

Predicting subgroup treatment effects for a new study

Giulia Capestro and **Silvia Zaoli**, Data Scientists

AMLD 2022, Lausanne

March 28, 2022

What is subgroup identification and why we need it

Phase III clinical trial



Submission to regulatory agency fails
(inadequate efficacy wrt SoC)



This situation is relatively common:

- **50%** of drugs fail first submission, **13.2%** of them due to inadequate efficacy wrt Standard of Care
- **16%** among drugs that are never approved

Sacks et al, *Scientific and Regulatory Reasons for Delay and Denial of FDA Approval of Initial Applications for New Drugs, 2000-2012*, JAMA

What is subgroup identification and why we need it

Patients are heterogeneous, and so is their response to a drug



Baseline covariates or biomarkers

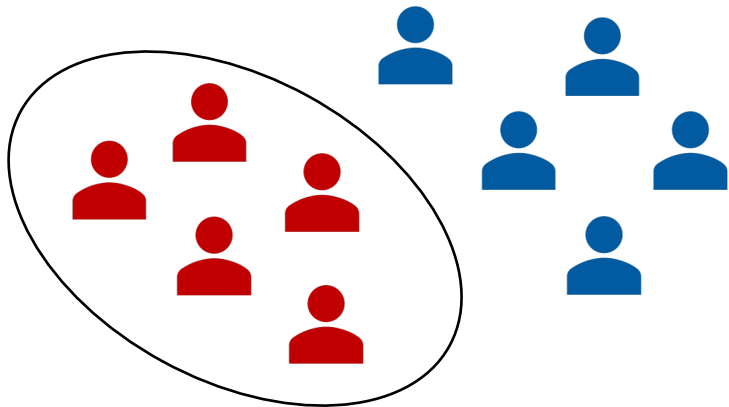
- Demographic (age, sex, ...)
- Disease sub-types, severity scores...
- Genetic biomarkers...

Covariates can be:

- **Prognostic** : impact the outcome regardless of treatment received
- **Predictive** : inform about the effect of treatment

What is subgroup identification and why we need it

If we find out which baseline covariates are predictive, we can identify a *subgroup with increased treatment effect*



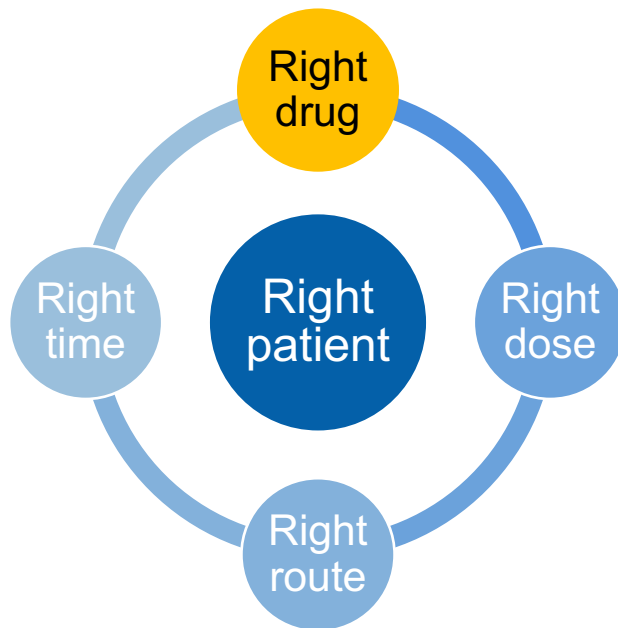
Ex: patients younger than 60 that have symptom X

Subgroup identification



Clustering

Subgroup identification as precision medicine



What is subgroup identification and why we need it

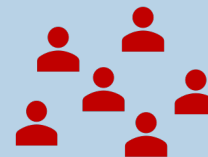
Phase III clinical trial



Submission to regulatory agency fails
(inadequate efficacy wrt SoC)



Plan follow-up trial
on subgroup



Finding a subgroup which will replicate in a new trial is an extremely hard problem:

- Trial was not designed with this purpose
- Treatment effect in subgroups noisy due to small sample size
- Example: Aspirin harmful for people born under Libra and Gemini!



Crucial to find reliable methods, but the problem remains challenging!

Overview of existing learning methods

Tree-based

- VirtualTwin
- SIDES
- GUIDE
- MOB
- ...

- Decision trees to split patients based on their characteristics
- Criteria to choose best split depends on method
- Model returns combination of thresholds which define the subgroup

Regression-based

- Lasso & Ridge, GLMnet
- Boosting
- 'FindIT' (SVT+Lasso)
- STIMA (hybrid)
- ...

- Identify predictive variables thanks to the regression on the outcome
- Does not directly return subgroup definition

The challenge aims

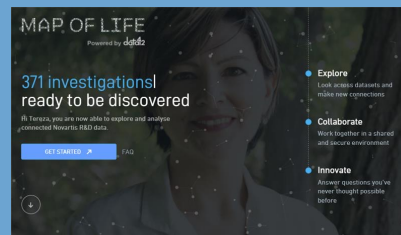
Realistic setting

- Assess teams in a real situation
- Subgroup tested on unseen data, to verify if it replicates

Innovative way of learning

Opportunity to test and compare various methods

Novartis data42 platform



- Large amount of clinical and RWE data
- Several data analysis tools
- Fosters collaboration and reproducibility

The challenge data

Challenge reproduces realistic situation:

- Identified subgroup is tested on new, unseen data
- Allows to test reproducibility

Training dataset

4 Phase III randomized clinical trials in the same therapeutic area were provided to all participants

Scoring dataset

One more clinical trial, not available to participants

- Same inclusion criteria
- 90+ Baseline covariates

The challenge data

Endpoint

Binary response index

Combination of measures of improvement e.g.:

- patient global assessment
- physician global assessment
- result of health questionnaire
- results of lab tests



Treatment effect

$$TE = p(\text{treatment}) - p(\text{control})$$

The challenge task

Participants had to submit:

- 1 A definition of the subgroup for which they predict increased treatment effect in the new trial (ex. “AGE<60”)
- 2 Their prediction of the treatment effect to be observed for the subgroup in the new trial:
$$\delta_{pred} = p(\text{treatment}) - p(\text{control})$$
and its uncertainty σ_{pred}
- 3 A description of their methodology, with clinical/biological justification of the subgroup

How we scored the submissions

Does the subgroup have increase treatment effect in the new trial?

- Probability p_i of patient i to respond modeled as

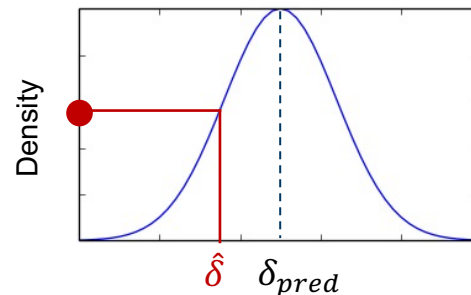
$$\text{logit}(p_i) = \beta_0 + \beta_{trt}t_i + \beta_s s_i + \beta_{interaction}t_i s_i + x_i' \beta$$

- t_i = treatment (0 – control, 1 – treatment)
- s_i = subgroup (1 – subgroup, 0 – complement)
- x_i covariates as in the primary analysis model for the new trial

- Score obtained as: $\frac{\hat{\beta}_{interaction}}{s.e.(\hat{\beta}_{interaction})}$

Is the prediction of treatment effect accurate?

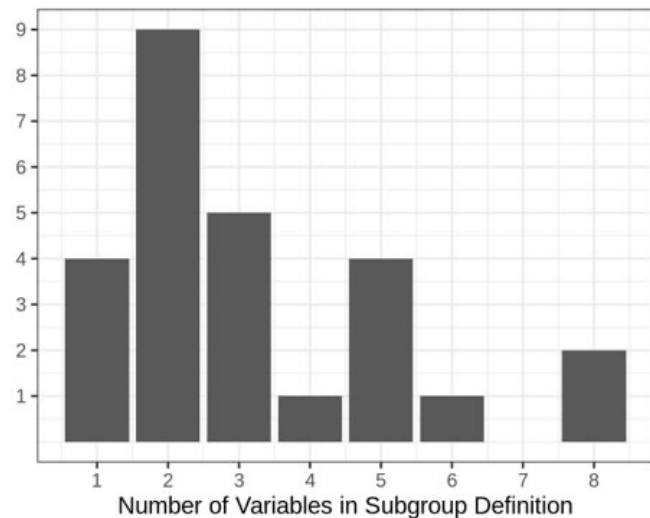
- $\hat{\delta}$ = treatment effect observed in the subgroup in the new trial
- The score is the log-likelihood of $\hat{\delta}$ according to $N(\delta_{pred}, \sigma_{pred})$



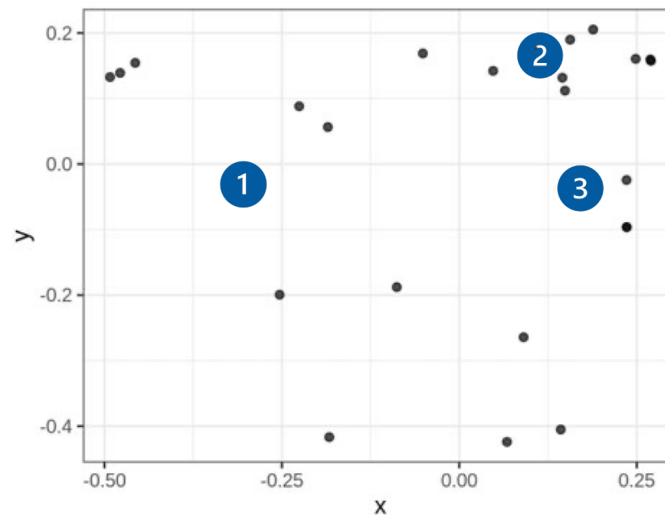
Treatment difference in subgroup

Challenge results

Typically few covariates used in subgroup definition
A few variables were used very often (e.g. age)

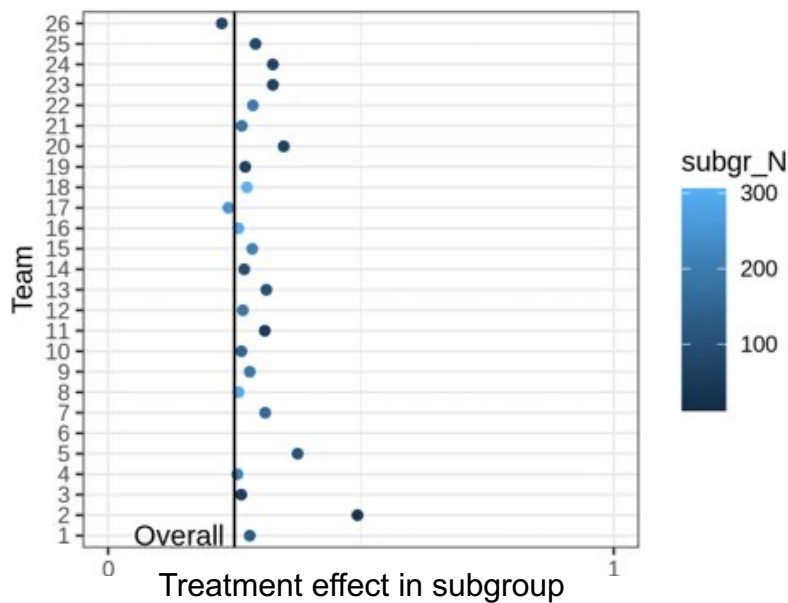


Proposed subgroups are quite different, also the top 3

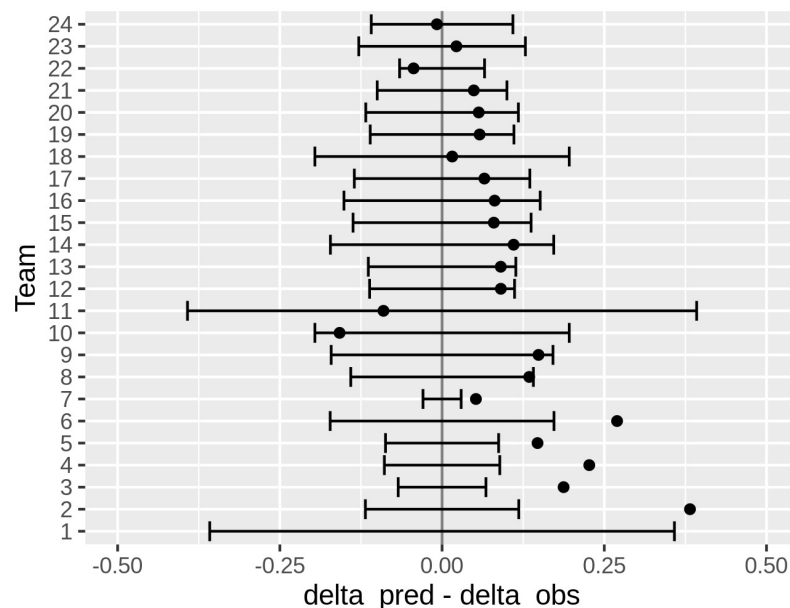


Challenge results

All but two teams identified a subgroup with tr. eff. higher than overall in the new trial

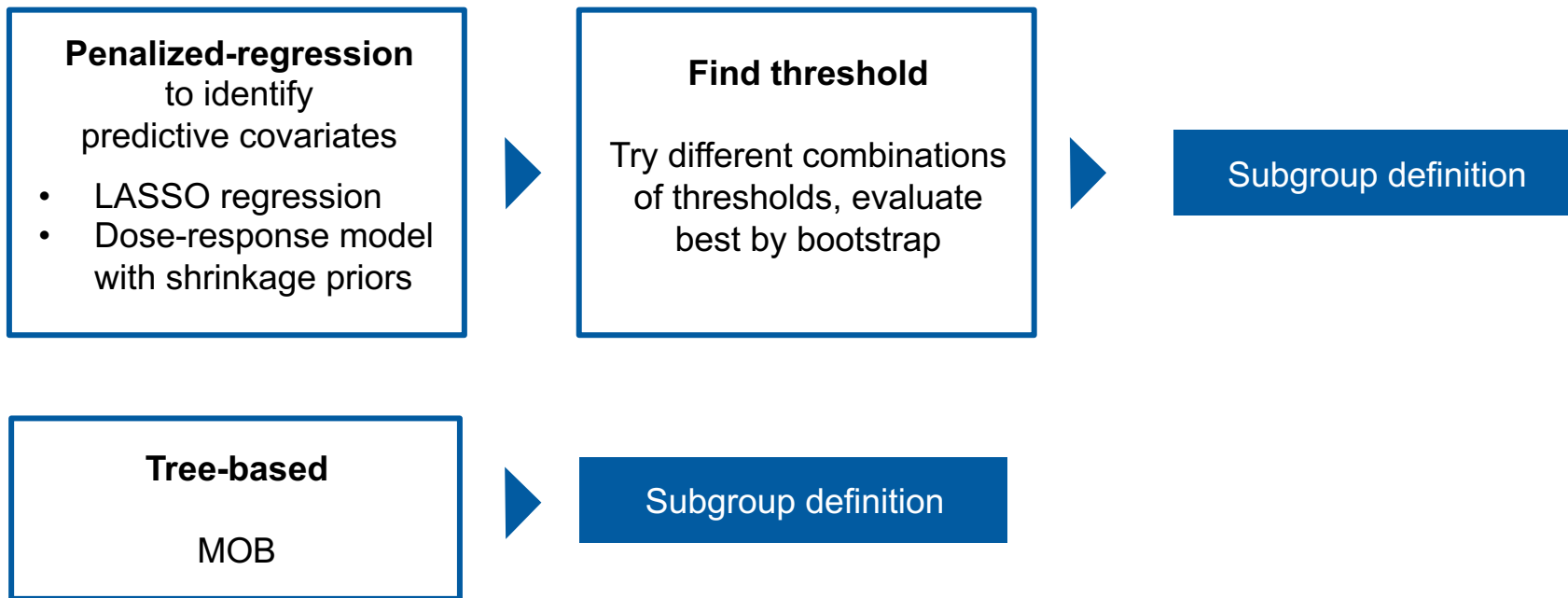


Systematic overestimation of treatment effect (regression to the mean)



Methods used by the participants

Focusing on top teams:



Learnings and insights from the participants

HARD PROBLEM

- No obvious solution
- Various methods could identify different subgroups with increased tr. eff.

REPRODUCIBILITY

- Cross-validation with hold-out sets
- Clinical insights

DATA NOT SUFFICIENT?

- Even with the best method, need to complement data with external information

Many thanks to

- The other organizers: Bjorn Bornkamp, Carsten Müller, Conor Moloney, Mark Baillie, Michela Azzarito, Ruvie Martin, Jana Starkova
- The participants of the challenge
- data42
- All of you for listening!