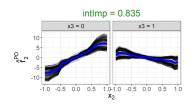
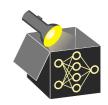
Interpretable Machine Learning

Regional Effects Interaction importance



Learning goals

- Interaction quantification
- REPID interaction importance



INTERACTION QUANTIFICATION

It's helpful to know not just how another feature changes the marginal effect of x_S but how strong that interaction is and want to rank features by it.

Approaches:

- H-Statistics: Variance of the deviation between the joint PDP and the sum of marginal PDPs (larger variance ⇒ stronger interaction).
- **Greenwell's Interaction Index:** Difference between variance of the PDP and the mean variance of centered ICE curves for the same feature pair.
- SHAP interaction index (Herbinger 2022 , Lundberg 2018): Proportion of all two-way interactions with x_i to which the j-th feature contributes.



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Pitfalls:

- The values of H-Statistic and the Greenwell's Interaction Index are influenced by the main effects of the two regarded features.
- SHAP interaction index does not suffer from main effect problem. However, correlation between the two features can bias the interaction value. Same applies to the H-Statistic.

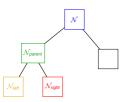


On parent node level (for \mathcal{N}_{parent}):

$$\textit{intImp}(\mathcal{N}_{\textit{parent}}) = \frac{\mathcal{R}(\mathcal{N}_{\textit{parent}}) - (\mathcal{R}(\frac{\mathcal{N}_{\textit{left}}}) + \mathcal{R}(\frac{\mathcal{N}_{\textit{right}}}{\mathcal{R}(\mathcal{N})})}{\mathcal{R}(\mathcal{N})}$$



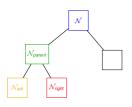
Interpretation: Reduction of ICE curve variance after one split of \mathcal{N}_{parent} into \mathcal{N}_{left} and \mathcal{N}_{right} relative to the ICE curve variance in the root node \mathcal{N} .

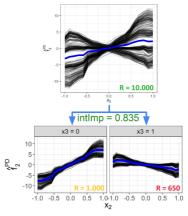


On parent node level (for \mathcal{N}_{parent}):

$$\textit{intImp}(\mathcal{N}_{\textit{parent}}) = \frac{\mathcal{R}(\mathcal{N}_{\textit{parent}}) - (\mathcal{R}(\mathcal{N}_{\textit{left}}) + \mathcal{R}(\mathcal{N}_{\textit{right}}))}{\mathcal{R}(\mathcal{N})}$$

Interpretation: Reduction of ICE curve variance after one split of \mathcal{N}_{parent} into \mathcal{N}_{left} and \mathcal{N}_{right} relative to the ICE curve variance in the root node \mathcal{N} .





Split reduces 83.5% of variance.

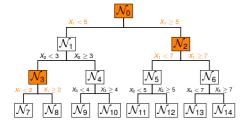
On feature level (for x_i):

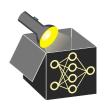
$$intImp_j = \sum_{i \in \mathcal{B}_j} intImp(\mathcal{N}_i)$$

where \mathcal{B}_j indexes parent nodes split by x_j .

Interpretation: Overall reduction of ICE curve variance due to splits by X_j (in %).

Example: For $X_1 \Rightarrow \mathcal{B}_1 = \{0, 2, 3\}$





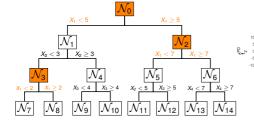
On feature level (for x_i):

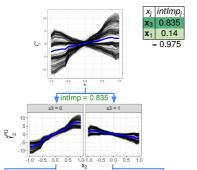
$$intImp_j = \sum_{i \in \mathcal{B}_i} intImp(\mathcal{N}_i)$$

where \mathcal{B}_j indexes parent nodes split by x_j .

Interpretation: Overall reduction of ICE curve variance due to splits by X_i (in %).

Example: For $X_1 \Rightarrow \mathcal{B}_1 = \{0, 2, 3\}$





Note: *intlmp* can also be used as a stopping criterion.



OUTPERFORMING SOTA

Simulation setting

- ullet Draw 1000 i.i.d. samples from $X_1,\ldots,X_4\sim \mathcal{U}(-1,1)$
- True underlying function:

$$f(\mathbf{x}) = \sum_{j=1}^{4} \mathbf{x}_j + \mathbf{x}_1 \mathbf{x}_2 + \mathbf{x}_2 \mathbf{x}_3 + \mathbf{x}_1 \mathbf{x}_3 + \mathbf{x}_1 \mathbf{x}_2 \mathbf{x}_3 + \epsilon$$

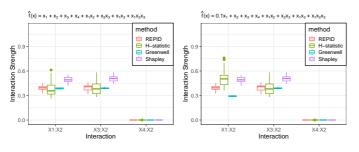
- ullet Fit a correctly specified linear model (interactions with ${f x}_4$ are excluded)
- ullet 30 reps, measure interaction strength between ${f x}_2$ and all other 3 features

Which methods are sensitive to changes in main effect sizes or feature correlations?



Pitfall	REPID	H-Statistic	Greenwell	SHAP
sensitive to changes of main effect	No	Yes	Yes	No
sensitive to changes of correlation be-	No	Yes	No	Yes
tween \mathbf{x}_j and other features				

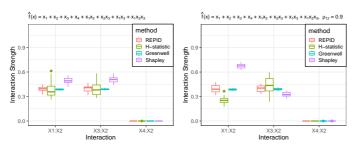
OUTPERFORMING SOTA





- Left (initial setting): Interaction strength of x₁:x₂ and x₃:x₂ similar; x₄:x₂ no interaction
- **Right**: Set main effect $\beta_1 = 0.1$
 - Expectation: Interaction strengths should not change
 - Fail: H-statistic $(\mathbf{x}_1:\mathbf{x}_2 > \mathbf{x}_3:\mathbf{x}_2)$ and Greenwell $(\mathbf{x}_1:\mathbf{x}_2 < \mathbf{x}_3:\mathbf{x}_2)$

OUTPERFORMING SOTA

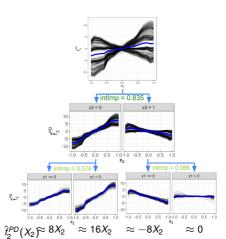




- Left (initial setting): Interaction strength of x₁:x₂ and x₃:x₂ similar; x₄:x₂ no interaction
- **Right**: Increase correlation $\rho(\mathbf{x}_1, \mathbf{x}_2) = 0.9$
 - Expectation: Interaction strengths should not change
 - Fail: H-statistic $(\mathbf{x}_1:\mathbf{x}_2 < \mathbf{x}_3:\mathbf{x}_2)$ and Shapley $(\mathbf{x}_1:\mathbf{x}_2 > \mathbf{x}_3:\mathbf{x}_2)$
- $\rightarrow\,$ REPID is the only method which always leads to correct rankings for these settings

LIMITATIONS OF REPID

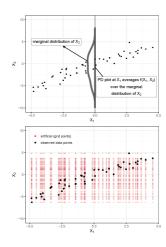
- 1) Restricted to one feature of interest
 - \Rightarrow Different regions for different features





LIMITATIONS OF REPID

- Restricted to one feature of interest
 ⇒ Different regions for different features
- 2) Restricted to PD (global) and ICE (local) as feature effect methods
 ⇒ Inherits extrapolation problem (unlikely combinations of feature values)
- → Follow-up GADGET [under review]





CONCLUSION

Summary of Contributions (REPID):

- Regional effects in interpretable regions
- Additive decomp. of feature effect
- Quantify feature interactions
- Outperforms SOTA interaction indices

Summary of Contributions (GADGET):

- Unique regions for multiple features
- Additive decomp. of prediction function
- Extension to ALE and Shapley Dependence
- Test to identify significant interactions

Further Directions:

Pruning, GADGET as a predictor, comparing regions across models, efficient implementation, more efficient testing and splitting approach, ...

