#### Identifying causal links between tectono-geomorphic processes and biodiversity with a coupled landscapebiodiversity evolution model

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#### Mountains are anomalously diverse...but why?

Hoorn et al., 2013; Badgley et al., 2017; Antonelli et al., 2018; Rahbek et al., 2019; Perrigo et al., 2020; Ott, 2020



From: Rahbek et al., Science, 2019.

## How does landscape evolution influence biodiversity?

Landscape evolution model (LEM)



We contribute to this question using a coupled LEM-Bio model

Mechanistic SEED model for biodiversity (speciation, evolution, extinction, dispersal)

## DAC (Divide and Capture): Coupled numerical and analytical LEM



Advantages of DAC:

- Computationally efficient
- Rivers are more dynamic sub-grid analytical solutions for rivers and divide
- Dynamic irregular, dynamic grid (nodes can be added/removed and move in space)





The location and elevation of each divide are found iteratively by solving analytical equations for the pair of tributary channels and hillslopes that define the divide.



The sub-grid analytical solutions for tributary channels and hillslopes allow rivers to be more dynamic than a model with solutions limited to the grid.







This results in more frequent river captures.

Bishop, 1995



The dynamic grid also allows for tectonic forcing in multiple directions
Vertical uplift + Horizontal advection ------

#### DAC: Numerical rivers and analytical tributaries

Detachment-limited stream power model of bedrock river incision:



Howard, 1994; Howard and Kerby, 1983; Siedl and Dietrich, 1992

#### DAC: Analytical hillslopes for finding divides

Hillslopes in DAC can be either (1) threshold or (2) Combination of linear diffusion and threshold (whichever results in lower divides).

**Linear diffusion** 

$$z_{hs}(x) = \frac{e_b}{2\alpha}(x_c^2 - x^2)$$



After Davis, 1892; Gilbert, 1909; Culling, 1960, 1963, 1965

 $x_c$  = Hillslope length

- $e_b$  = Incision rate at base of hillslope
- $\alpha$  = Diffusivity
- $\theta_c$  = Threshold hillslope angle

#### **Threshold hillslopes**

$$z_{hs}(x) = (x_c - x) \tan \theta_c$$



After Kirkby, 1987; Anderson and Humphrey, 1990; Howard, 1994



All nodes (not just channel head nodes) have a sub-grid analytical solution for a tributary and hillslope associated with each neighboring node.

#### DAC-Bio: Sub-grid structure based on analytical divides

We used these solutions to find the topography of each node's Voronoi cell. Each cell was split into many smaller triangles and for each small triangle we found the range in elevation as well as the slope and aspect.





#### Modeling biodiversity in DAC-Bio: Definitions

**Habitat patch** = Contiguous nodes defined as habitable using parameters acquired from simulated DEM



#### Modeling biodiversity in DAC-Bio: Definitions

Habitat patch = Contiguous nodes defined as habitable using parameters acquired from simulated DEM
Population = Inhabited nodes that are considered connected
Species = Grouping of 1 or more populations; genetic mixing between populations of same species when merged

Example: One species composed of two populations



- 1. Habitability requirements of species to be simulated using parameters acquired from simulated DEM:
  - Fraction of Voronoi cell that needs to be within habitable range
  - Aquatic/Terrestrial
  - Elevation
  - Slope
  - Aspect
  - Discharge



**Habitat patch** = Contiguous nodes defined as habitable

- 2. Dispersal abilities of species to be simulated
  - Dispersal rate (distance per time step)
- Uninhabitable grid node
   Unoccupied habitable node
  - Occupied habitable node

# All contiguous habitable nodes are considered connected.



- 2. Dispersal abilities of species to be simulated
  - Dispersal rate (distance per time step)
  - Ability to disperse across geographic barriers (uninhabitable nodes)
  - Uninhabitable grid nodeUnoccupied habitable node
  - Occupied habitable node

All nodes within dispersal distance per time step are considered connected regardless of habitability of intervening nodes.



3. Speciation rate, isolation time needed to become a new species

time 3 – time 2 > isolation time needed to become a new species



3. Speciation rate, isolation time needed to become a new species

#### Populations merge before required isolation time has elapsed







inhabited nodes

#### Tectonic scenarios simulated

Model input

Model output

- 1. Change in rock uplift rate: Step-increase or step-decrease in uplift rate.
- 2. Orogenic wedge: Steady shortening (horizontal movement of rock/nodes), e.g., Taiwan, Olympic Mountains, Apennine Mountains, Caucasus Mountains.





capture.

Model input

2. Terrestrial species: Defined by elevation, slope, aspect and with varying dispersal abilities.

Confined to channel network and limited by river discharge of 3 km<sup>2</sup>, but with instantaneous dispersal throughout river basin.



initial populations

Uniform vertical uplift, steady shortening (max advection at lower boundary, zero advection at upper boundary)



Observations: Landscape in flux steady-state but topology continuously changes with river capture of smaller pro-wedge basins by larger pro-wedge basins and or larger pro-wedge basins by retro-wedge basins.

Speciation time = 0.5 Myr; drainage area limit = 9 km<sup>2</sup>

Max advection rate:



- Total number of extant species rises through time and with max advection rate
- Diversification rates are fairly steady throughout but rise with max advection rate
- Means and standard deviation in richness and endemic richness rise with max advection rate.
- Number of captures is steady throughout and rises with max advection rate.

River captures drive genetic exchange.

Speciation time = 1.0 Myr; drainage area limit = 9 km<sup>2</sup>

Max advection rate:



With a longer speciation time, higher advection rate does not increase the number of species or species richness because river capture and genetic mixing occur before speciation time has elapsed.

Richness rises in retro-wedge rivers because of river capture from pro-wedge to retro-wedge basins richness 0.0e+00 4 6 8 10 12 14 16 2.0e+01

#### Aquatic species response to pulse of rock uplift rate



Elevation (and consequently slope and aspect) change but river network topology does not.

#### Aquatic species response to pulse of rock uplift rate



0.1

Time (Myr)

No large enough changes in river network topology to drive genetic mixing.

#### Terrestrial species response to changes in rock uplift

- Mid-elevation species, high slope, south-facing aspect
- No dispersal over barriers but instantaneous dispersal within habitat patches
- Speciation time = 3 Myr



#### Terrestrial species response to changes in rock uplift

- High elevation species, low slope, no aspect requirements
- No dispersal over barriers still but slower dispersal rate of 10 km/10 kyr within habitat patches.
- Speciation time = 3 Myr



#### Terrestrial species response to changes in rock uplift

- Mid-elevation species, high slope, south-facing aspect
- No dispersal over barriers but instantaneous dispersal within habitat patches
- Speciation time = 3 Myr



Terrestrial species response to changes in rock uplift with different dispersal rules

- Mid-elevation species, high slope, south-facing aspect
- Speciation time = 3 Myr

No dispersal over barriers; instantaneous dispersal within habitat patches Dispersal over barriers with dispersal rate of 2 km/ 10,000 yrs

![](_page_32_Figure_5.jpeg)

#### Current limitations of DAC-Bio

- Simulations require that initial conditions contain habitable terrain – i.e., species must be initialized they cannot be born as new terrain comes into existence.
- Computationally expensive such that simulation of full mountain ranges with tens of thousands of species takes a long time.

## Moving forward

- Add adaptation/evolution to enable simulation of mountain building and decay.
- More complex mountain building simulations.

Thanks for checking out my presentation! Feel free to get in touch at helen.beeson@erdw.ethz.ch