

Identification of Health Risk Factors in Developing Countries using Intrinsic Model Selection Approaches

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Master's Thesis

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Introduction



Objective:

- Identification of risk factors of two common disease burdens in sub-Saharan Africa.
- Statistically, how to approach moderate dimensional regression where effect selection is necessary, and how to approach predictive modelling with binomial data where inference on the underlying risk is desired.

Methodology:

- Component-wise (model-based) boosting with intrinsic variable selection and model choice.

Data Source: Demographic and Health Surveys (DHS)

- Large N household surveys in low- and middle income countries collect data on important population health and socio-economic characteristics.
- Often used in the epidemiological literature due to it's temporal compatibility and representative samples, e.g., in the research of determinants of disease burdens.
- I use the Madagascar 2021 Standard DHS and the Mali 2021 Malaria Indicator Survey (MIS).



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Component-wise boosting for variable selection and model choice



Component-wise boosting

Functional gradient boosting: estimate function by numerical optimisation in function space (Friedmann 2001).

Very popular in the literature given it's superiority in many tasks (XGBoost). Generally boosted trees but a model based approach is also possible (Bühlmann and Yu 2003, Bühlmann and Hothorn 2007).

Boosting additive models (component-wise). In a generalised additive regression:

$$E(y|\mathbf{x}) = h(\eta(\mathbf{x}))$$
$$\eta(\mathbf{x}) = \beta_0 + \sum_{j=1}^J f_j(\mathbf{x}).$$

We define the following optimisation problem

$$\arg \min_{\eta} E(\rho(y, \eta))$$

where ρ is the negative log-likelihood (i.e., loss) and replace the expectation with the empirical risk

$$R = n^{-1} \sum_{i=1}^n \rho(y_i, \eta).$$

Component-wise boosting

Init $\hat{\eta}^{[0]}$ and define a set of base-learners $b_l, l = 1, \dots, L$. In each iteration m refit each to the negative gradient

$$u_i = -\frac{\partial}{\partial \eta} \rho(y_i, \eta) \Big|_{\eta = \hat{\eta}^{[m-1]}(\mathbf{x}_i)}$$

and select the best-fitting learner b_{l^*} by residual-sum-of-squares.

Update $\hat{\eta}^{[m]}$

$$\hat{\eta}^{[m]} = \hat{\eta}^{[m-1]} + \nu \hat{b}_{l^*}$$

where the parameter ν is $0 < \nu \ll 1$.

Early stopping (to avoid overfitting and improve generalisation error) can be achieved through holdout sets and resampling methods (k-fold cv, bootstrap etc.).

- Intrinsic selection of learners as in each iteration exactly *one* learner is added to the additive predictor.
- Effect selection by decomposition of smooth effects (Kneib et al. 2009). Allows to choose none, linear, non-linear effects.
- Many statistical tasks covered: survival analysis, quantile regression (Fenske et al. 2011), multivariate distributions (Strömer et al. 2021) and copulas (Hans et al. 2022).

Component-wise boosting

Distributional regression (or GAMLSS: Generalised Additive Models for Location, Scale and Shape)

- Allows modelling of each distribution parameter with a separate additive predictor.
- Algorithm: non-cyclical boosting. In each iteration both the learner *and* the parameter are selected jointly for an update. (see Thomas et al. 2018)

Uncertainty quantification

- Subsampling replications or bootstrap replications of the model, but: no theoretical guarantees of coverage.
- Use it to assess stability of estimated coefficients.
- Stability selection (Meinshausen and Bühlmann 2010) allows for finite sample control of Type 1 error for variable selection, but: very conservative.



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Case Studies



Case Study 1: Childhood malnutrition in Madagascar

Objective: Identification of risk factors (or determinants).

Outcome: child is stunted yes / no
(height-for-age score is more than 2σ below the reference)

Explanatory Covariates:

- Individual-level risk factors (age, gender, mother's bmi, if twin, etc.) ,
- household- (no. of household members, DHS wealth index, etc.),
- and community-level (urbanicity, distance to healthcare facilities etc.).

Additional Specifications:

- Decomposition of smooth effects for continuous covariates to allow for effect selection.
- Markov random field for administrative regions (first-order neighbourhood structure).

Case Study 2: Geographic malaria risk in Mali

Objective: Identification of environmental correlates of malaria prevalence and inference of risk.

Outcome: k children out of n tested positive in cluster c , i.e., binomial.

- Following Dong and Wakefield 2021, I model the outcome with a beta-binomial distribution that accounts for cluster overdispersion due to within-cluster variability.

Explanatory Covariates:

- Elevation, land surface temperature (day/night), rainfall - aggregated annually (mean / sum).
- Vegetation indices, NDVI and EVI.
- Population (Global Human Settlement Layer Data).
- Urbanicity variable to account for survey design.

Additional Specifications:

- Decomposition of smooth effects for continuous covariates to allow for effect selection.
- Bivariate tensor P-spline to model spatial effects.



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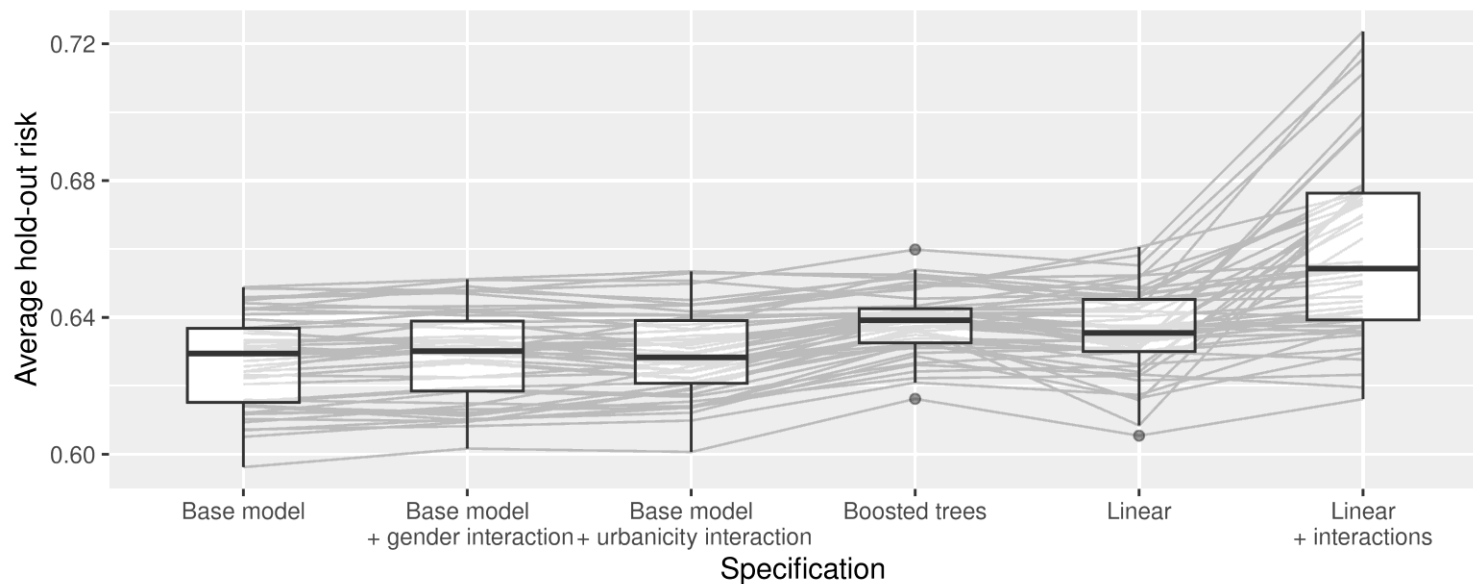
Results



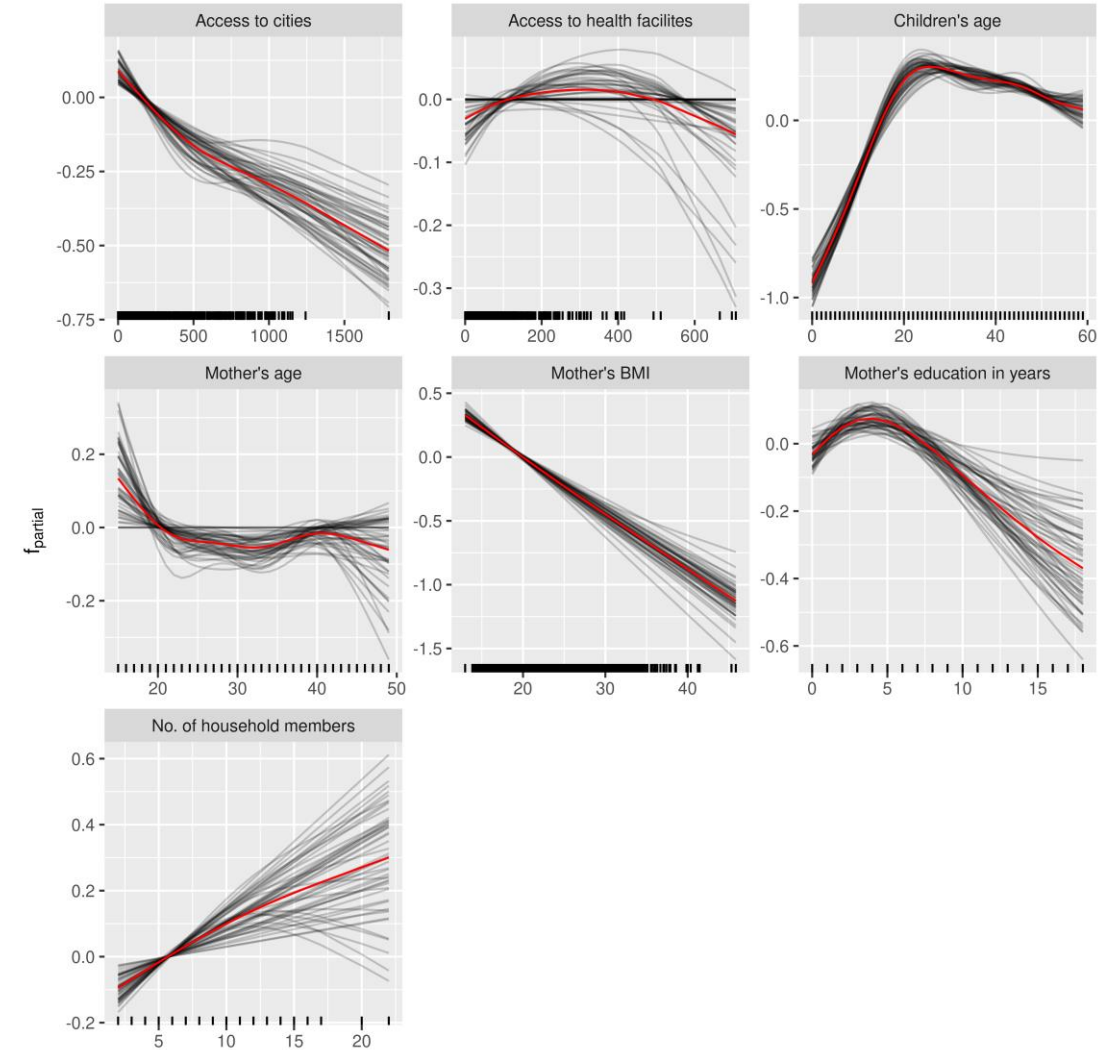
Childhood malnutrition in Madagascar

Model selection

- by three-way holdout method (70/20/10), no. of boosting iterations selected optimal performance on validation set.
- Following results based on 50 subsampling replications. Red line indicates pointwise average.



Childhood malnutrition in Madagascar



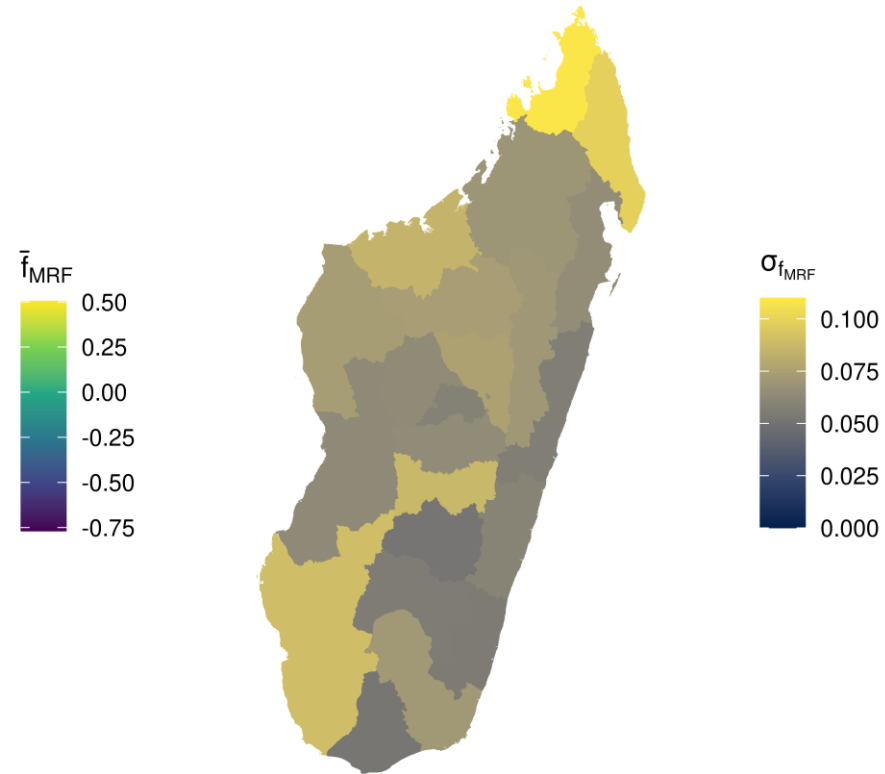
- Estimated effects of the continuous covariates.

Childhood malnutrition in Madagascar

A



B



- Markov random field effect for admin 1 regions, mean (A) and standard deviation (B) of the subsampling replications.

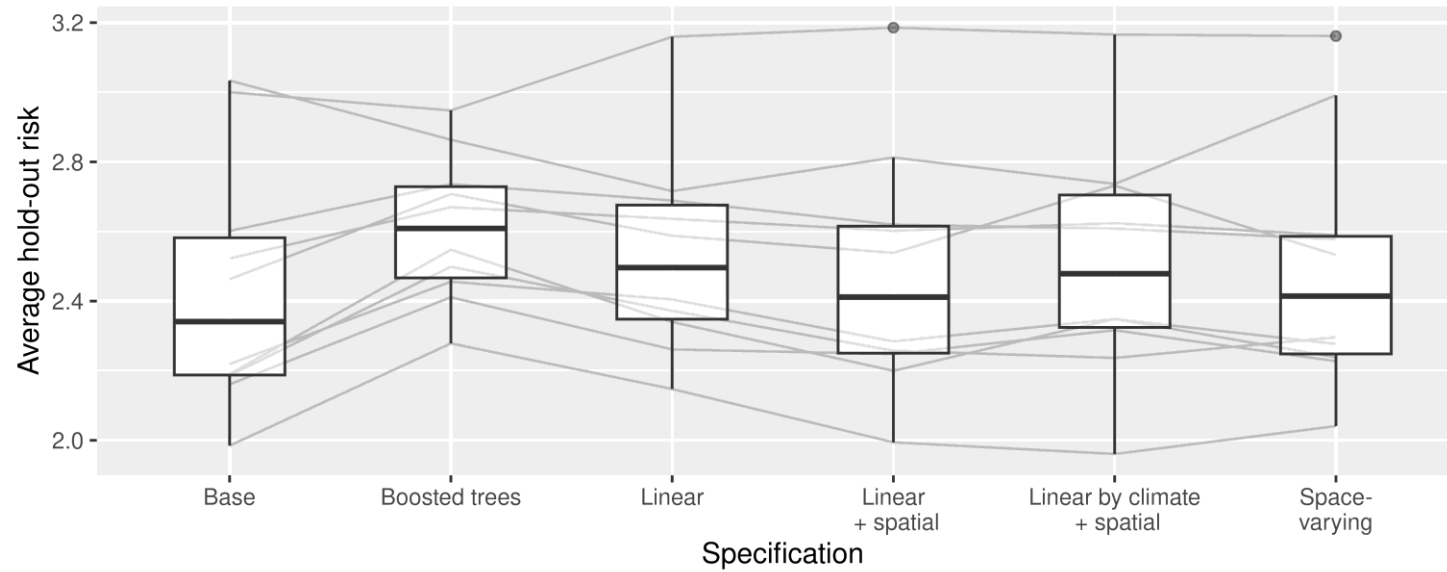
Model validation and selection

- by nested cross-validation (10-fold, stratified by region)
- comparison of base specification to boosted trees and
 - Linear
 - Linear + bivariate tensor P-spline
 - Linear + climate interactions + bivariate tensor P-spline
 - Linear + spatially-varying coefficient

Early stopping by 10-fold cross-validation. Uncertainty quantification with bootstrap samples.

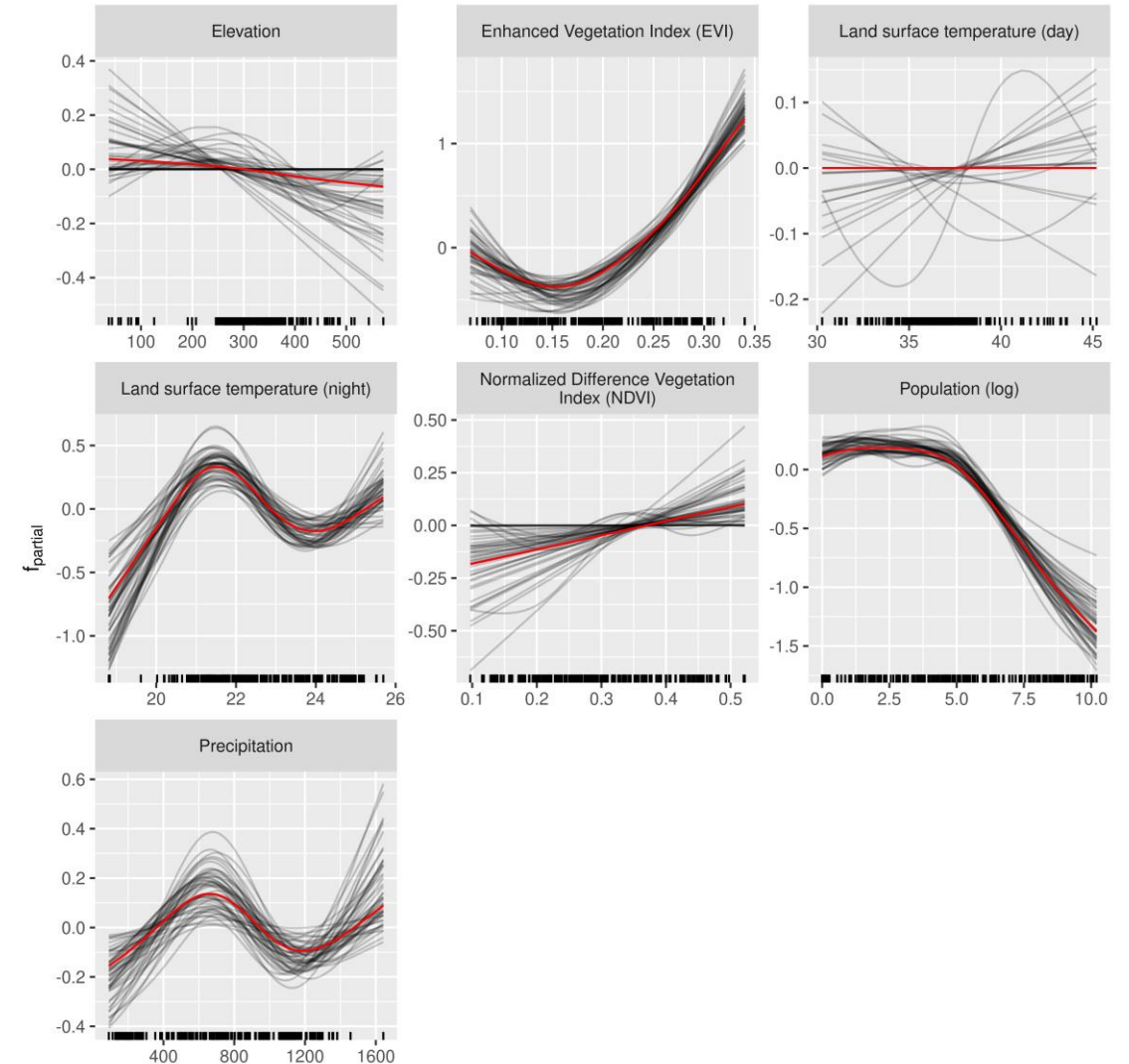
Geographic malaria risk in Mali

Model	Bias	MAE	RMSE	80% PI	90% PI	95% PI
Beta binomial	-0.005	0.093	0.131	0.861	0.944	0.963
Binomial	-0.007	0.091	0.131	0.597	0.708	0.759



Geographic malaria risk in Mali

- Red line / dot indicates estimate of the principal model.
- Uncertainty quantification based on 50 bootstrap samples.

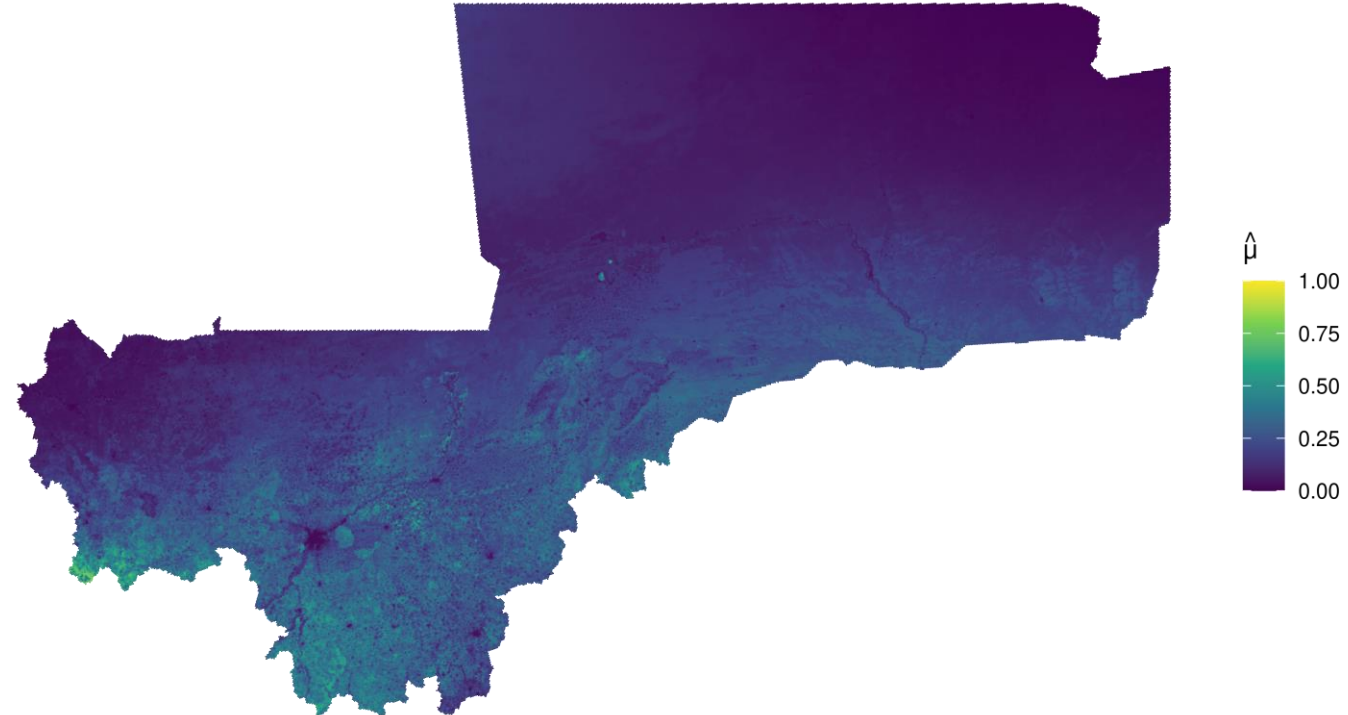


Geographic malaria risk in Mali



- Spatial effect (left) and standard error of bootstrap samples (right).

Geographic malaria risk in Mali



- Predicted malaria risk.

Discussion



Component-wise boosting for risk identification?

- Yes, can allow for interesting insights in moderate dimensional datasets where a priori the functional form of an effect is not known, but difficult if rigorous notion of statistical inference is required.

Case Study 1 (Malnutrition)

- If effect *type* selection of interest – great. But difficult to achieve controls for variable selection: stability selection is very conservative in low dimensional settings.
- Probably more useful: hierarchical modelling of main factors to distinguish regional differences and deviations from country-level relationship.

Case Study 2 (Malaria)

- Likely competitive and interpretable approach compared to Bhatt et al. 2017 and Weiss et al. 2015 with respect to variable selection and predictive accuracy (and: appropriate response distribution).
- High accuracy masks large uncertainties in predicted risk, if admin 2 estimates are the objective probably not the right approach (since uncertainty is central).



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Q&A





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References



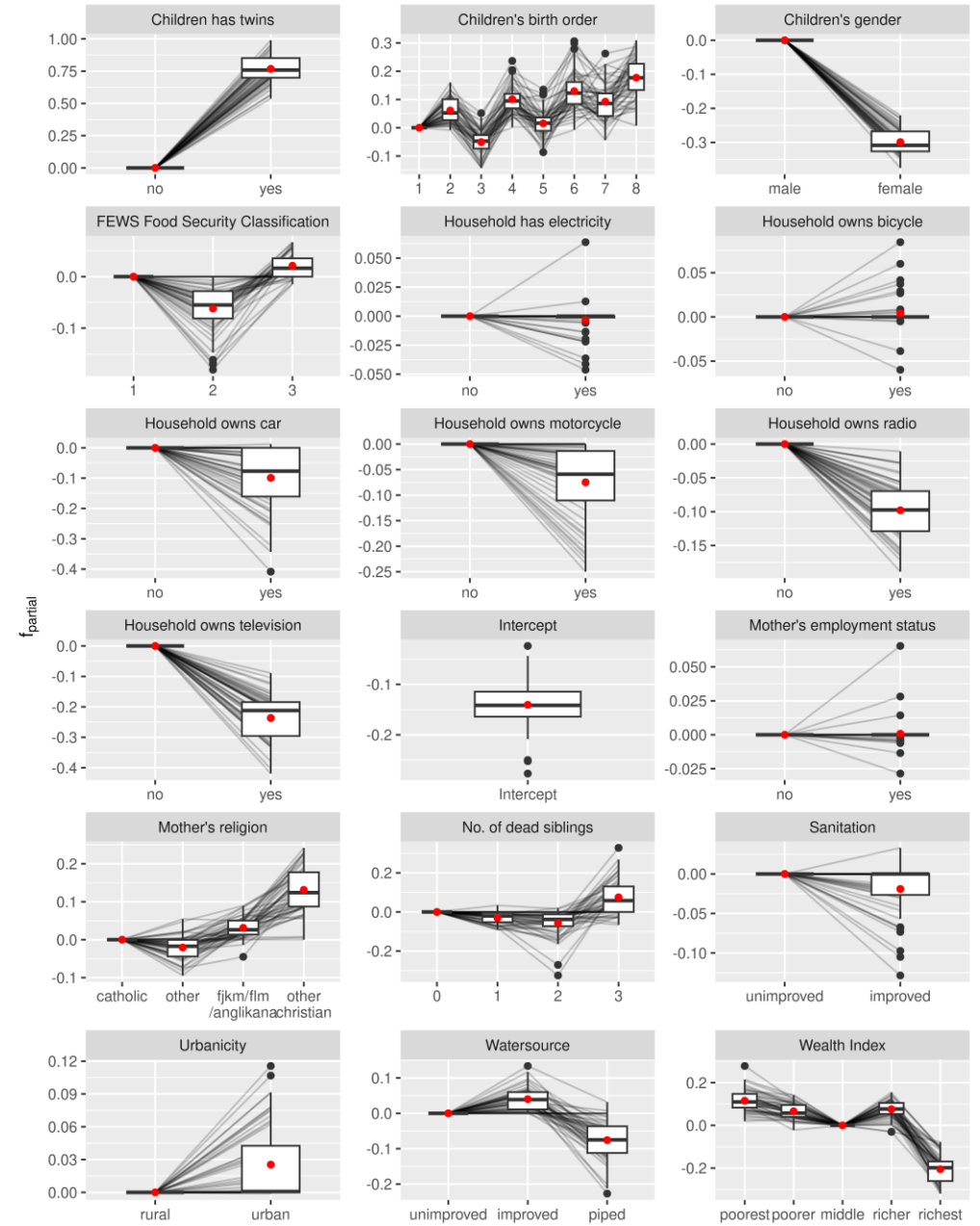
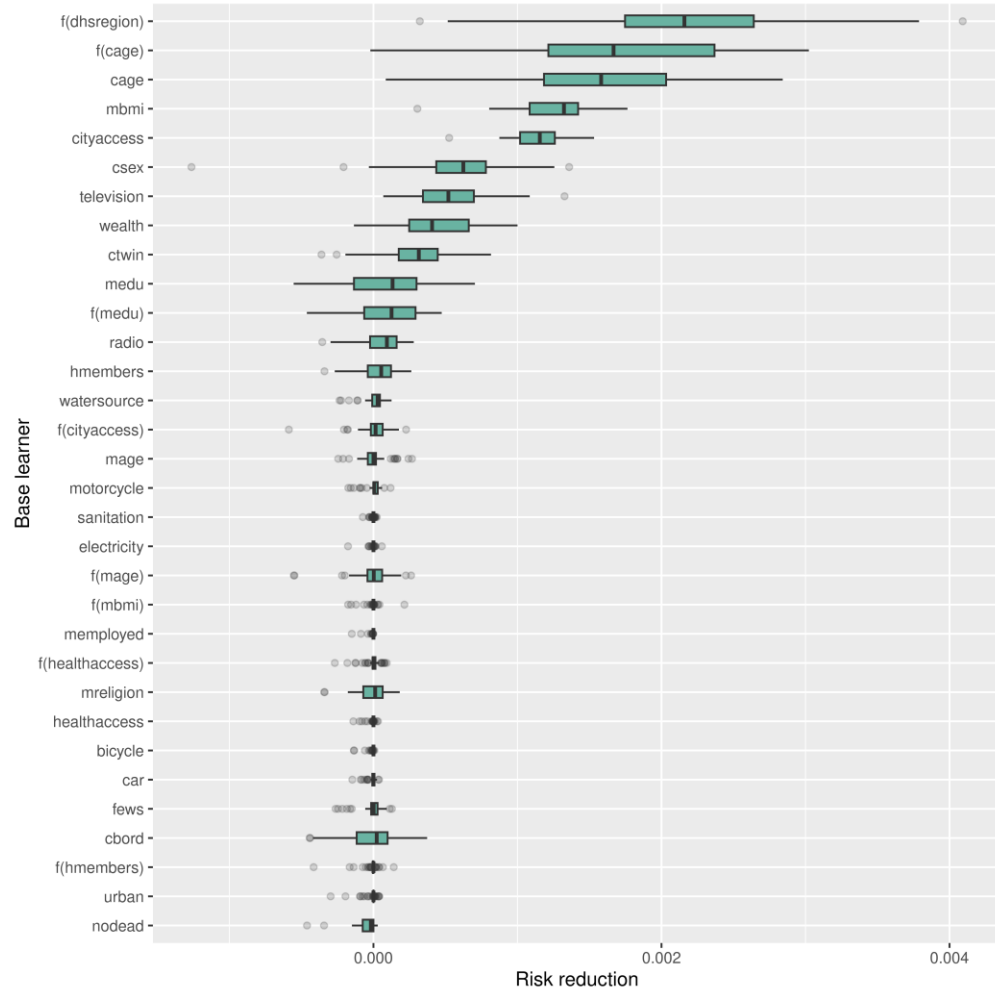
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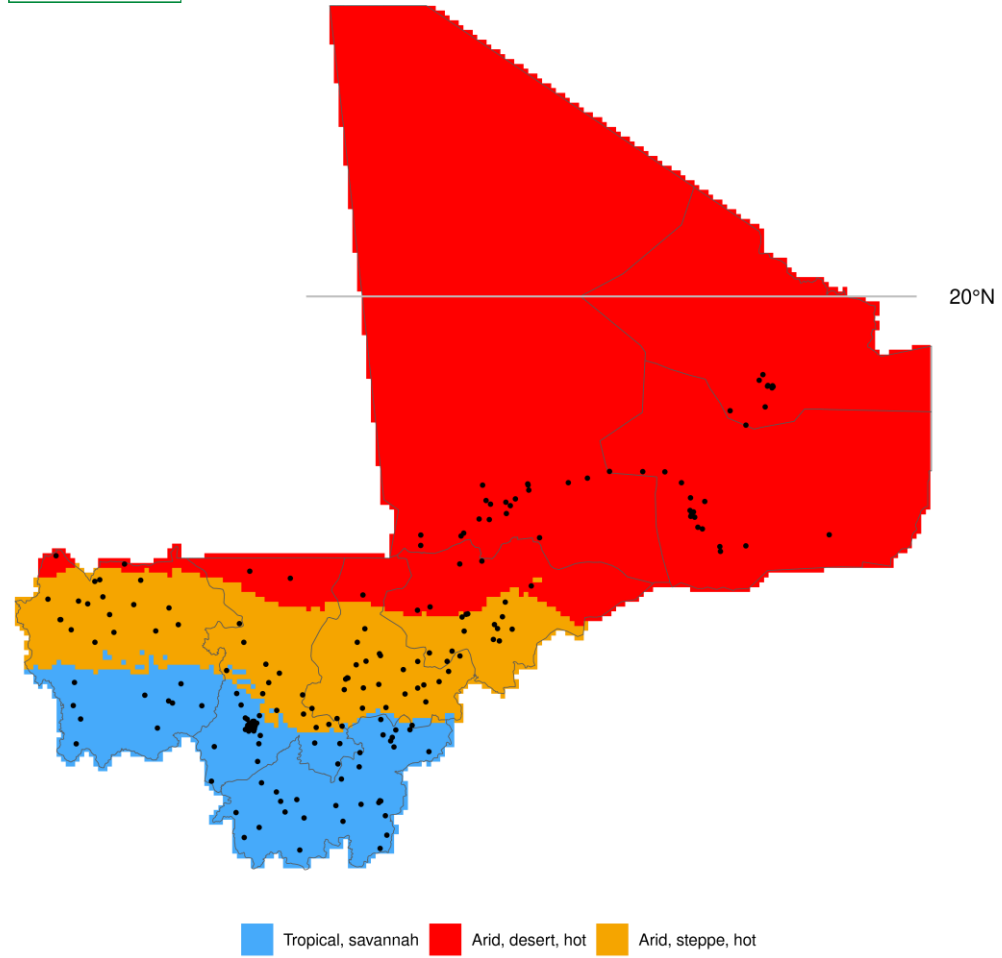


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Additional Figures







A



B



C



