Coalescence times of ancestral lineages in two-dimensional logistic branching random walks

Matthias Birkner

Joint work with Andrej Depperschmidt and Timo Schlüter

Stochastic Processes in Evolutionary Biology CIRM, 21 May 2024



(Wright-)Malécot formula (S. Wright 1943, G. Malécot 1948)

Assume:

- a population lives, reproduces and evolves in a two-dimensional space, offspring disperse (only) locally around parent's location
- habitat \approx homogeneous in space and time, population "in equilibrium"
- neutral genetic variation (according to infinite alleles)

Sample two individuals: one from 0, one from *x* ($\in \mathbb{R}^2$, say)

 $\phi(x) := \mathbb{P}(\text{the two sampled individuals have the same type})$

(Wright-)Malécot formula

 $\phi(x) := \mathbb{P}(\text{two sampled individuals with separation } x \text{ have same type})$

$$\phi(\mathbf{x}) \approx \frac{1}{2\pi\sigma^2\delta + K_0(\sqrt{2\mu}\,\kappa/\sigma)} K_0\left(\sqrt{2\mu}\,\|\mathbf{x}\|/\sigma\right) \quad \text{for } \|\mathbf{x}\| \ge \kappa$$

with

- $\delta > 0 \dots$ local population density (i.e., in a region A one should find on average $\delta |A|$ many individuals)
- $\sigma > 0 \dots$ standard deviation of the spatial displacement between a typical individual and its parent (viewed backwards in time)
- $\mu > \mathsf{0} \dots$ mutation probability per generation
- $\kappa > 0 \dots$ a "local scale" parameter (approximation breaks down for distances $< \kappa$)

 $K_0(\cdot)$ modified Bessel function of the second kind of order 0

$$K_0$$
 solves $t^2 \frac{d^2}{dt^2} K_0(t) + t \frac{d}{dt} K_0(t) - t^2 K_0(t) = 0, t > 0$
with boundary behaviour $K_0(t) \sim \sqrt{\frac{\pi}{2t}} \exp(-t)$ for $t \to \infty$,
 $K_0(0) \sim \log(1/t)$ for $t \to 0$.

G. Malécot originally derived this formula by proposing a recursion formula ('backwards analysis')

$$\phi(\mathbf{y}) = (1-\mu)^2 \left(\frac{1-\phi(\mathbf{0})}{\delta} \int_{\mathbb{R}^2} g_1(\mathbf{y}-\mathbf{z})g_1(\mathbf{z}) d\mathbf{z} + \int_{\mathbb{R}^2 \times \mathbb{R}^2} g_1(\mathbf{z})g_1(\mathbf{z}')\phi(\mathbf{y}+\mathbf{z}-\mathbf{z}') d\mathbf{z}d\mathbf{z}'\right)$$

 $(g_1(\cdot))$ is the 2d standard normal density), then taking the Fourier transform and (formally) inverting it

Very nice explanations and discussion e.g. in

- N. H. Barton, F. Depaulis, A. M. Etheridge, *Neutral evolution in spatially continuous populations*, Theor. Pop. Biol. 61(1):31–48, (2002).
- A. M. Etheridge, *Evolution in fluctuating populations*, Mathematical statistical physics, Elsevier B. V., 2006, pp. 489–545.
- A. M. Etheridge, *Spatial population models*, 23rd Brazilian school of probability, Sociedade Brasileira de Matemática, 2019, pp. 75–186.

An alternative view on Malécot's formula

Assume:

Two ancestral lineages cannot merge when separated by more than κ , the difference of their spatial embeddings is a 2*d* Brownian motion $(B_t)_{t\geq 0}$ (variance $2\sigma^2$).

$$egin{aligned} & \tau := \inf\{t \geq 0: \|B_t\| \leq \kappa\}. \ & ext{For } \mu \geq 0 ext{ put } \ & f_\mu(x) = \mathbb{E}_x[\exp(-2\mu au)\phi(\kappa)], \quad x \in \mathbb{R}^2 \end{aligned}$$

We have

$$\sigma^2 \Delta f_\mu(x) - 2\mu f_\mu(x) = 0, \quad ||x|| > \kappa,$$

$$f_\mu(x) = \phi(\kappa), \quad ||x|| \le \kappa.$$

By radial symmetry, $f_\mu(x) = g_\mu(\|x\|).$

 g_μ solves (using the Laplace operator in polar coordinates)

$$g_\lambda^{\prime\prime}(x)+rac{1}{r}g_\lambda^\prime(r)-rac{2\mu}{\sigma^2}g_\lambda(r)=0, \quad r\geq\kappa$$

and $g_{\lambda}(\kappa) = \phi(\kappa)$, $g_{\lambda}(\infty) = 0$. Hence $f_{\mu}(x) = \phi(x)$.

Known problems with Malécot's formula

- No explicit underlying forwards model: critical branching Brownian motions die out in *d* = 2
 (J. Felsenstein's 'pain in the torus' 1975, O. Kallenberg 1977)
- (2) No consistent way of extending to larger sample sizes

Known problems with Malécot's formula

 No explicit underlying forwards model: critical branching Brownian motions die out in *d* = 2 (J. Felsenstein's 'pain in the torus' 1975, O. Kallenberg 1977)

(2) No consistent way of extending to larger sample sizes

Possible remedies:

(a) discretise space and enforce constant local population sizes (stepping stone model):

elegant sampling formulas via duality with coalescing random walks, but deterministic size restriction seems artificial (and removes 'ecology')

(b) consider branching random walks with local regulation or relatives (either in continuous space or in discrete space): however, little hope for explicit sampling formulas

(c) Spatial-A-Fleming Viot processes: in principle elegant sampling formulas, very versatile approach, arguably implicitly takes a large (local) population density limit

N. H. Barton, A. M. Etheridge, A. Véber 2010 and ...

(d) consider a compact space [cf. P. Koepernik, The Brownian spatial coalescent, arxiv:2401.08557] **Remark** (Remedy (a) is not "too bad"). Malécot's formula fits well also to 2-dim. stepping stone models (with suitably adjusted parameters) already for quite modest distances, as observed e.g. in Barton, Depaulis, Etheridge 2002.



Comparison with IBD probability in a stepping stone model on \mathbb{Z}^d : N = 10, symmetric nearest neighbour migration at rate $m = 0.05 (= 2\sigma^2)$, $\mu = 10^{-6}$ (with choice $\kappa = 0.33$)

Remedy (b): Branching random walk with local density-dependent feedback

- Offspring distribution supercritical when there are few neighbours, subcritical when there are many neighbours
- Possible and natural extension of the stepping stone model (and of branching random walks and of the contact process)

e.g. Bolker & Pacala (1997), Murrell & Law (2003), Etheridge (2004), Fournier & Méléard (2004), Hutzenthaler & Wakolbinger (2007) Blath, Etheridge & Meredith (2007), B. & Depperschmidt (2007), Pardoux & Wakolbinger (2011), Greven, Sturm, Winter, Zähle (2015), Maillard & Penington (2022), ... Remedy (b): Branching random walk with local density-dependent feedback

- Offspring distribution supercritical when there are few neighbours, subcritical when there are many neighbours
- Possible and natural extension of the stepping stone model (and of branching random walks and of the contact process)

e.g. Bolker & Pacala (1997), Murrell & Law (2003), Etheridge (2004), Fournier & Méléard (2004), Hutzenthaler & Wakolbinger (2007) Blath, Etheridge & Meredith (2007), B. & Depperschmidt (2007), Pardoux & Wakolbinger (2011), Greven, Sturm, Winter, Zähle (2015), Maillard & Penington (2022), ...

Rest of this talk: Focus on (b) in the 'flavour' considered in B. & Depperschmidt (2007), recover an asymptotic version of Malécot's formula in that framework

Large sampling distance, small mutation rate: limits

Observation.

Assume

$$x = Ny$$
 with $y \in \mathbb{R}^2 \setminus \{0\}$ and $\mu = \mu_N = mN^{-2\gamma}$

with $m \in (0,\infty)$ and $\gamma \geq 1$ (all other parameters fixed).

Malécot's formula yields

$$\begin{split} \phi(\mathbf{x}) &= \frac{K_0\left(\sqrt{2m}||\mathbf{y}||N^{1-\gamma}/\sigma\right)}{2\pi\sigma^2\delta + K_0\left(\sqrt{2m}\,\kappa N^{-\gamma}/\sigma\right)} \\ &\sim \frac{-\log\left(\sqrt{2m}||\mathbf{y}||N^{1-\gamma}/\sigma\right)}{-\log\left(\sqrt{2m}\,\kappa N^{-\gamma}/\sigma\right)} \xrightarrow[N \to \infty]{} 1 - \frac{1}{\gamma} \end{split}$$

(using $K_0(t) \sim \log(1/t)$ for $t \downarrow 0$)

(Our version of) Logistic branching random walks

Particles 'live' in \mathbb{Z}^d in discrete generations, $\eta_n(x) = \#$ particles at $x \in \mathbb{Z}^d$ in generation *n*.

Given η_n ,

each particle at *x* has Poisson $((m - \sum_{z} \lambda_{z-x}\eta_n(z))^+)$ offspring, m > 1, $\lambda_z \ge 0$, $\lambda_0 > 0$, symmetric, finite range.

(Local competition: Ind. at *z* reduces average reproductive success of focal ind. at *x* by λ_{z-x})

(Our version of) Logistic branching random walks

Particles 'live' in \mathbb{Z}^d in discrete generations, $\eta_n(x) = \#$ particles at $x \in \mathbb{Z}^d$ in generation *n*.

Given η_n ,

each particle at *x* has Poisson $((m - \sum_{z} \lambda_{z-x}\eta_n(z))^+)$ offspring, m > 1, $\lambda_z \ge 0$, $\lambda_0 > 0$, symmetric, finite range.

(Local competition: Ind. at *z* reduces average reproductive success of focal ind. at *x* by λ_{z-x})

Children take an independent random walk step to *y* with probability p_{y-x} , $p_{xy} = p_{y-x}$ symmetric, aperiodic finite range random walk kernel on \mathbb{Z}^d .

(Our version of) Logistic branching random walks

Particles 'live' in \mathbb{Z}^d in discrete generations, $\eta_n(x) = \#$ particles at $x \in \mathbb{Z}^d$ in generation *n*.

Given η_n ,

each particle at *x* has Poisson $((m - \sum_{z} \lambda_{z-x}\eta_n(z))^+)$ offspring, m > 1, $\lambda_z \ge 0$, $\lambda_0 > 0$, symmetric, finite range.

(Local competition: Ind. at *z* reduces average reproductive success of focal ind. at *x* by λ_{z-x})

Children take an independent random walk step to *y* with probability p_{y-x} , $p_{xy} = p_{y-x}$ symmetric, aperiodic finite range random walk kernel on \mathbb{Z}^d .

Given η_n ,

$$\eta_{n+1}(y) \sim \operatorname{Poi}\Big(\sum_{x} p_{y-x}\eta_n(x) \big(m - \sum_{z} \lambda_{z-x}\eta_n(z)\big)^+\Big), \quad ext{independent}$$

Remarks

$$\eta_{n+1}(y) \sim \operatorname{Poi}\Big(\sum_{x} p_{y-x}\eta_n(x) \big(m - \sum_{z} \lambda_{z-x}\eta_n(z)\big)^+\Big), \quad \text{independent}$$

- For $\lambda \equiv 0$, (η_n) is a branching random walk.
- (η_n) is a spatial population model with local density-dependent feedback:
 Offspring distribution supercritical when there are few neighbours, subcritical when there are many neighbours
- System is in general *not* attractive.
- Conditioning¹ on η_n(·) ≡ N for some N ∈ N ("effective local population size") yields a discrete version of the stepping stone model
- Dynamics can be generalised (e.g. form of feed-back function or offspring distribution)

¹and considering types and/or ancestral relationships

Survival, complete convergence, stationary regime

Theorem (B. & Depperschmidt, 2007).

Assume $m \in (1, 3)$, $0 < \lambda_0 \ll 1$, $\lambda_z \ll \lambda_0$ for $z \neq 0$.

 (η_n) survives for all time globally and locally with positive probability for any non-trivial initial condition η_0 . Given survival, η_n converges in distribution to its unique non-trivial equilibrium $\overline{\nu}$.

Survival, complete convergence, stationary regime

Theorem (B. & Depperschmidt, 2007).

Assume $m \in (1, 3)$, $0 < \lambda_0 \ll 1$, $\lambda_z \ll \lambda_0$ for $z \neq 0$.

 (η_n) survives for all time globally and locally with positive probability for any non-trivial initial condition η_0 . Given survival, η_n converges in distribution to its unique non-trivial equilibrium $\overline{\nu}$.

Consider the stationary process $(\eta_n^{\text{stat}})_{n \in \mathbb{Z}}$ with $\mathcal{L}(\eta_n^{\text{stat}}) = \overline{\nu}$ for all $n \in \mathbb{Z}$, enriched with "enough book-keeping" to follow ancestries of particles. Let $x \in \mathbb{Z}^d$, $x \neq 0$, sample one individual from η_0^{stat} at 0 and one from x $X = (X_k)_{k \in \mathbb{N}_0}$, X_k = position of ancestor k generations into the past of particle sampled at 0

 $X' = (X'_k)_{k \in \mathbb{N}_0}, X'_k$ = position of ancestor k generations into the past of particle sampled at x

 au_{coal} = time (in generations) to MRCA of the two sampled particles

Theorem (B., Depperschmidt, Schlüter 2024). Let d = 2, assume $m \in (1, 3)$, $0 < \lambda_0 \ll 1$, $\lambda_z \ll \lambda_0$ for $z \neq 0$.

$$\lim_{N \to \infty} \mathbb{P}_{Nx} \big(\tau_{\text{coal}} > N^{2\gamma} \big) = \frac{1}{\gamma} \quad \text{ for } \gamma \geq 1.$$

(\mathbb{P}_{Nx} refers to sampling at separation Nx, $x \neq 0$)

Theorem (B., Depperschmidt, Schlüter 2024). Let d = 2, assume $m \in (1, 3)$, $0 < \lambda_0 \ll 1$, $\lambda_z \ll \lambda_0$ for $z \neq 0$.

$$\lim_{N\to\infty}\mathbb{P}_{Nx}\big(\tau_{\text{coal}}>N^{2\gamma}\big)=\frac{1}{\gamma}\quad\text{ for }\gamma\geq1.$$

(\mathbb{P}_{Nx} refers to sampling at separation Nx, $x \neq 0$)

Corollary. ("asymptotic analogue of Malécot's formula") This implies for $\mu_N = mN^{-2\gamma}$ ($\gamma \ge 1$, $m \in (0, \infty)$)

$$\phi_N(Nx) = \mathbb{E}_{Nx} \left[\left(1 - \mu_N \right)^{2\tau_{\text{coal}}} \right] \underset{N \to \infty}{\longrightarrow} 1 - \frac{1}{\gamma}$$

Theorem (B., Depperschmidt, Schlüter 2024). Let d = 2, assume $m \in (1, 3)$, $0 < \lambda_0 \ll 1$, $\lambda_z \ll \lambda_0$ for $z \neq 0$.

$$\lim_{N\to\infty}\mathbb{P}_{Nx}\big(\tau_{\mathrm{coal}}>N^{2\gamma}\big)=\frac{1}{\gamma}\quad\text{ for }\gamma\geq1.$$

(\mathbb{P}_{Nx} refers to sampling at separation Nx, $x \neq 0$)

Corollary. ("asymptotic analogue of Malécot's formula") This implies for $\mu_N = mN^{-2\gamma}$ ($\gamma \ge 1$, $m \in (0, \infty)$)

$$\phi_{N}(Nx) = \mathbb{E}_{Nx} \left[\left(1 - \mu_{N}\right)^{2\tau_{\text{coal}}} \right] \underset{N \to \infty}{\longrightarrow} 1 - \frac{1}{\gamma}$$

 $\begin{array}{ll} \mbox{Proof of corollary:} & \mathbb{E}_{Nx} \big[(1 - \mu_N)^{2\tau_{\rm coal}} \big] \sim \mathbb{E}_{Nx} \big[\exp(-2mN^{-2\gamma}\tau_{\rm coal}) \big] \\ \mbox{For } \varepsilon > 0 \mbox{ small and } N \mbox{ large} \end{array}$

$$\begin{split} \exp(-2m\mathsf{N}^{-\varepsilon})\mathbb{P}_{\mathsf{N}\mathsf{X}}\big(\tau_{\operatorname{coal}} \leq \mathsf{N}^{2\gamma-\varepsilon}\big) \\ & \leq \mathbb{E}_{\mathsf{N}\mathsf{X}}\big[\exp(-2m\mathsf{N}^{-2\gamma}\tau_{\operatorname{coal}})\big] \leq \mathbb{P}_{\mathsf{N}\mathsf{X}}\big(\tau_{\operatorname{coal}} \leq \mathsf{N}^{2\gamma+\varepsilon}\big) + \exp(-2m\mathsf{N}^{\varepsilon}) \end{split}$$

hence

$$\Big(1-\frac{1}{\gamma-\frac{\varepsilon}{2}}\Big)\big(1-o(1)\big) \leq \mathbb{E}_{Nx}\big[(1-\mu_N)^{2\tau_{\text{coal}}}\big] \leq \Big(1-\frac{1}{\gamma+\frac{\varepsilon}{2}}\Big)\big(1+o(1)\big)$$

then take $\varepsilon \downarrow 0$

Remark (Hitting times for two-dimensional random walk, Erdős-Taylor 1960).

Let $S = (S_k)_{k \in \mathbb{N}_0}$ be 2*d* (say, symmetric simple) random walk, $\tau_0 := \inf\{k : ||S_k|| = 1\}$ the hitting time of (neighbourhood of) the origin. For ||x|| = N and $\gamma \ge 1$,

$$\mathbb{P}_x(\inf\{k: \|S_k\|=1\} > N^{2\gamma}) = rac{1+o(1)}{\gamma} \quad \text{as } N = \|x\| \to \infty.$$

Remark (Hitting times for two-dimensional random walk, Erdős-Taylor 1960).

Let $S = (S_k)_{k \in \mathbb{N}_0}$ be 2*d* (say, symmetric simple) random walk, $\tau_0 := \inf\{k : ||S_k|| = 1\}$ the hitting time of (neighbourhood of) the origin. For ||x|| = N and $\gamma \ge 1$,

$$\mathbb{P}_x\big(\inf\{k: \|S_k\|=1\} > N^{2\gamma}\big) = \frac{1+o(1)}{\gamma} \quad \text{as } N = \|x\| \to \infty.$$

Idea:

$$\inf\{k: \|S_k\| = 1\} \asymp N^{2\gamma} \quad "\iff" \quad \|S\| \text{ hits } N^{\gamma} \text{ before } 1,$$

 $\mathbb{Z}^2 \ni x \mapsto \log(||x||)$ is 'almost' harmonic for S in $\mathbb{Z}^2 \setminus \{0\}$ (literally harmonic for 2*d* BM), thus

$$\mathbb{P}_{N}(\|S\| \text{ hits } N^{\gamma} \text{ before 1}) \approx \frac{\log(N) - \log(1)}{\log(N^{\gamma}) - \log(1)} = \frac{1}{\gamma}$$

Ancestral lines as random walks in dynamic random environment

- X_k = position of ancestor k generations into the past of particle sampled at 0
- X'_k = position of ancestor k generations into the past of particle sampled at x

X and X' are random walks in the dynamic random environment generated by (the time reversal of) $\eta^{\rm stat}$

Given η^{stat} and $X_k = x$, $X_{k+1} = y$ w. prob.

$$\frac{p_{x-y}\eta_{-k-1}^{\text{stat}}(y)(m-\sum_{z}\lambda_{z-y}\eta_{-k-1}^{\text{stat}}(z))^{+}}{\sum_{y'}p_{x-y'}\eta_{-k-1}^{\text{stat}}(y')(m-\sum_{z}\lambda_{z-y'}\eta_{-k-1}^{\text{stat}}(z))^{+}}$$

(note: a Poisson vector conditioned on its total sum is multinomial)

and analogously for X'

Note: even conditioned on η^{stat} , *X* and *X'* are correlated when closer than interaction range

Tools and proof ideas

• Joint regeneration construction for X and X' under the 'annealed' law (averaging over η^{stat} and the dynamics of the two ancestral lineages at the same time)

```
such that
```

```
\mathbb{P}(\text{more than } \ell \text{ steps until regeneration}) \leq \text{const.} \times \ell^{-\beta}
uniformly in the initial separation x and
```

```
total variation distance between
```

```
\mathcal{L}((X, X') \text{ until next regeneration } | \text{ initial separation } x)
```

and

 $\mathcal{L}((X, X'') \text{ until next regeneration } | \text{ initial separation } x)$ is $\leq \text{const.} \times ||x||^{-\beta}$ for some (large) $\beta > 2$, where X'' moves in an independent copy of η^{stat} . (Extending B., Černý, Depperschmidt 2016, where a single lineage is studied.)

- X X'', observed along regeneration times, has i.i.d. increments (with suff. high moments), thus X X'' behaves like 2*d* Brownian motion over large space-time scales.
- Couple (*X*, *X*') and (*X*, *X*'') with controlled error to transfer asymptotics

Tools and proof ideas, 2

Proof of survival and complete convergence of (η_n) and also the (joint) regeneration construction of two ancestral lineages uses

corresponding deterministic system

$$\zeta_{n+1}(y) = \sum_{x} p_{y-x} \zeta_n(x) \left(m - \sum_{z} \lambda_{z-x} \zeta_n(z)\right)^+$$

has unique (and globally attracting) non-triv. fixed point

• strong coupling properties of η

Tools and proof ideas, 2

Proof of survival and complete convergence of (η_n) and also the (joint) regeneration construction of two ancestral lineages uses

corresponding deterministic system

$$\zeta_{n+1}(y) = \sum_{x} p_{y-x} \zeta_n(x) \left(m - \sum_{z} \lambda_{z-x} \zeta_n(z) \right)^+$$

has unique (and globally attracting) non-triv. fixed point

- strong coupling properties of η
- coarse-graining and (lots of) comparisons with supercritical directed percolation.



Coupling: An essential proof ingredient



 $m = 1.5, p = (1/3, 1/3, 1/3), \lambda = (0.01, 0.02, 0.01)$

Starting from any two initial conditions η_0 , η'_0 , copies (η_n) , (η'_n) can be coupled such that if both survive, $\eta_n(x) = \eta'_n(x)$ in a space-time cone.

Coupling: An essential proof ingredient



 $m = 1.5, p = (1/3, 1/3, 1/3), \lambda = (0.01, 0.02, 0.01)$

Starting from any two initial conditions η_0 , η'_0 , copies (η_n) , (η'_n) can be coupled such that if both survive, $\eta_n(x) = \eta'_n(x)$ in a space-time cone.

Coupling: An essential proof ingredient



Modulus of difference

 $m = 1.5, p = (1/3, 1/3, 1/3), \lambda = (0.01, 0.02, 0.01)$

Starting from any two initial conditions η_0 , η'_0 , copies (η_n), (η'_n) can be coupled such that if both survive, $\eta_n(x) = \eta'_n(x)$ in a space-time cone.

Supercritical oriented percolation

"Eventually, everything is caught by the cluster started at the (space-time) origin."

(No information comes from outside at late times when *p* sufficiently large)



(Here, p = 0.77, $U = \{-1, 0, 1\}$, $\widetilde{U} = \{-2, -1, 0, 1, 2\}$)

Idea for constructing regeneration times

Find time points along the path such that:

- a cone (with fixed suitable base diameter and slope)
 centred at the current space-time position of the walk covers the path and everything it has explored so far (since the last regeneration)
- configuration η^{stat} at the base of the cone is "good"
- "strong" coupling for $\eta^{\rm stat}$ occurs inside the cone

Then, the conditional law of future path increments is completely determined by the configuration η^{stat} at the base of the cone (= a finite window around the current position)



Idea for constructing regeneration times

Find time points along the path such that:

- a cone (with fixed suitable base diameter and slope) centred at the current space-time position of the walk covers the path and everything it has explored so far (since the last regeneration)
- configuration η^{stat} at the base of the cone is "good"
- "strong" coupling for $\eta^{\rm stat}$ occurs inside the cone



Then, the conditional law of future path increments is completely determined by the configuration η^{stat} at the base of the cone (= a finite window around the current position)

• For joint regeneration of two lineages, we use corresponding *double cones*.

Outlook

- Results "conceptual" rather than practical: Can you get numbers out of it??
 (e.g. variance of lineages from parameters of forwards model? "in principle"-answer from regeneration construction, in practice: simulations)
- 'Abstract' regeneration construction can cover more general forwards models.
 Include continuous space models with discrete particles?
- Larger sample sizes?
 (note B., Gantert, Steiber 2019 for Brownian web limit in *d* = 1)
- Adding selection?

Thank you!

M.B., Andrej Depperschmidt, Timo Schlüter, Quenched CLT for ancestral lineages of logistic branching random walks, arXiv:2403.08567 (2024)

M.B., Andrej Depperschmidt, Timo Schlüter, Pair coalescence times of ancestral lineages of twodimensional logistic branching random walks, arXiv:2405.02090 (2024)