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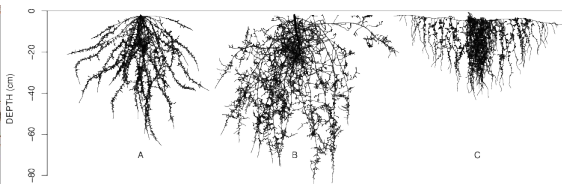
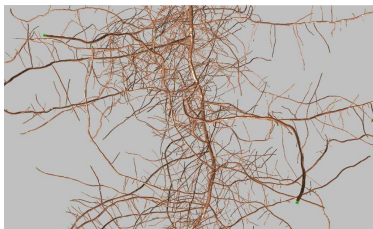
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Usefulness of Sensitivity Analysis for Approximate Bayesian Computation

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Overview

- 1 Review of ABC concepts
- 2 The root system model
- 3 Sensitivity Analysis for statistics
- 4 Sensitivity Analysis for MSE criterion
- 5 Conclusion and discussion

1. ABC concepts

- Approximate Bayesian Computing (ABC) is a free likelihood method to estimate model parameters
- Definition of statistics (or descriptors)
- Fast computing model

Notations:

Observed data D and simulated data D^*

θ is the vector of parameters with Prior $\pi(\cdot)$

$s(\cdot)$: function that computes a set of statistics (descriptors)

$S = s(D)$ vector of statistics for data D

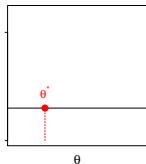
$S^* = s(D^*)$ vector of statistics for data D^*

1. ABC: a free likelihood method

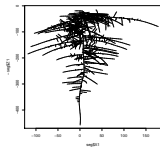
Algorithm (Accept/Reject)

- 0: Suppose we have observed data D and $S = s(D)$
- 1: Generate θ^* from $\pi(\cdot)$
- 2: Generate D^* from $f(\cdot|\theta^*)$
- 3: Compute statistics S^* for D^*
- 4: Accept θ^* if $d_W(S, S^*) \leq \epsilon$ and return to (1)

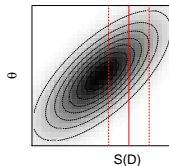
Prior
 $\pi(\theta)$



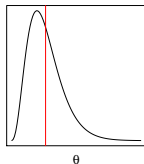
Simulation
 D^*



Joint Distribution
 (θ^*, S^*)



Posterior
 $\pi(\theta | d_W(S, S^*) \leq \epsilon)$



1. ABC: a free likelihood method

This algorithm gives an approximation of $\pi(\theta|D)$.

Two important points for the approximation:

- The threshold ϵ :
smaller $\epsilon \rightarrow$ *better* approximation
- D^* is summarised by the statistics S^* :
better statistics \rightarrow *better* approximation

2. The root system model

Complexity of plant root system:

Functioning is linked to the dynamics of the architecture. Water and nutrient uptake depend on the root surface..

Plant root system modelling:

Integration of knowledge and test of new hypotheses

Summarize data into a low number of key values

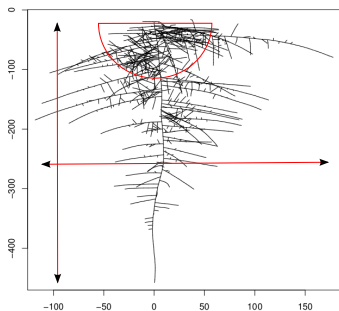
The stochastic model:

Number of parameters: 14

Output of the model: image of root system

3. The root system model

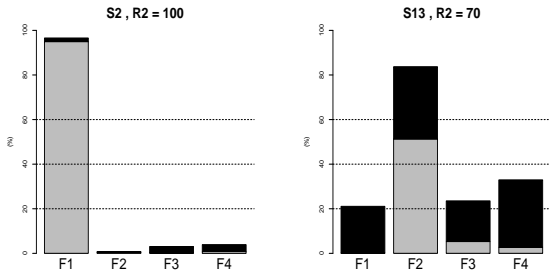
- **4 parameters** over 14 are estimated with images.
- **15 statistics** are computed: size and shape of the root system, density of pixels in different areas, ...



3. Sensitivity analysis of statistics

- Can parameters be estimated with the statistics ?
- Anova: 4 factors with 5 levels, interaction of order 3

Gray: Principal
Black: Interaction



- About 8-10 statistics over the 15 seem to be sufficient to estimate parameters

4. Sensitivity analysis of MSE

- Find the best weights W of d_W to minimize MSE criterion ?
- Point estimate: $\hat{\theta} = \text{Mean}\{\theta^* : d_W(S, S^*) \leq \epsilon\}$ with

$$d_W^2(S, S^*) = \sum_{i=1}^{N_S=15} w_i (S_i - S_i^*)^2 \text{ and } w_i > 0, \sum_{i=1}^{N_S} w_i = 1.$$

- Criterion to evaluate point estimate $\hat{\theta}$:

$$\text{MSE}_{\theta}(W) = \sum_{k=1}^{N_{\theta}=4} \frac{(\hat{\theta}^{(k)} - \theta^{(k)})^2}{\sigma_{\theta^{(k)}}^2}$$

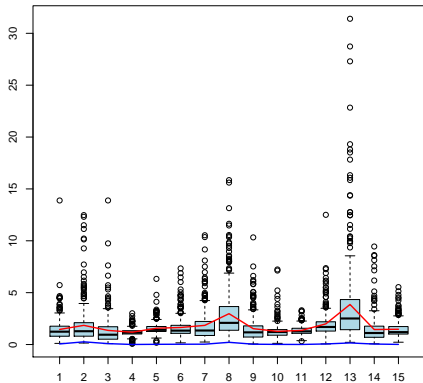
4. Sensitivity analysis of MSE

- Generate uniformly a R -sample of weights $W^r, r = 1, \dots, R$ with $W^r = (w_1^r, \dots, w_{N_S}^r)$ and $\sum_{i=1}^{N_S} w_i^r = 1$
- Generate a N -sample $\theta_l, l = 1, \dots, N$ from $\pi(\theta)$.
- For each $\theta_l, l = 1, \dots, N$
 - Compute $MSE_{\theta_l}(W^r), r=1, \dots, R$
 - Fit a canonical polynomial of degree 2:
$$MSE_{\theta_l}(W) = P_l(W) + e, l = 1, \dots, N$$

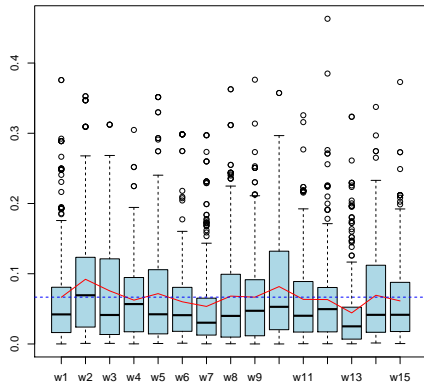
with
$$P_l(W) = \sum_{i=1}^{N_S} \delta_{ii} w_i^2 + \sum_{i=1}^{N_S} \sum_{i < j}^{N_S} \delta_{ij} w_i w_j$$
 - Sensitivity indices by comparing nested polynomials models.

4. Sensitivity analysis of MSE

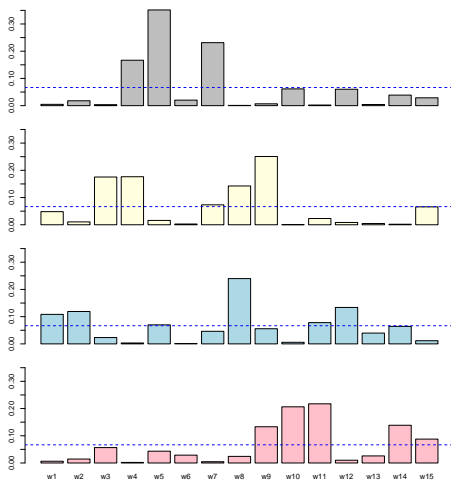
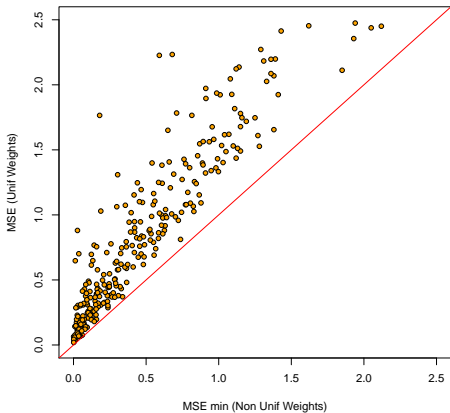
Sensitivity indices



Minimum weights



4. Sensitivity analysis of MSE



5. Conclusion

Conclusion

- Difficult to find an optimal distance (for all θ)
- Interaction between weights associated to statistics
- ABC with three steps:
 - ① Pilot ABC (\rightarrow first approximation $\tilde{\theta}$)
 - ② Determine optimal weights associated to $\tilde{\theta}$
 - ③ ABC with the optimal weights (\rightarrow second approximation $\hat{\theta}$)

Future work

- Optimal weights determined by global optimum of P_W
- Study based on the expectations of the statistics (rather one observation)

References

Beaumont, M., Zhang, W., Balding, D.J. (2002). Approximate bayesian computation in population genetics. *Genetics*.

Cornell, J. (2002). Experiments with mixtures. J. Wiley and sons, N. Y., 3rd edition.

Joyce, P., Marjoram, P. (2008). Approximately sufficient statistics and bayesian computation. *Stat. Appl. Genet. Mol. Biol.*

Pagès, L. (2011). Links between root developmental traits and foraging performance. *Plant, Cell and Environment*.

Factor F3 and F4:

