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nts in breedR

:/developments.html

Since Jaca…

- June's training workshop: `breedR v0.10`
- Today: `breedR v0.10-14`

Two important fixes were notified to `breedR`'s mailing list

1. Memory issues (reported by Jan Kowalczyk in GitHub)
2. Bug in the `variogram()` plot

Memory issues

- Under certain scenarios, the AR model consumed lots of memory
- Even with data of moderate size
- Two problems:

  1. The AR model builds a regular grid containing all the individuals. The size of the grid can be much larger than N.
  2. (Most importantly) AR was building unnecessary copies of matrices in non-sparse format

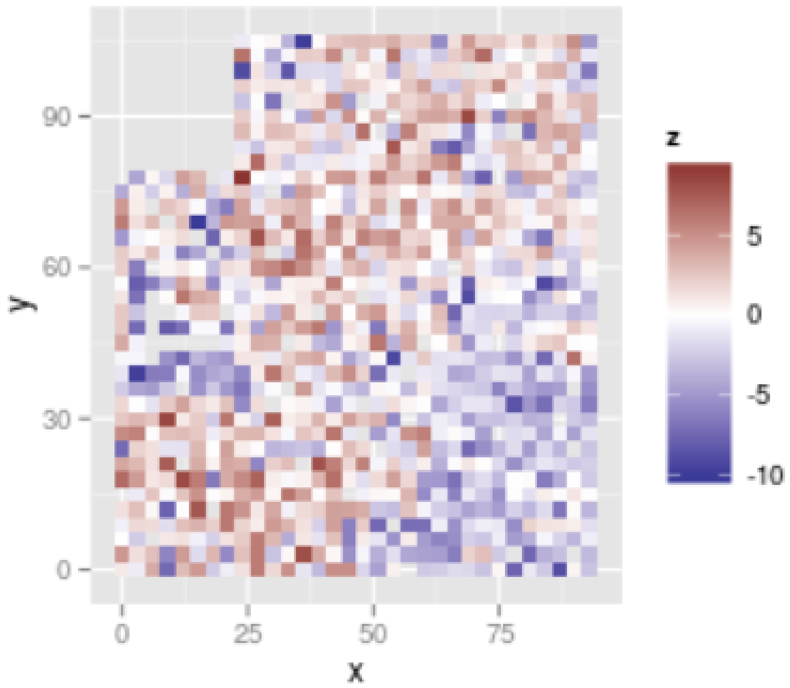
- Fixed from `breedR v0.10-9`

The bug in the variogram plot

- Affects the calculation of the variograms under **some** circunstances.
- When there were many *holes* in the field, it was treating the empty spaces as **observations with a value of 0**.
- The problem **did not affect** in any way the results of the models fitted with `remlf90()`. So your **results were correct** and reliable.

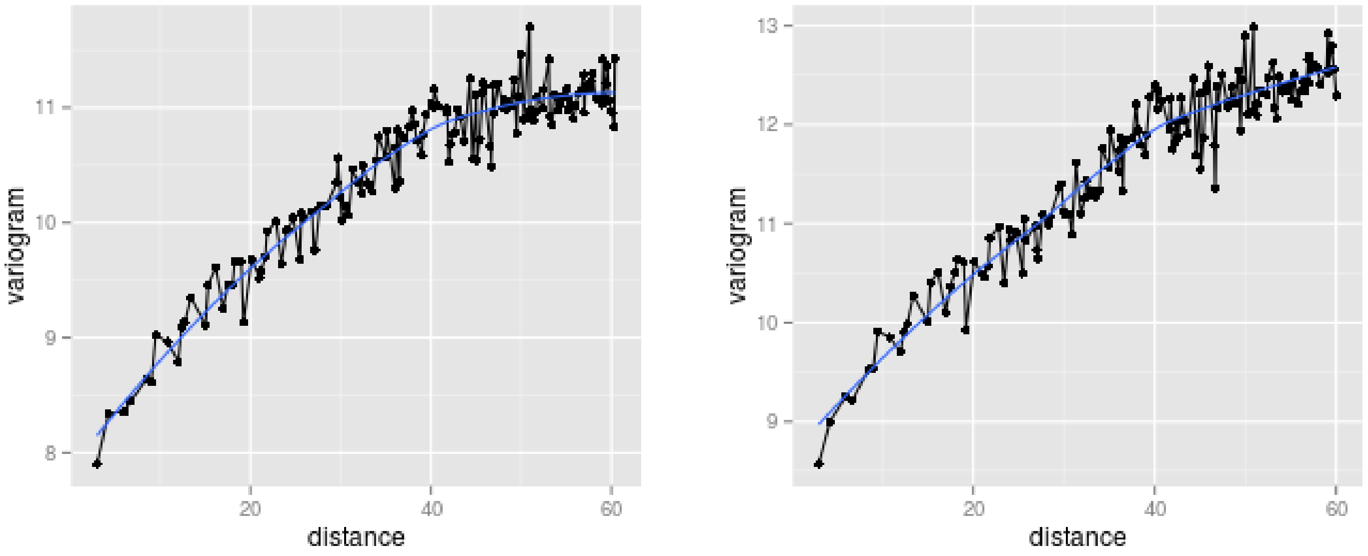
Scenario 1

Model residuals in a field trial with little or no holes



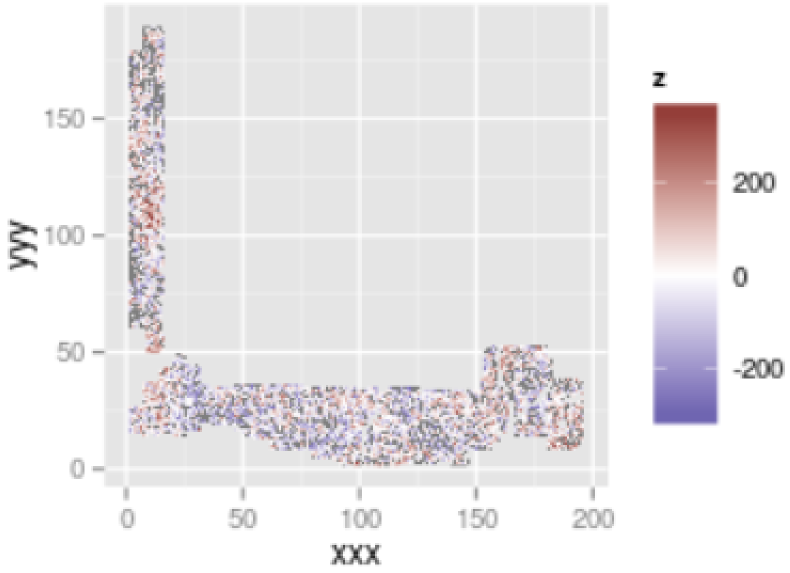
Difference in variograms

Before and after the fix



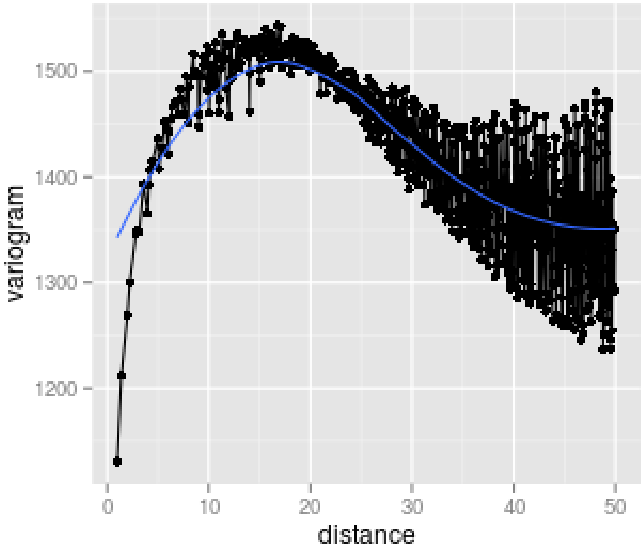
Scenario 1

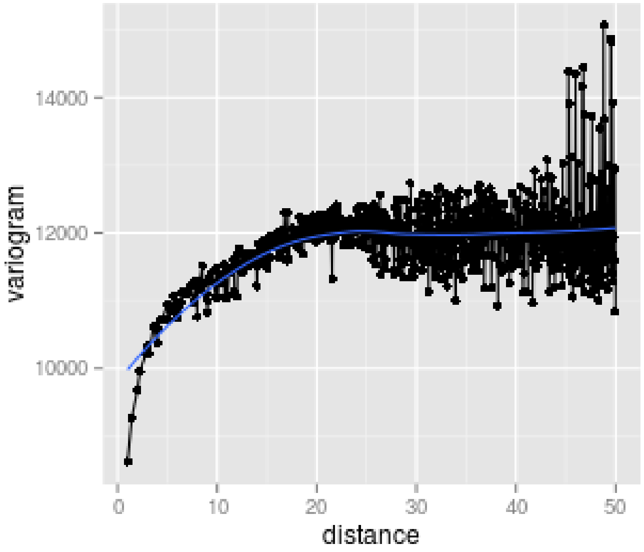
Model residuals in a field trial with lots of holes



Difference in variograms

Before and after the fix





Solution

- Adapt the function `fields::vgram.matrix()` for `breedR`
- Side effects
    - Remove dependency with package `fields`
    - Reported another bug in the function to `fields` maintainer
    - Return number of pairs for each variogram bin
- Fixed from `breedR v0.10-13`

Computation of heritability and its SE

Possible alternative calculations

$$h^2 = \frac{\sigma_a^2}{\sigma_{\mathrm{phenot}}^2} = \frac{\sigma_a^2}{\sigma_a^2 + \cdots + \sigma_e^2}$$

- Some authors **exclude** the variance of the spatial effect from the denominator (e.g. for comparability among sites)
- Need **flexibility** to compute it in different ways
- Sensible **default**: include all variance components in the denominator

Approach:

1. General interface to `OPTIONS` in `PROGSF90`
2. Exploit option `se_covar_function` in `AI-REML` which allows estimating a function of the variance components, and its SE
3. Generate default formula for heritability including all variance components, unless otherwise indicated by the user
4. Parse results and display in the summary()

Updates of **PROGSF90** binaries

Goals

- Avoid distributing binaries for all 3 main platforms with `breedR`
- Stop distributing 32bit programs only: take advantage of 64bit architectures (memory)

Approach

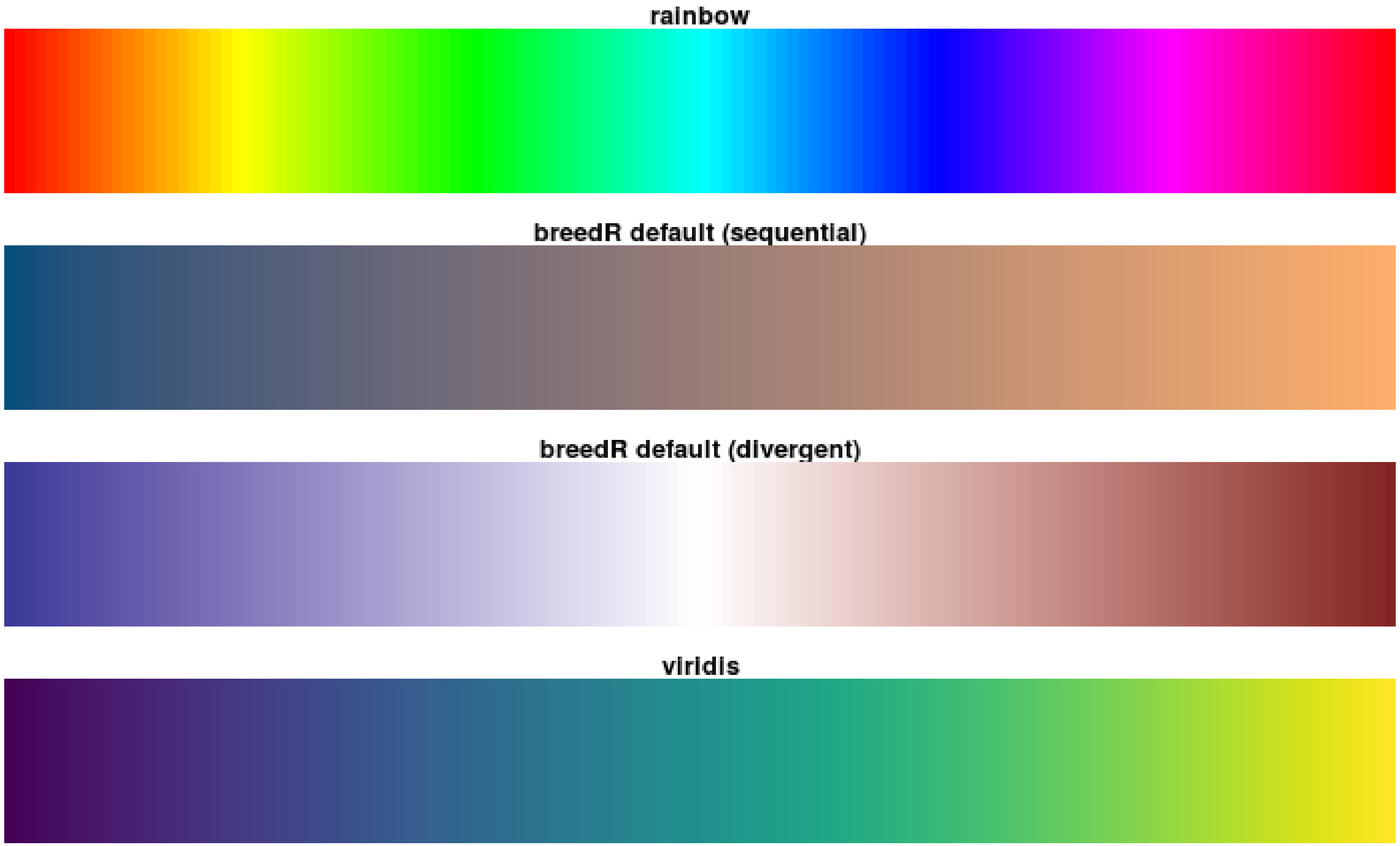
- Separate the R package (frontend) from the Mixed Model engine (backend)
- Download (automatically) the appropriate backend at installation time

Implications

- More complex installation $=$ more oportunities for issues
- Can not simply download latest binaries from PROGSF90: uncontrolled changes could break `breedR`
- Need to maintain a repository with the latest *tested* binaries
- The 64bit binaries for Windows require yet additional libraries from Intel. Alternatives:
  - distribute dll (easy, but Intel does not like)
  - give installation instructions to the user (yet another installation step)

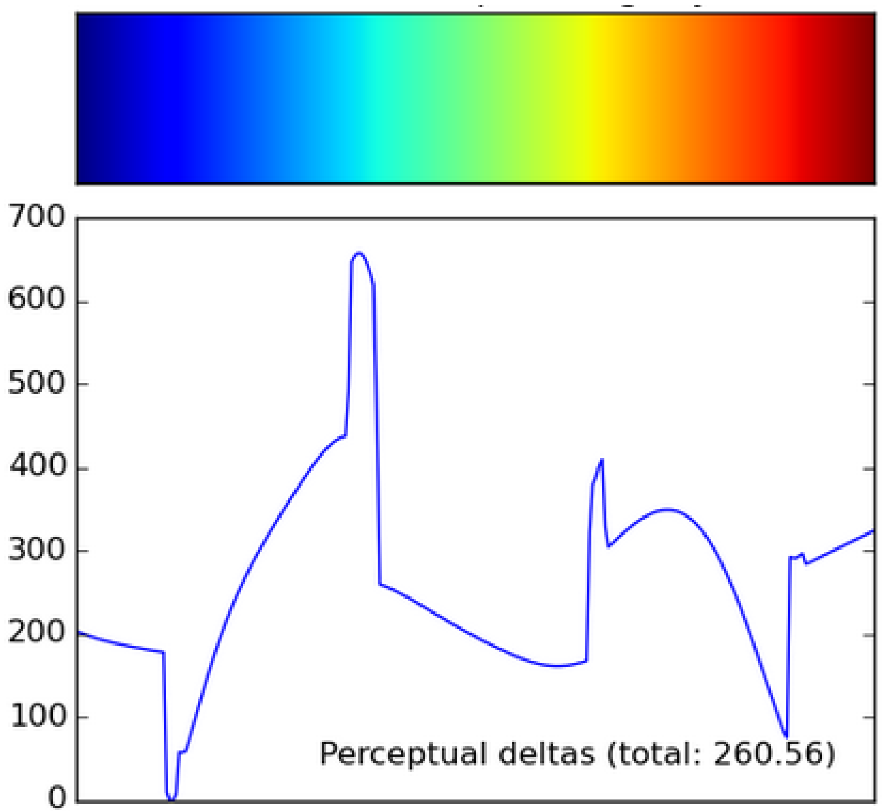
Default colour map

Colour palettes



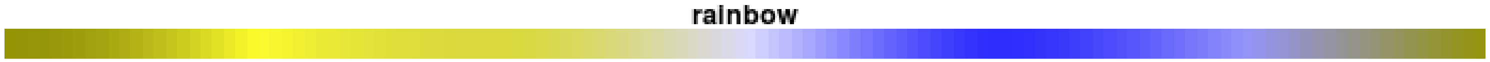
Concern 1

Perceptual uniformity



Concern 2

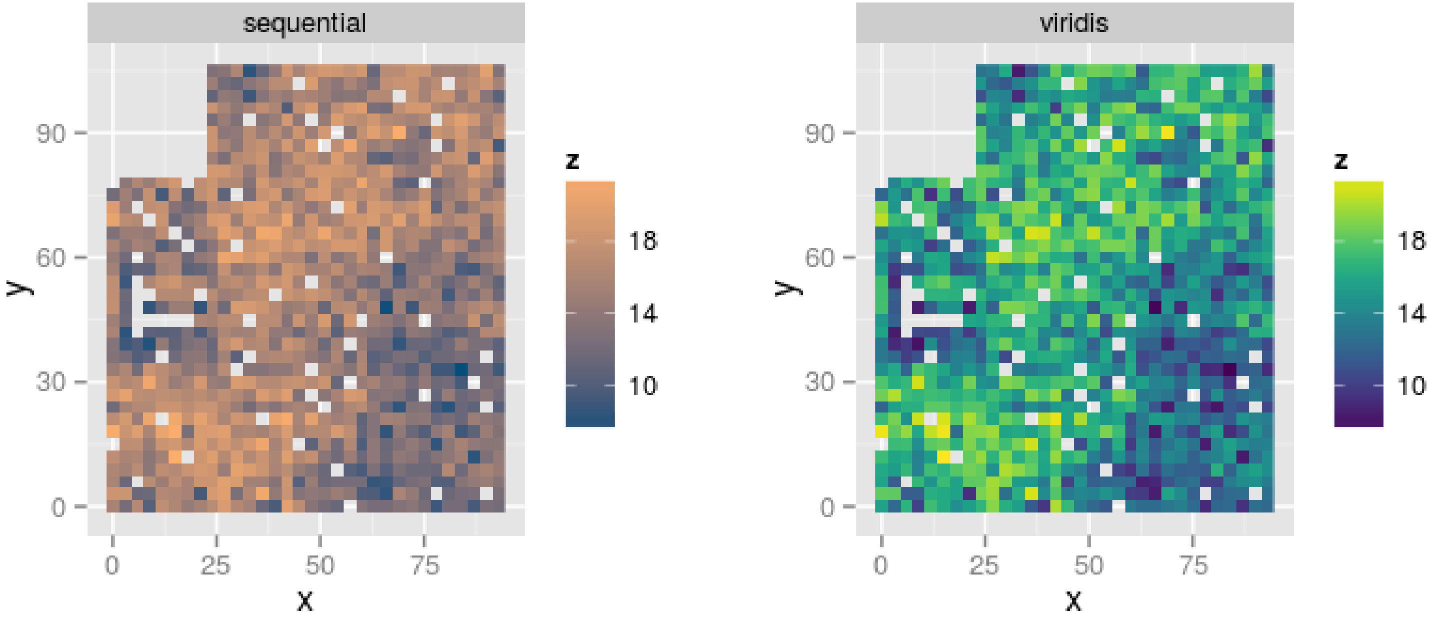
Colour blindness



Concern 3

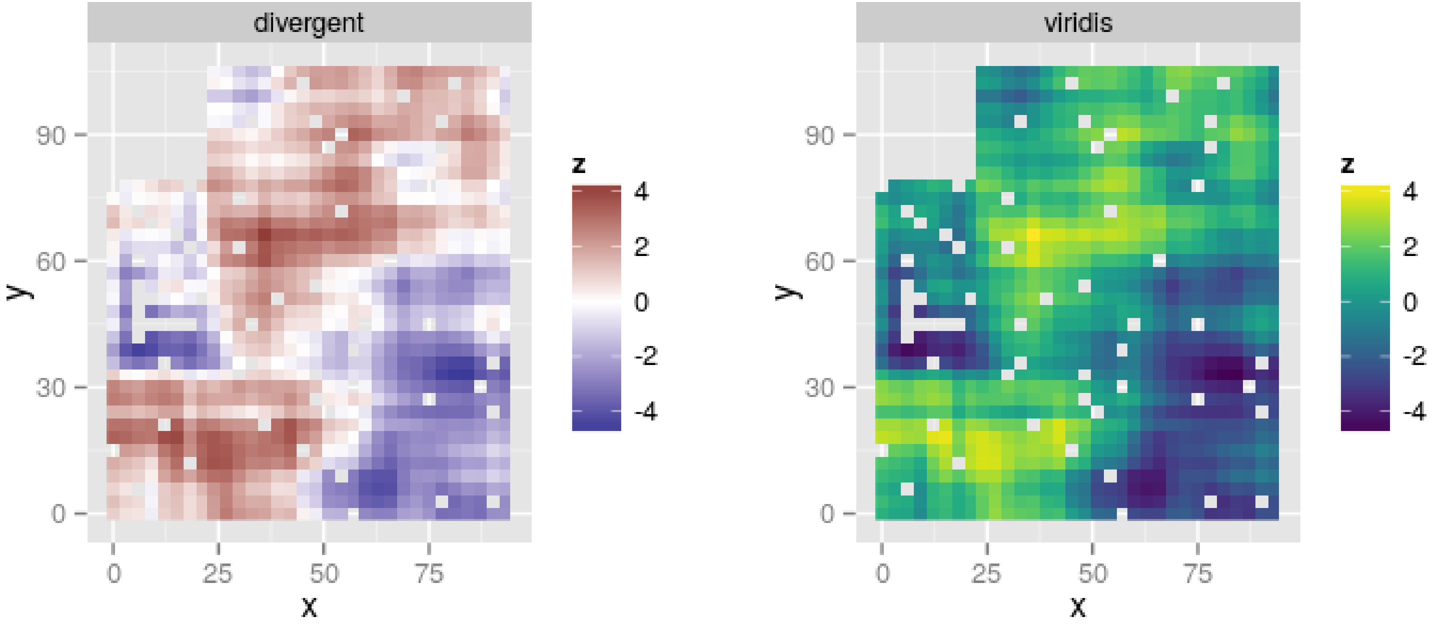
Black & White (printed) readability

Adopt `viridis` for sequential variables



Not so sure about divergent variables

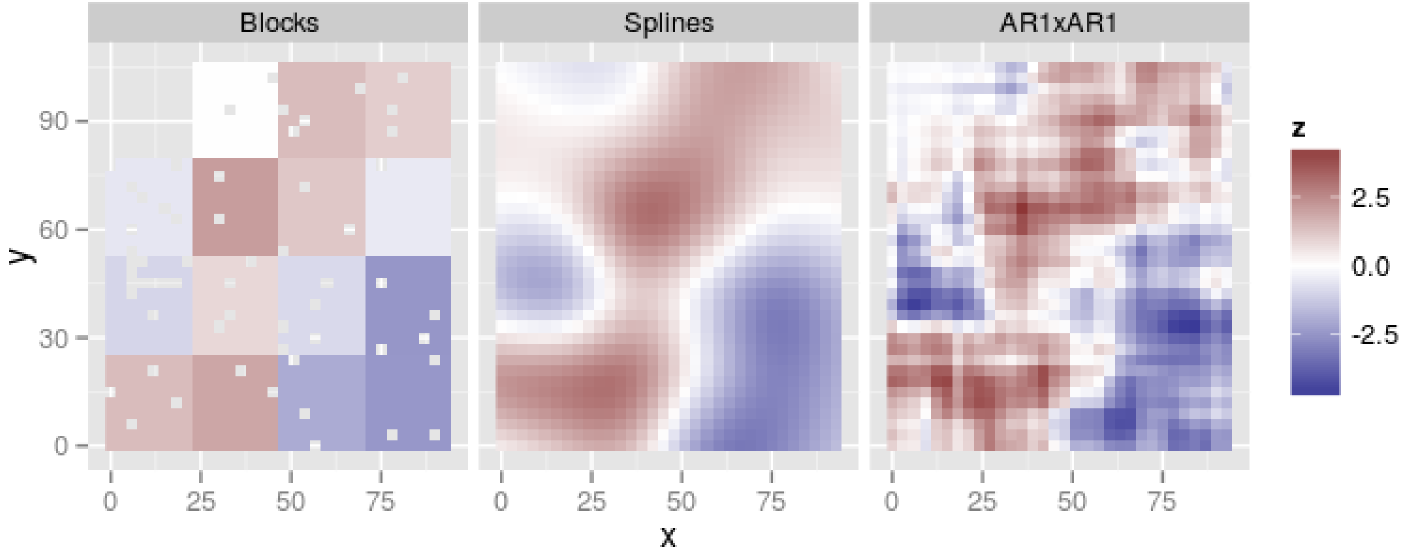
- What do **you** think?



Comparison of spatial models

Goals

- Study the relative performance of `blocks`, `splines` and `AR` in a diversity of scenarios



Approach

- Cross-Validation study with several datasets of diverse characteristics

(Advance of) results

- The `splines` and `AR` models clearly outperform the `blocks` model
- `AR` is usually slightly better than `splines` in most situations
- We detected some (suspected) sensitivity with `AR` under certain situations where `splines` may be more conservative (and safer). **This is work in progress**
- General recommendation: **run both**, compare, evaluate and decide.
- If both models agree, then everything is ok.

Thanks!