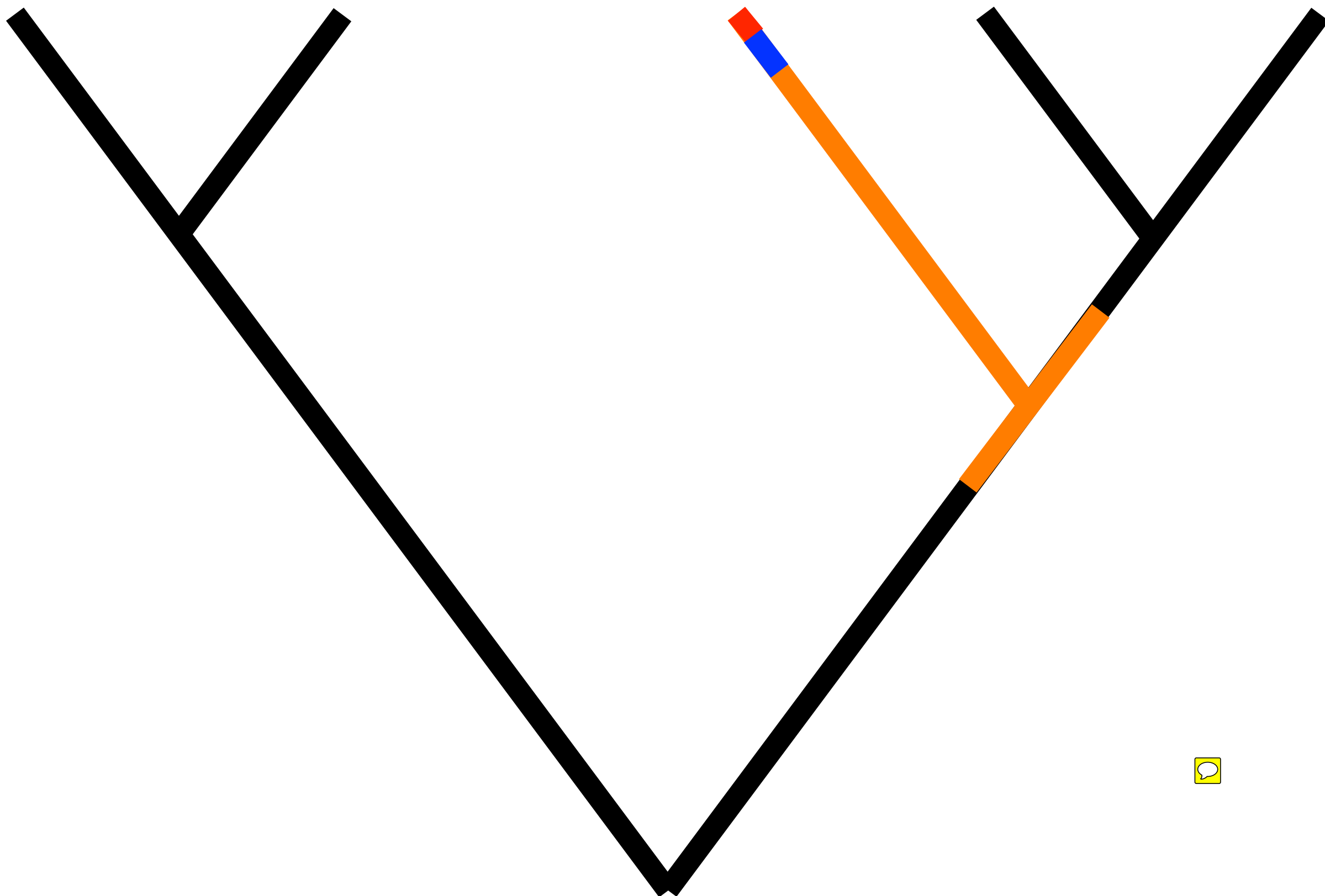$$dX_T = \sigma \times dW_T + \alpha(\theta - X_T)$$

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...

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

$$\sigma_i$$
$$\alpha_i$$
$$\theta_i$$

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

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

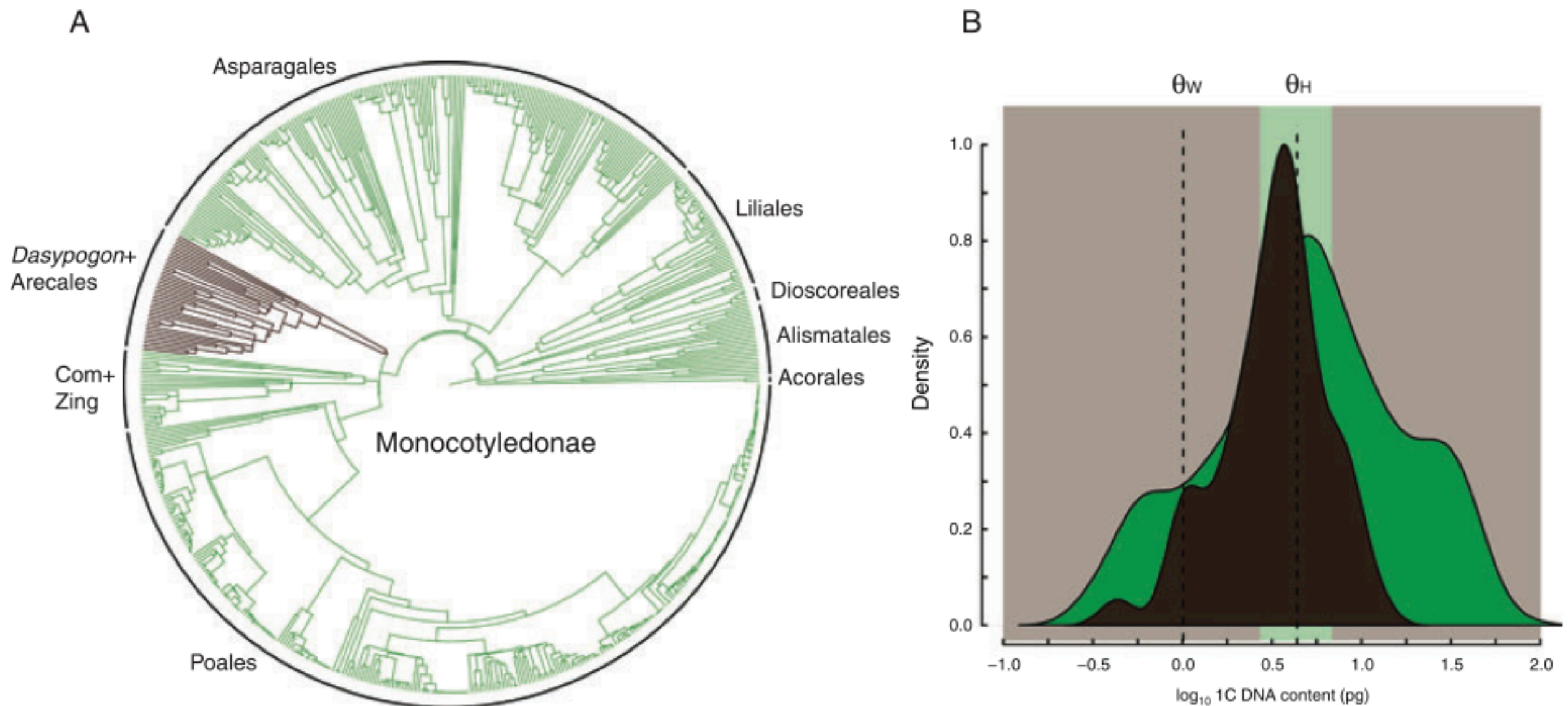Beaulieu, Jhwueng, Boettiger, O'Meara 2012

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.

Beaulieu, Jhwueng, Boettiger, O'Meara 2012

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

Beaulieu, Jhwueng, Boettiger, O'Meara 2012

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	$\pm \infty$

Beaulieu, Jhwueng, Boettiger, O'Meara 2012

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How do we figure out painting?

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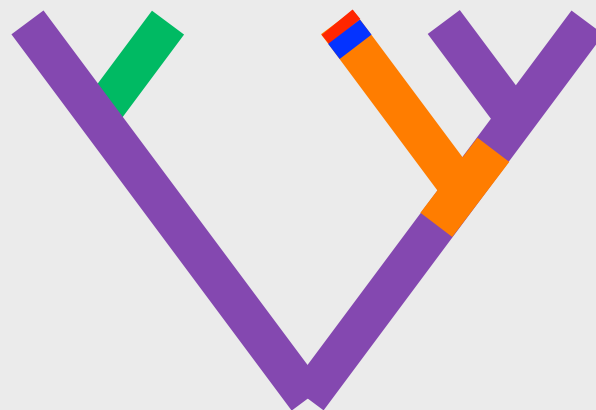- Slice by time (pre and post KT)

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
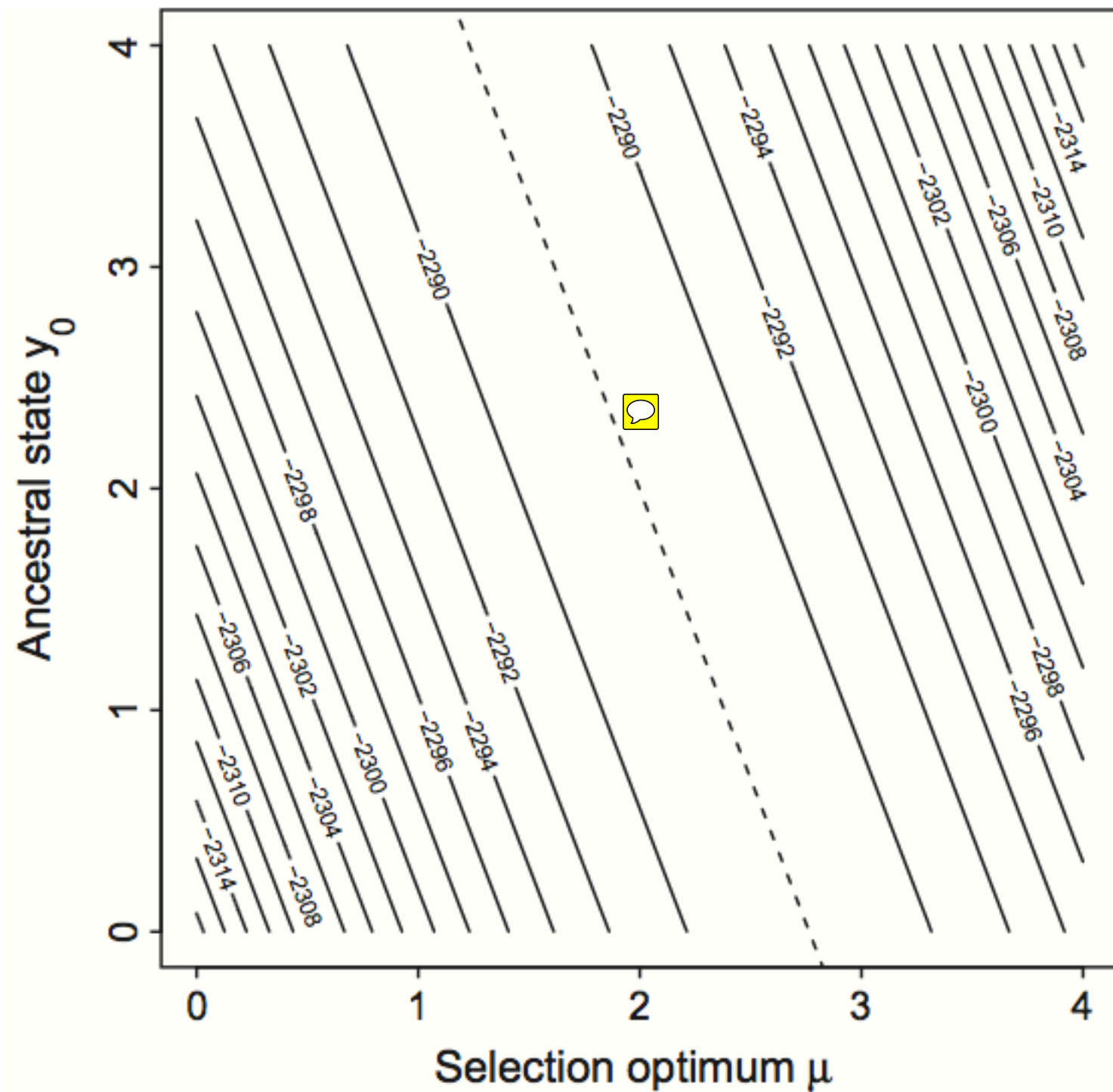
Fig. 1. Log likelihood surface with respect to (y_0, μ) from data simulated on a 4507-taxon tree, with other parameters fixed to their ML values. The dash line $y_0 e^{-\hat{\alpha}T} + \mu(1 - e^{-\hat{\alpha}T}) = 1 \cdot 998$ is where the likelihood achieves its maximum.
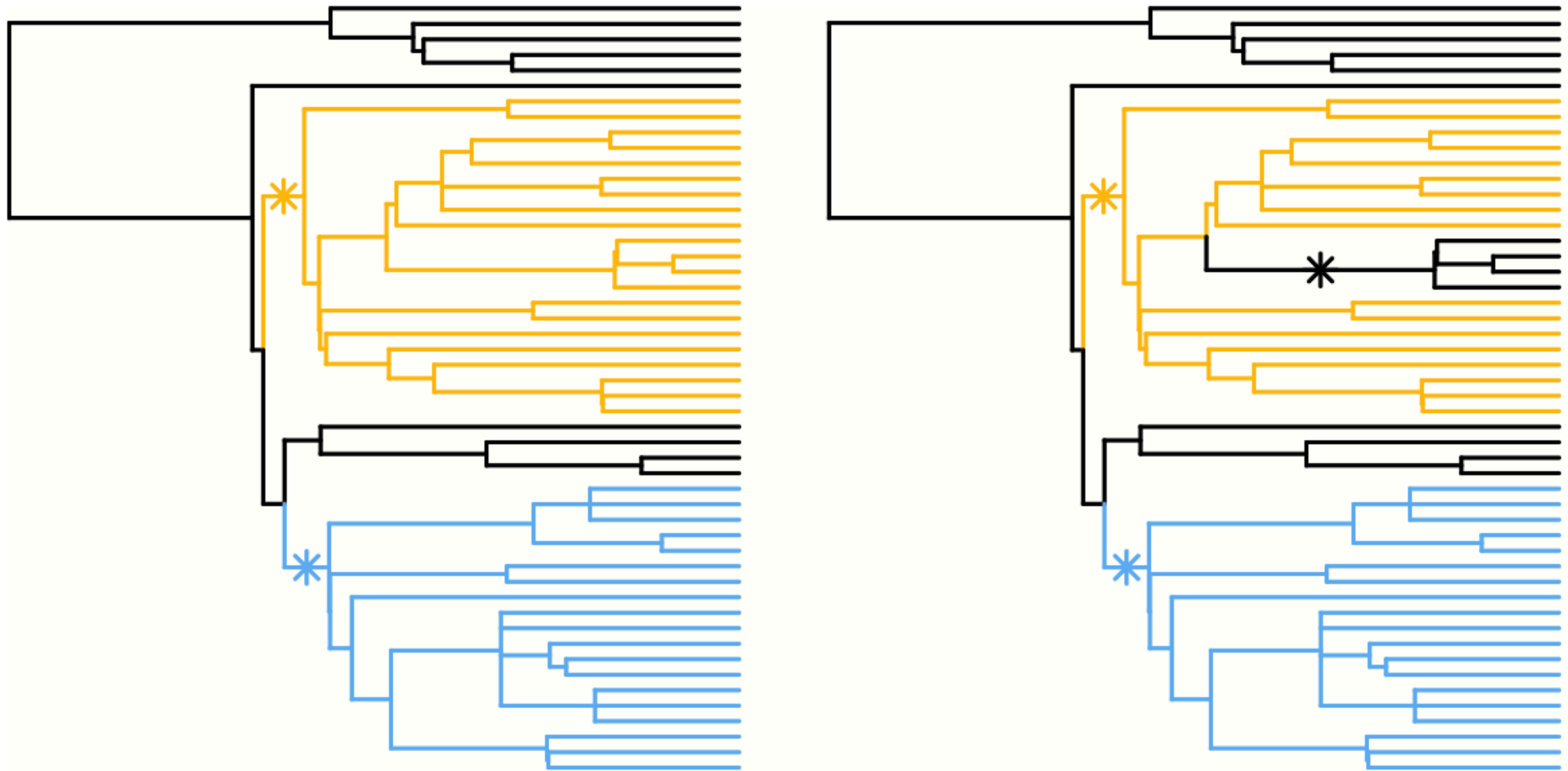
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Fig. 2. Edges are 'painted' according to their selection regime, with one optimum μ_ℓ for each colour. Unidentifiability case (left): every selection regime forms a connected component. Identifiability case (right): one regime (black) covers two disconnected parts in the tree.

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