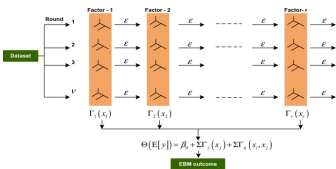
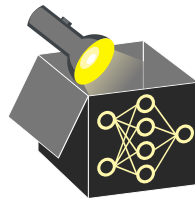


Interpretable Machine Learning

Explainable Boosting Machines (EBM)



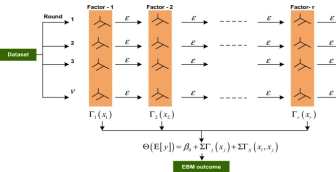
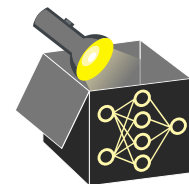
Learning goals

- Understand link between GAM and EBM
- Learn univariate EBMs
 $\hat{=}$ GAM + boosting + shallow bagged trees
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- Detect interactions efficiently using FAST algorithm

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Explainable Boosting Machines (EBM)

Interpretable Models 1



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RECAP: SPLIT SELECTION DECISION TREE

- **Impurity (Regression):** Variance of target Y in a node:

$$\text{Var}(Y) = \frac{1}{n} \sum_{i=1}^n (y^{(i)} - \bar{y})^2 = \frac{1}{n} \sum_{i=1}^n (y^{(i)})^2 - \bar{y}^2$$

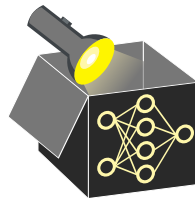
- **Sum of squared errors (SSE) = residual sum of squares (RSS):**

$$\text{RSS} = n \cdot \text{Var}(Y) = \sum_{i=1}^n (y^{(i)} - \bar{y})^2 = \dots = \sum_{i=1}^n (y^{(i)})^2 - \frac{1}{n} \left(\sum_{i=1}^n y^{(i)} \right)^2$$

Hence: $\text{RSS} = SS_n - \frac{S_n^2}{n}$ with $S_n = \sum_{i=1}^n y^{(i)}$, $SS_n = \sum_{i=1}^n (y^{(i)})^2$

- **Split criterion:**

- **Minimize post-split RSS:** $\text{RSS}_{\text{split}} = \text{RSS}_L + \text{RSS}_R$
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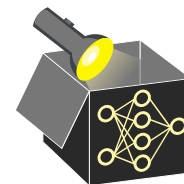
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NAIVE SPLIT SELECTION: EXPLICIT COMPUTATION

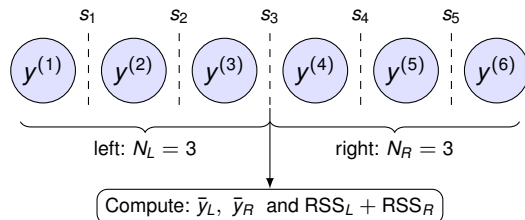
- For a given feature X_j , sort the pairs $(x_j^{(i)}, y^{(i)})$ by increasing $x_j^{(i)}$.
- For each of the $n - 1$ potential split points at $s_k = \frac{1}{2}(x_j^{(k)} + x_j^{(k+1)})$:
 - Define partitions: $\mathcal{I}_L = \{i : x^{(i)} \leq s_k\}$, $\mathcal{I}_R = \{i : x^{(i)} > s_k\}$
 - Compute group means and counts after splitting at s_k :

$$\bar{y}_L = \frac{1}{N_L} \sum_{i \in \mathcal{I}_L} y^{(i)}, \quad \bar{y}_R = \frac{1}{N_R} \sum_{i \in \mathcal{I}_R} y^{(i)}, \quad \text{with } N_L = |\mathcal{I}_L|, \quad N_R = |\mathcal{I}_R|$$

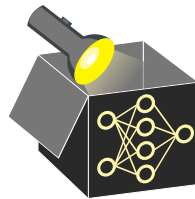
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- Select split point s_k that minimizes $\text{RSS}_{\text{split}}(s_k)$
- **Computational cost:** $O(n^2)$ per feature (recompute mean & RSS at each split)



$O(n^2)$ operations (recompute for each split s_i per feature)



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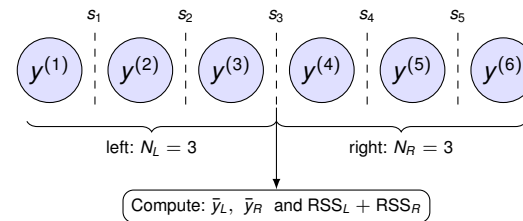
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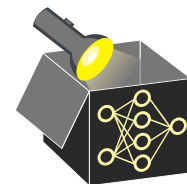
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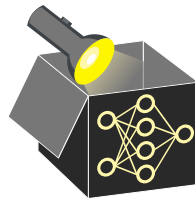
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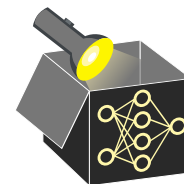
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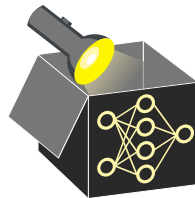
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All squared-target terms SS_L , SS_R cancel. Only first-order sums are needed.

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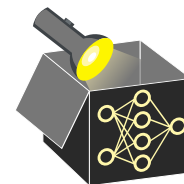
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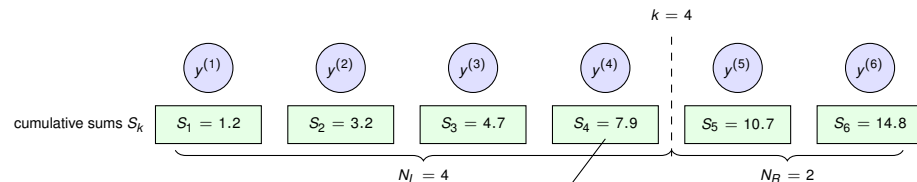
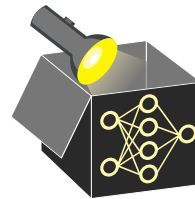
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EFFICIENT SPLIT SELECTION - EXAMPLE

$$y^{(1)} = 1.2, y^{(2)} = 2.0, y^{(3)} = 1.5, y^{(4)} = 3.2, y^{(5)} = 2.8, y^{(6)} = 4.1 \quad (x_j^{(1)} \leq \dots \leq x_j^{(6)})$$

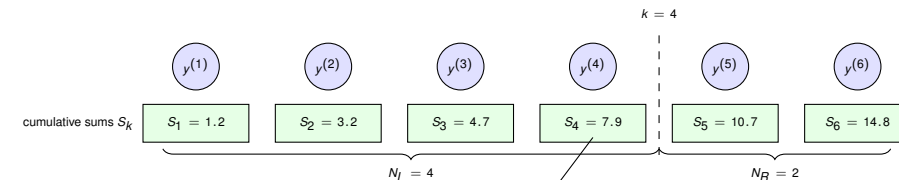
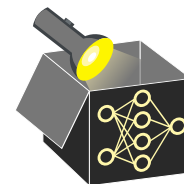


$$G(k=4) = \frac{S_4^2}{4} + \frac{(S_6 - S_4)^2}{2} = \frac{7.9^2}{4} + \frac{(14.8 - 7.9)^2}{2} \approx 39.41$$

- $G(k)$ omits $-S_n^2/n$ (identical for all splits \Rightarrow does not affect arg max).
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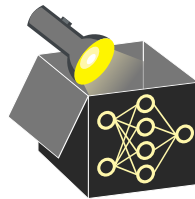
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EXPLAINABLE BOOSTING MACHINES (EBM)



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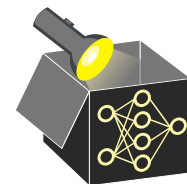
$$g(\mathbb{E}[y \mid \mathbf{x}]) = \theta_0 + f_1(x_1) + f_2(x_2) + \dots + f_p(x_p),$$

- One shape function f_j per feature x_j
 \rightsquigarrow **Feature-level interpretability**
- Captures non-linear univariate effects
 \rightsquigarrow **Better performance / more flexible than GLMs**

Idea of EBM: GAMs trained with **gradient boosting** over **shallow bagged trees**

- **GAMs** - provide feature-wise interpretability via separate shape functions $f_j(x_j)$
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- **Gradient Boosting** - incrementally fits residuals to improve predictive performance while retaining additivity
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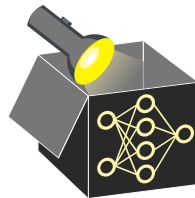
EBM - TWO-STAGE MODEL CONSTRUCTION

1 Stage 1: Fit Main Effects (Univariate Terms) ▶ Lou et al. 2012

- Train EBM using only feature-wise shape functions $f_j(x_j)$
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2 Stage 2: Add Selected Pairwise Interactions ▶ Lou et al. 2013

- Apply **FAST** to rank all $O(p^2)$ feature pairs by potential reduction in RSS
- Select top K pairwise interactions and store them in \mathcal{K}
- Use boosting to fit pairwise interaction terms $f_{ij}(x_i, x_j)$ on residuals
- Final model: $\hat{f}(\mathbf{x}) = \sum_{j=1}^p f_j(x_j) + \sum_{(i,j) \in \mathcal{K}} f_{ij}(x_i, x_j)$



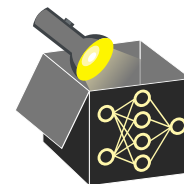
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UNIVARIATE EBM - INITIALIZATION

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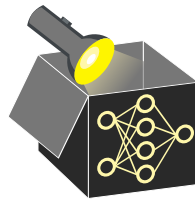
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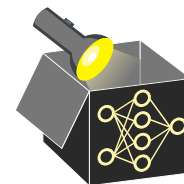
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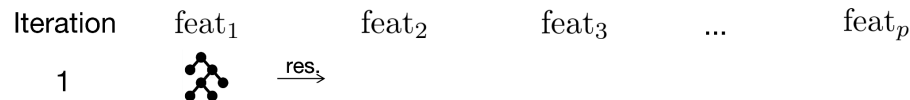
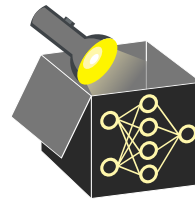
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UNIVARIATE EBM – FIRST FEATURE UPDATE



- Fit shallow bagged tree $T_1^{[1]}$ (2–4 leaves) to training data $\left\{ (x_1, \tilde{r}^{[0]})^{(i)} \right\}_{i=1}^n$
 \rightsquigarrow Use only feature x_1 as input and $\tilde{r}^{[0]}$ as target
- Update first shape function with learning rate η :

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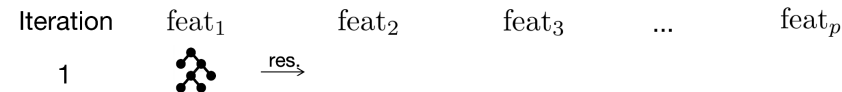
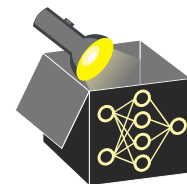
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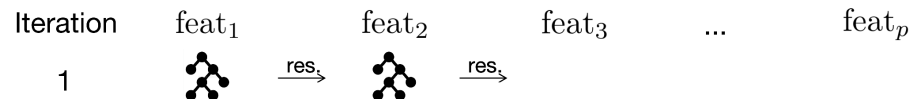
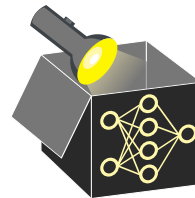
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UNIVARIATE EBM – CYCLE THROUGH FEATURES



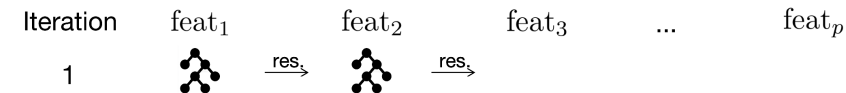
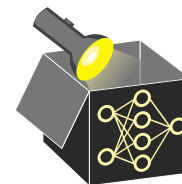
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- After one full pass over features, we complete one boosting iteration

UNIVARIATE EBM CYCLE THROUGH FEATURES



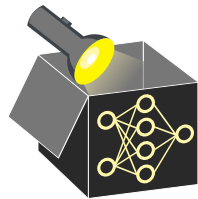
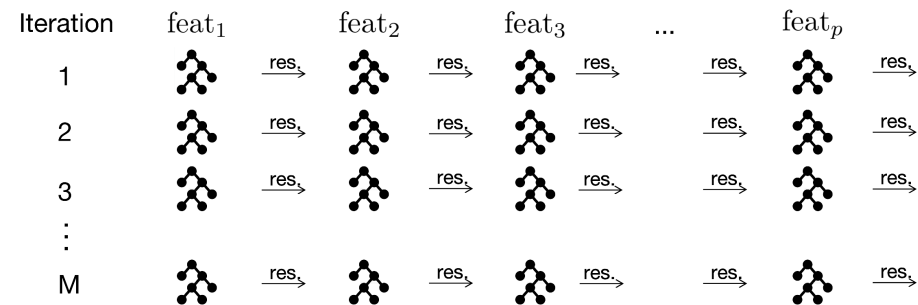
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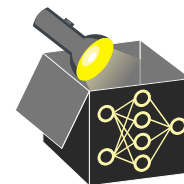
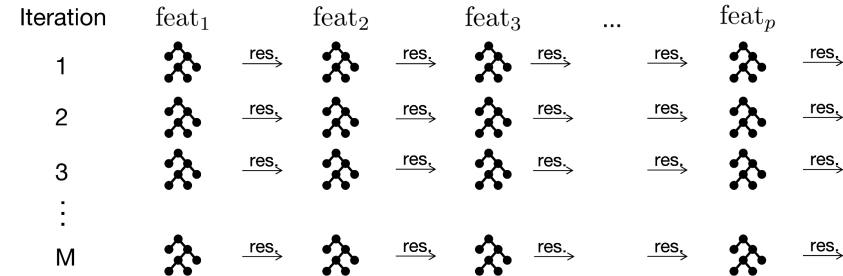
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UNIVARIATE EBM – ITERATE BOOSTING PROCESS



- Repeat feature-wise updates for M boosting iterations (e.g., $M = 10000$)
- In each boosting iteration:
 - Cycle over all features $j = 1, \dots, p$ individually
 - Update only one f_j at a time using residuals from previous state
- Use small learning rate η to ensure smooth updates and order-invariance

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UNIVARIATE EBM - PREDICTION & INTERPRETABILITY

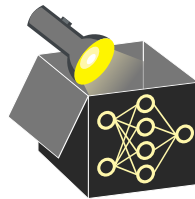
- Final model consists of M shallow trees per feature:

$$\text{EBM Model} = \sum_{j=1}^p \sum_{m=1}^M \eta \cdot T_j^{[m]}(x_j)$$

- For each feature x_j , combine its M trees into a shape function:

$$\hat{f}_j(x_j) = \sum_{m=1}^M \eta \cdot T_j^{[m]}(x_j)$$

- Plot $\hat{f}_j(x_j)$ vs. $x_j \rightsquigarrow$ Shows univariate marginal effect of feature j
- One plot per feature \rightsquigarrow Model is fully explainable via p additive plots



UNIVARIATE EBM - PREDICTION & INTERPRETABILITY

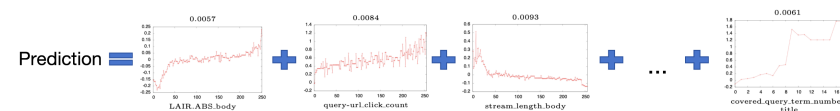
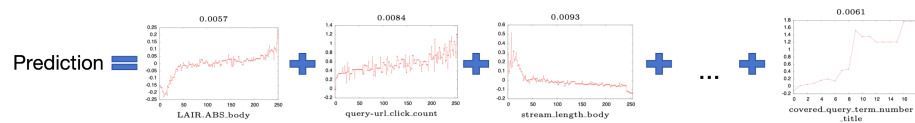
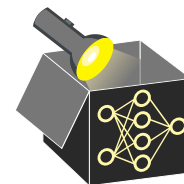
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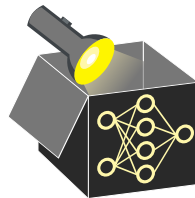
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EBM WITH PAIRWISE INTERACTIONS

Generalized Additive Models plus Interactions (GA2M):

$$g(\mathbb{E}[y \mid \mathbf{x}]) = \theta_0 + \sum_{j=1}^p f_j(x_j) + \sum_{i < j} f_{ij}(x_i, x_j)$$

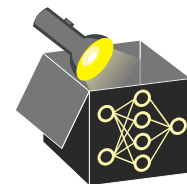


- **Motivation:** Univariate EBM does not model interactions
- **Challenge:** $O(p^2)$ potential pairwise interactions \rightsquigarrow often infeasible
- **Solution - FAST algorithm** ► Lou et al. 2013:
 - Efficiently estimates importance of all feature pairs
 - Ranks pairs by reduction in residual sum of squares (RSS)
 - Avoids fitting EBM with each pairwise interaction
- **Result:** Add only top-ranked interactions f_{ij} via a second-stage boosting step
 \rightsquigarrow Performed after the univariate EBM has been trained
- **Interpretability preserved:** Each $f_{ij}(x_i, x_j)$ visualized as a 2D heatmap

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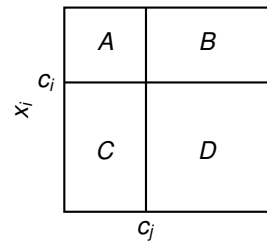
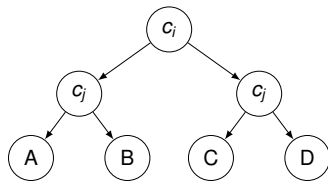
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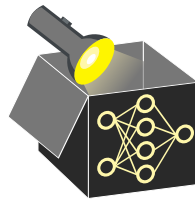
FAST: PAIR-WISE INTERACTION STRENGTH

We evaluate a 4-leaf, axis-aligned tree T_{ij} over the 2D feature projection (x_i, x_j) .



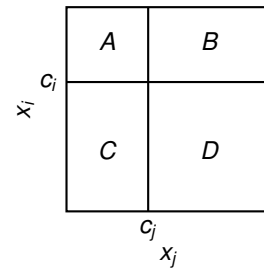
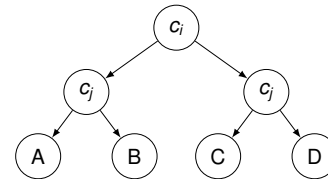
tree T_{ij} with 4 leaves

- 1 **Discretize** : Map each axis to $b \leq 256$ ordered bins (quantile or equal-width).



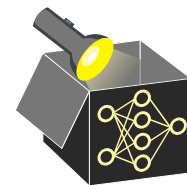
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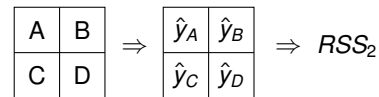
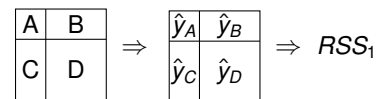
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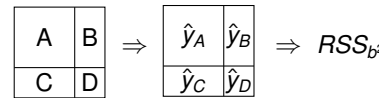


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❶ **Discretize** : Map each axis to $b \leq 256$ ordered bins (quantile or equal-width).

❷ **Iterate** over b^2 candidate cuts (c_i, c_j) .

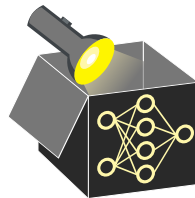
❸ **Fit** : For each cut, assign a constant $\hat{y}_r = \text{mean}(y \in r)$ to $r \in \{A, B, C, D\}$.

❹ **Compute RSS summed over all regions:**

$$RSS(c_i, c_j) = \sum_r \sum_{(x,y) \in r} (y - \hat{y}_r)^2$$

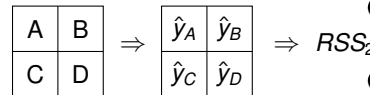
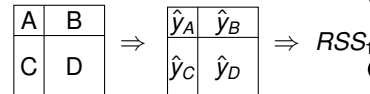
$$= \sum_r \left(\sum_{(x,y) \in r} y^2 - \frac{1}{n_r} \left(\sum_{(x,y) \in r} y \right)^2 \right)$$

❺ **Select** : Keep the split with minimal RSS.
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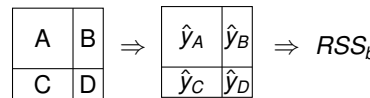


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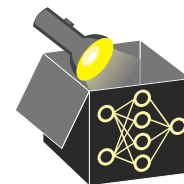
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To evaluate a cut pair (c_i, c_j) , we use precomputed per-region statistics:

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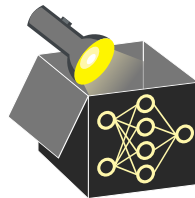
$$S_r = \sum_{(x,y) \in r} y, \quad n_r = |\{(x,y) \in r\}|, \quad \hat{y}_r = S_r/n_r$$

- Plug into RSS summed over all regions:

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- For a candidate cut, compute **RSS drop**:

$$\begin{aligned} \Delta \text{RSS}(c_i, c_j) &= \text{RSS}_{\text{parent}} - \text{RSS}(c_i, c_j) \\ &= \left(\sum_{i=1}^n (y^{(i)})^2 - \frac{S_n^2}{n} \right) - \sum_r \sum_{(x,y) \in r} y^2 + \sum_r \frac{S_r^2}{n_r} \end{aligned}$$



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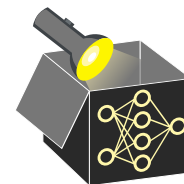
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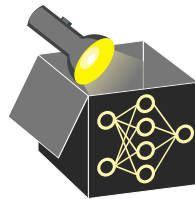
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The parent term S_n^2/n is constant across all cuts. Hence

$$\textbf{maximize } \Delta \text{RSS}(c_i, c_j) = \sum_r \frac{S_r^2}{n_r} \iff \textbf{minimize } \text{RSS}(c_i, c_j).$$

Why is this efficient?

- Precompute cumulative sums of y and counts across the binned grid
- Enables fast lookup of region statistics S_r, n_r for any cut
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- For the best cut: Compare and select the largest $\Delta \text{RSS}(c_i, c_j)$.



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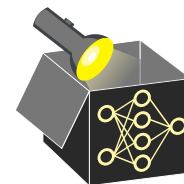
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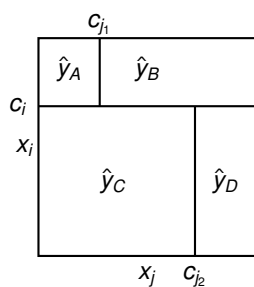
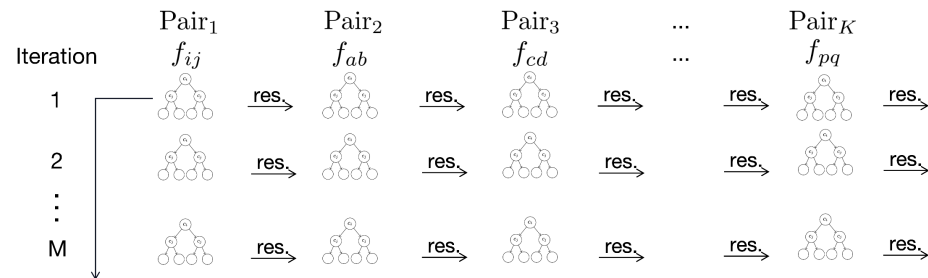
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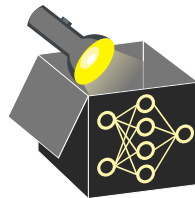
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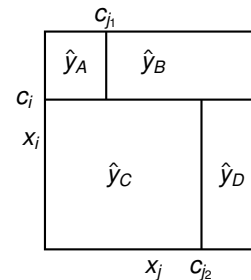
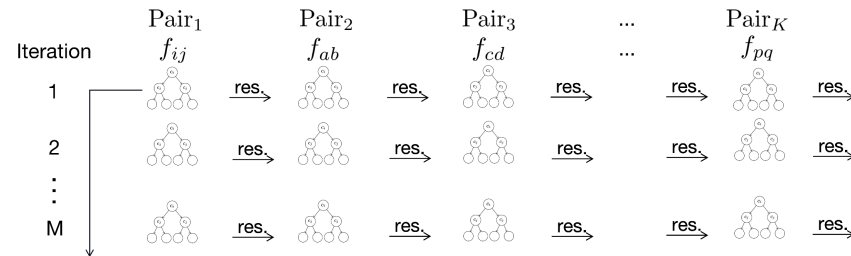
EBM - BOOSTING PAIRWISE INTERACTIONS



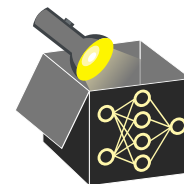
- **Goal:** Fit each selected interaction $f_{ij}(x_i, x_j)$ on residuals from main effects
- Use tree-like predictor, inspired by FAST
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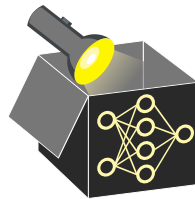
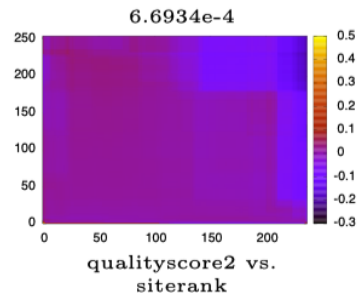


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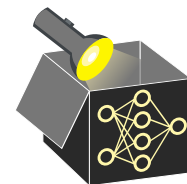
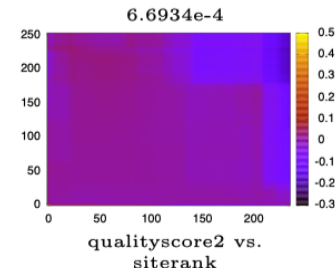
EBM - PREDICTION WITH PAIRWISE INTERACTIONS

- Each selected pair (x_i, x_j) is modeled by M boosted predictors trained on their residual interaction
- These are aggregated into a single bivariate function $f_{ij}(x_i, x_j)$
- The function is visualized as a 2D heatmap:
 - Axes: feature values of x_i and x_j
 - Color: contribution to the final prediction
 - Preserves human interpretability
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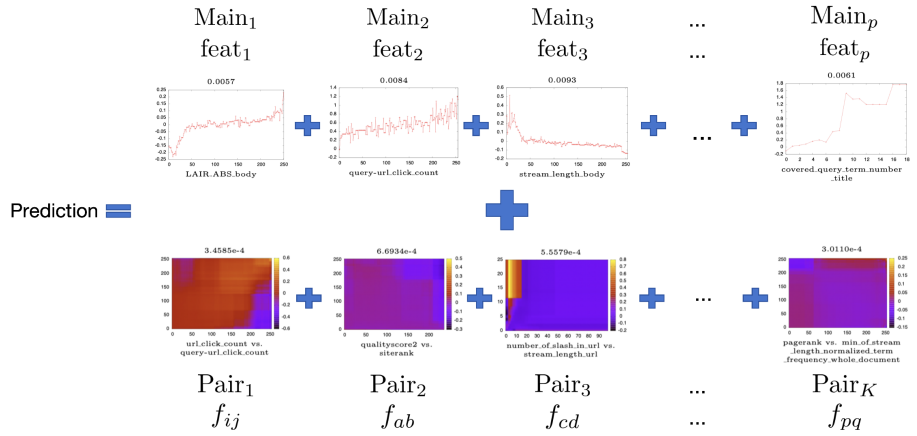
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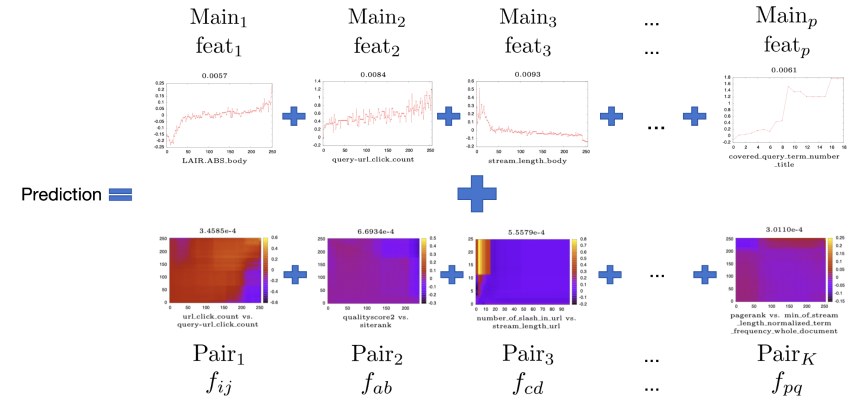
EBM - FINAL MODEL STRUCTURE

- **Main effects:** One shape function $f_j(x_j)$ per feature (visualized as 1D plots)
- **Pairwise interactions:** Selected functions $f_{ij}(x_i, x_j)$ added for top K pairs (visualized as 2D heatmaps)
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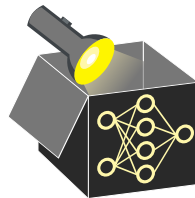
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EBM VS. MODEL-BASED BOOSTING

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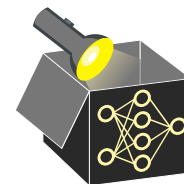
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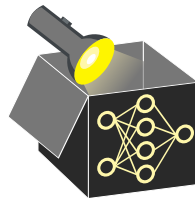
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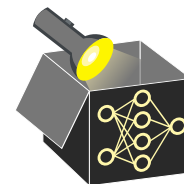
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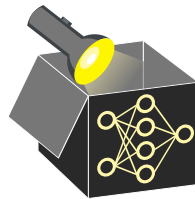
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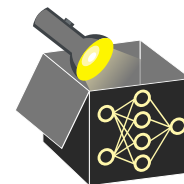
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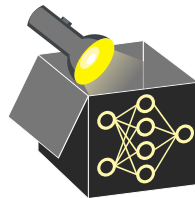
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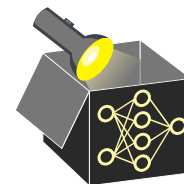
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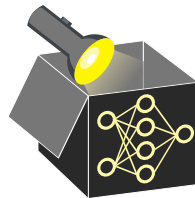
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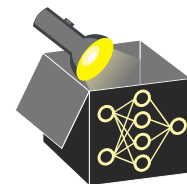
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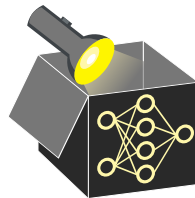
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