## Comparing Modern Machine Learning Methods for Predicting Individual Treatment Effect

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- Characterizing this heterogeneity in intervention effects is key to improving patients outcomes.

#### to estimate Individual Treatment Effects.

## To compare state-of-the-art **Statistical models and Machine Learning algorithms**.

- PITE is a method to estimate individual treatment effects.
- PITE consists of the difference between **experimental(E)** and **control (C) prediction** for each individual [Jaki et al., 2024].

$$\mathsf{PITE}_i = f_E(\boldsymbol{X}_i) - f_C(\boldsymbol{X}_i), \qquad f(\cdot) \text{ is a predictor}$$

# The predicted individual treatment effects (**PITE**) framework

#### challenge

PITE is unobserved. The outcome is observed for a given patient only under either the **experimental(E)**  $f_E(\mathbf{x}_i)$  or **control (C) condition**  $f_C(\mathbf{x}_i)$ 

a natural question

Which method is the best to estimate PITE?

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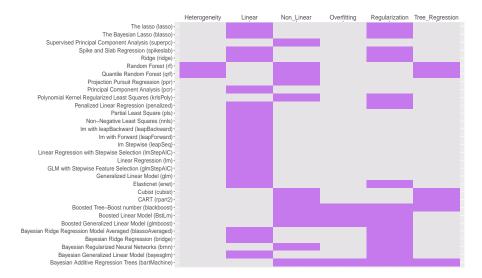
#### Predictive models should address

- population heterogeneity,
- complex structures (linear/non-linear)
- and high-dimensionality [Lamont et al., 2016].

#### important!

- The best method to estimate the PITE is not **necessarily** the best fitted model.
- An essential part is **to delineate this heterogeneity** based on the baseline covariates (features).

## Regressions approaches applied



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• Sensitivity (Detect PITE direction)

$$\mathsf{Same Direction}_i = egin{cases} 1 & \mathsf{if } \mathsf{tPITE}_i imes \mathsf{PITE}_i > 0 \ -1 & \mathsf{otherwise} \end{cases}$$

true  $tPITE_i$  and estimated  $PITE_i$ .

$$\frac{1}{n} \sum_{i=1}^{n} \mathbf{1}_{tPITE_i \times PITE_i > 0}$$

For each method, calculate the proportion of individuals whose estimated PITE have the same direction as the true PITE.

• Risk (Expected Squared Error)

$$\frac{1}{n}\sum_{i=1}^{n}(\mathsf{tPITE}_{i}-\mathsf{PITE}_{i})^{2}\times100$$

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Sample size n = 40, 70, 100, 300, 400, 500, 1000, 1200, 1500 with allocation ratio 1:1 ( $n_C = n_T = n/2$ ).

$$y = \boldsymbol{X}\beta + t\boldsymbol{Z}\gamma + \epsilon, \quad \epsilon \sim N(0,1)$$

 $t \in (0,1) \Rightarrow \mathsf{benefit} \ \boldsymbol{Z}\gamma$ 

Leave-one-out cross-validation for validation

• Z Normal, Linear, Independent

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- $\boldsymbol{Z} \sim U[0.1, 0.5]$ , Non-Linear. Benefit:  $Z_1\gamma_1/(Z_2 + \gamma_2)$

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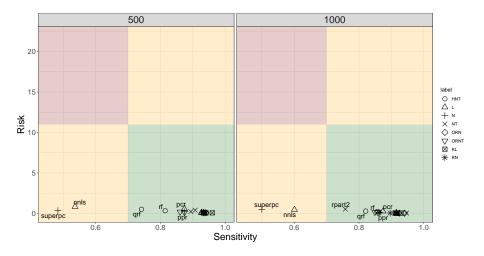
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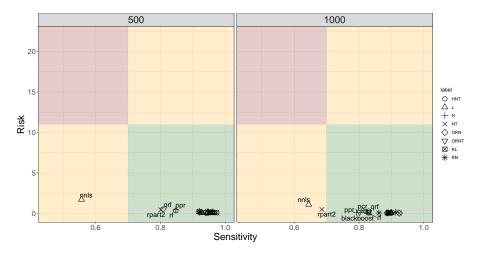
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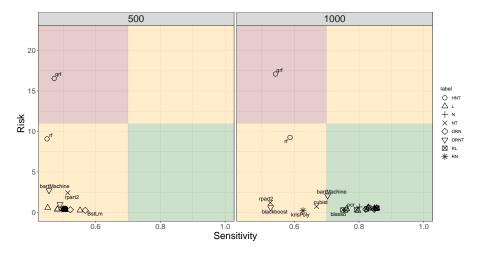
### Linear, no Interaction



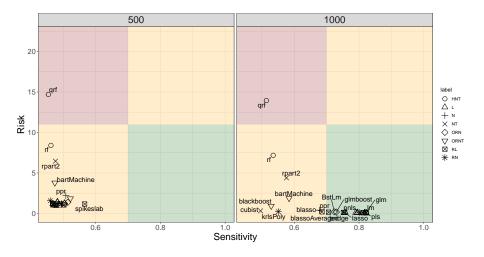
## Linear, with Interaction

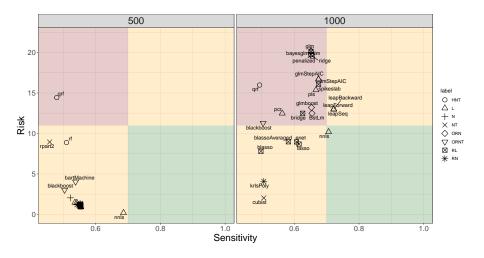


#### Linear, low Correlation

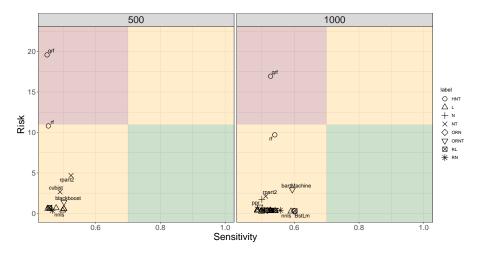


## Linear, high Correlation



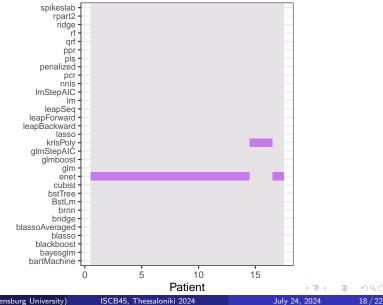


## No-Linear, Complex



## Difficult cases Non-linear Complex n = 500

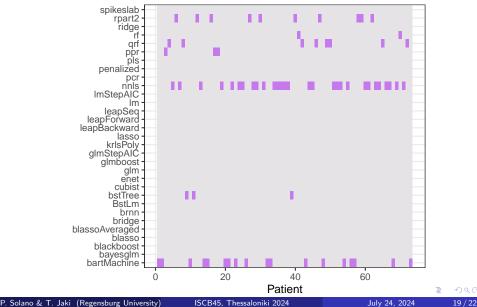
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## Difficult cases Non-linear Complex n = 1000

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- Effectiveness of Regularization in high-correlation scenarios.
- Methods based on trees (blackboost, bartMachine, rpart2) present typically low risk in non-linear cases, while linear approaches struggle with risk in simple non-linear data.
- Leave complex methods for large sample sizes.

- Thomas Jaki, Chi Chang, Alena Kuhlemeier, and M. Lee Van Horn. Predicting individual treatment effects: Challenges and opportunities for machine learning and artificial intelligence. KI - Künstliche Intelligenz, January 2024. ISSN 1610-1987. doi: 10.1007/s13218-023-00827-4. URL http://dx.doi.org/10.1007/s13218-023-00827-4.
- Andrea Lamont, Michael D Lyons, Thomas Jaki, Elizabeth Stuart, Daniel J Feaster, Kukatharmini Tharmaratnam, Daniel Oberski, Hemant Ishwaran, Dawn K Wilson, and M Lee Van Horn. Identification of predicted individual treatment effects in randomized clinical trials. *Statistical Methods in Medical Research*, 27(1):142–157, March 2016. doi: 10.1177/0962280215623981. URL https://doi.org/10.1177/0962280215623981.

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