

DisturPloidy

<https://github.com/rosemckeon/ploidy>

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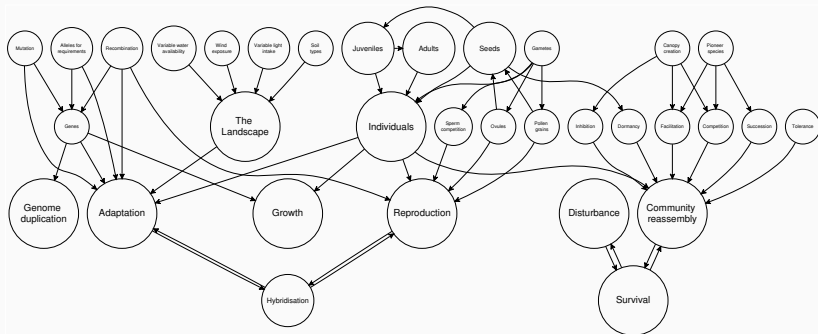
Individual-based models (IBMs)

IBMs emulate long-term evolutionary studies *in-silico* by simulating biological systems over virtual time.

- They allow for individual variation by representing all individuals in a population *explicitly*.
- This means fewer assumptions.
- Variables we're used to seeing in mathematical models (like N) become *emergent properties* of the simulation.
- IBMs are tailor made to simulate a specific system.

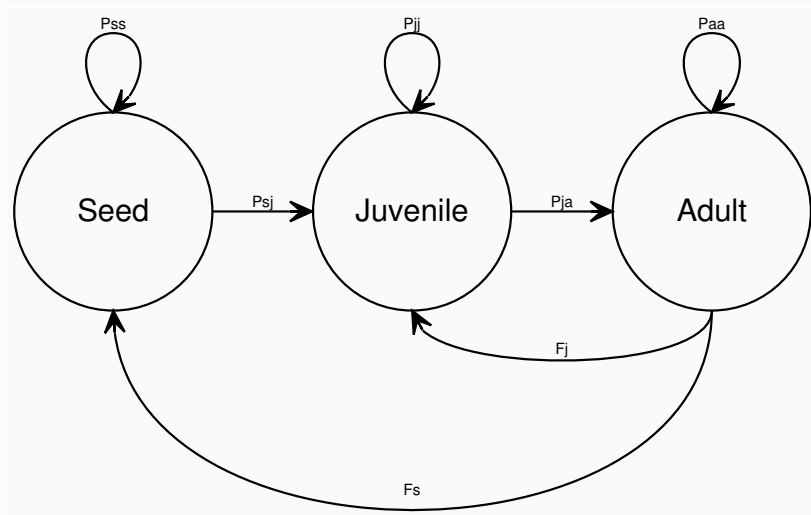
**How does disturbance on a
landscape affect the establishment
of new polyploid plant species?**

What I thought the model had to do



Basically, everything.

The Life Cycle



Costs

Reduce polyploid fitness:

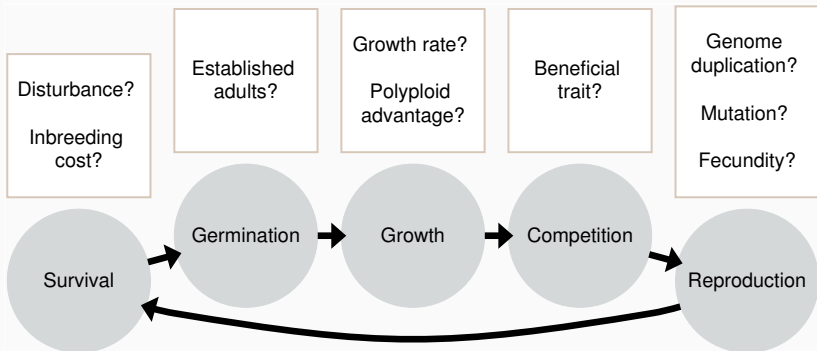
- **Triploid sterility** reduces fecundity.
- **Diploid pollen-swamping** reduces fecundity.

Benefits

Increase polyploid fitness:

- **Gigas-effects** reduce mortality.
- **Genetic buffering** reduces mortality.
- **Reversal of selfing inhibition** increases fecundity.

Model Flow










Plots here!

I learned more too.

Further work

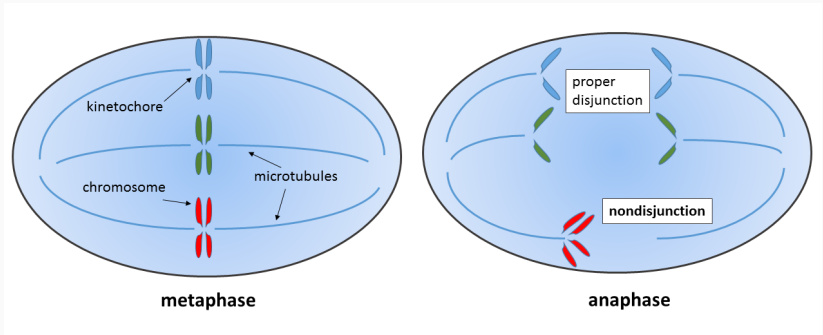
Version 2

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<input type="checkbox"/> ⓘ 7 Open ✓ 0 Closed		
<input type="checkbox"/> ⓘ	Consider including allopolyploids enhancement #104 opened 2 minutes ago by rosemckeon	
<input type="checkbox"/> ⓘ	Incorporate delayed maturity of polyploids enhancement #100 opened 4 days ago by rosemckeon	
<input type="checkbox"/> ⓘ	Allow polyploids to have increased ovule number enhancement #101 opened 4 days ago by rosemckeon	
<input type="checkbox"/> ⓘ	Improve disturbance enhancement #89 opened 14 days ago by rosemckeon	
<input type="checkbox"/> ⓘ	Improve cloning enhancement #88 opened 14 days ago by rosemckeon	
<input type="checkbox"/> ⓘ	Enable dormancy bug enhancement #98 opened 5 days ago by rosemckeon	
<input type="checkbox"/> ⓘ	Free up memory enhancement #103 opened 19 hours ago by rosemckeon	 3

Any questions?

Whole-Genome Duplication (WGD)



¹Wpeissner (2014). *Non-disjunction* [image]. Available at:
<https://commons.wikimedia.org/w/index.php?curid=32332257>

`ploidy_growth_benefit`

- Can take a value between 0 and 1.
- Any value above 0 allows the contribution of additional alleles for growth rate and so simulates *gigas-effects*.
- Smaller adults have lower fitness.
- Polyploids will have an advantage if `ploidy_growth_benefit` > 0.

¹Tested: 0, 0.5, and 1.

`inbreeding_cost`

- Can take a value between 0 and 1.
- Any value above 0 will increase winter mortality if an individual is homozygous at a specified locus.
- Polyploids will have better survival probabilities than their diploid counterparts, because the chance of being homozygous at any given locus is far smaller.

¹Tested: 0, 0.5, and 1.

Benefit: Reversal of selfing inhibition

selfing_polyploid_prob

- Takes a value between 0 and 1.
- Any value above 0 will give polyploids the ability to self-fertilise.
- This will increase fecundity, especially in the face of limited mate-choice (when `pollen_range` is low).
- Will convey a benefit to being polyploid when set to a value greater than that of diploids (default = 0).

¹Tested: 0, and 1 with pollen range reduced from the full landscape to $\frac{2}{3}$ and $\frac{1}{3}$.

`triploid_mum_prob`

- Takes a value between 0 and 1.
- Any value below `fertilisation_prob` will reduce the fecundity of triploids.
- Triploids in the model make 50/50 haploid/diploid gametes, so including triploid sterility also substantially reduces the chance of new polyploid lines arising.

¹Tested: 0, 0.375, and 0.75.

uneven_matching_prob

- Take a value between 0 and 1.
- Acts to affect fertilisation success when gametes possessing different ploidy levels meet (ie: a haploid gamete and a diploid gamete).
- Any value below **fertilisation_prob** will reduce the fecundity of polyploids, especially when diploid density (an emergent property) is high, and when mate-choice is not limiting (when **pollen_range** is high).
- This will reduce the appearance of triploids.

¹Tested: 0, 0.375, and 0.75.

`disturbance_freq`

- Takes a whole number between 0 and max generation.
- Any value above 0 enables a chance of disturbance during the winter survival period.
- The value represents the likely mean number of generations between disturbances.

`disturbance_mortality_prob`

- Takes a value between 0 and 1.
- Any value above 0 increases the chance of mortality during the survival period.

¹Tested: 0, 100, 50, 25, and 10.

The Individuals

ID	X	Y	life_stage	size	ploidy	gen	genome	growth_rate	inbreeding
0_94	4	5	2	4.219	2	3	—	1.616	FALSE
0_23	6	3	2	7.233	2	3	—	1.934	FALSE
0_62	7	0	2	3.004	2	3	—	1.443	FALSE
0_78	9	1	2	4.299	2	3	—	1.626	FALSE

allele	locus	value
1	1	48.64990
1	2	60.69052
2	1	89.82384
2	2	83.90019

