Introduction	Main Methodology	Genomic Application	Summary	Références

Floodgate: Inference for Model-free Variable Importance

Lu Zhang Joint work with Lucas Janson

> Department of Statistics Harvard University

August 26, 2020



Introduction ••••••	Main Methodology	Genomic Application	Summary O	Références
Summary				

Setup : data (Y, X, Z).

■ *Y* : response variable; *X* : the variable of interest; $Z := (Z_1, \dots, Z_p)$ confounders.

Q : how important each covariate (X) is in this relationship?

- A : introduce floodgate, a new inferential approach for variable importance.
 - Focus on an interpretable, sensitive and nonparametric MOVI : the mMSE gap.

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z\right])^2 \right] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z\right])^2 \right].$$

Provide valid and robust lower confidence bounds for the mMSE gap.

$$u^{\star} := \mathbb{E}\left[Y \,|\, X, Z\right], \quad f(\mu) := \frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{\star}(X, Z), \mu(X, Z) \,|\, Z)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}(\mu(X, Z) \,|\, Z)\right]}}, \quad f(\mu) \leq \mathcal{I} \text{ for any } \mu.$$

Allow flexible regression algorithms to obtain μ , good prediction \Rightarrow good accuracy. Genomic application to UKBB data : colored "Chicago" plot.

Zhang, Lu, and Lucas Janson. "Floodgate : inference for model-free variable importance." arXiv preprint arXiv:2007.01283 (2020).

Extensions : relax the assumption ; a different MOVI for binary responses ; group variable importance ; different covariate distribution ; adjusting for multiplicity and selection effects.

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Motivation

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

- Y a response variable of interest
- X a explanatory variable of interest (AKA treatment, covariate, feature)
- $Z := (Z_1, \dots, Z_p)$ a set of *p* further variables (AKA confounders, nuisance variables)

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

- Y a response variable of interest
- X a explanatory variable of interest (AKA treatment, covariate, feature)
- $Z := (Z_1, \dots, Z_p)$ a set of *p* further variables (AKA confounders, nuisance variables)

Question : is the variable X important or not?

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

- Y a response variable of interest
- X a explanatory variable of interest (AKA treatment, covariate, feature)
- $Z := (Z_1, \dots, Z_p)$ a set of *p* further variables (AKA confounders, nuisance variables)

Question : is the variable *X* important or not?

Assuming parametric models : testing whether the coefficients are zero.

Introduction	Main Methodology	Genomic Application	Références
0000			
Motivation			

- Y a response variable of interest
- X a explanatory variable of interest (AKA treatment, covariate, feature)
- $Z := (Z_1, \dots, Z_p)$ a set of *p* further variables (AKA confounders, nuisance variables)

Question : is the variable *X* important or not?

- Assuming parametric models : testing whether the coefficients are zero.
- Conditional independence testing (without parametric assumption) :

 $Y \perp\!\!\!\perp X \mid Z$

Introduction OOOO	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

- Y a response variable of interest
- X a explanatory variable of interest (AKA treatment, covariate, feature)
- $Z := (Z_1, \dots, Z_p)$ a set of *p* further variables (AKA confounders, nuisance variables)

Question : is the variable X important or not?

- Assuming parametric models : testing whether the coefficients are zero.
- Conditional independence testing (without parametric assumption) :

$Y \perp X \mid Z$

- Kernel-based conditional independence tests.
- Semi-parametric approaches.
- Model-X approaches : model-X knockoffs, conditional knockoffs, conditional randomization tests, conditional permutation tests, hold-out randomization tests and so on.
- Symmetry idea approaches : Gaussian mirrors and data splitting.

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

- Y a response variable of interest
- X a explanatory variable of interest (AKA treatment, covariate, feature)
- $Z := (Z_1, \dots, Z_p)$ a set of *p* further variables (AKA confounders, nuisance variables)

Question : is the variable X important or not?

- Assuming parametric models : testing whether the coefficients are zero.
- Conditional independence testing (without parametric assumption) :

$Y \perp X \mid Z$

- Kernel-based conditional independence tests.
- Semi-parametric approaches.
- Model-X approaches : model-X knockoffs, conditional knockoffs, conditional randomization tests, conditional permutation tests, hold-out randomization tests and so on.
- Symmetry idea approaches : Gaussian mirrors and data splitting.

Go beyond : how important each covariate is in this relationship?

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Confidence intervals on the parameters;

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

2 How to provide inference for it?

Introduction	Main Methodology	Genomic Application	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

```
2 How to provide inference for it?
```

A desirable MOVI (of the covariate X) should have

```
Validity : zero when Y \perp X \mid Z.
```

Introduction	Main Methodology	Genomic Application	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

2 How to provide inference for it?

A desirable MOVI (of the covariate *X*) should have

Validity : zero when $Y \perp X \mid Z$.

Sensitivity : able to detect nonlinear effects and interactions.

Introduction	Main Methodology	Genomic Application	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

How to provide inference for it?

A desirable MOVI (of the covariate X) should have

Validity : zero when $Y \perp X \mid Z$.

Sensitivity : able to detect nonlinear effects and interactions.

Interpretability : interpretable and ready for scientists and practitioners' use.

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

How to provide inference for it?

A desirable MOVI (of the covariate X) should have

Validity : zero when $Y \perp X \mid Z$.

Sensitivity : able to detect nonlinear effects and interactions.

Interpretability : interpretable and ready for scientists and practitioners' use.

A desirable inferential procedure for the MOVI should be

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

How to provide inference for it?

A desirable MOVI (of the covariate X) should have

Validity : zero when $Y \perp X \mid Z$.

Sensitivity : able to detect nonlinear effects and interactions.

Interpretability : interpretable and ready for scientists and practitioners' use.

A desirable inferential procedure for the MOVI should be

General

Introduction	Main Methodology	Genomic Application	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

How to provide inference for it?

A desirable MOVI (of the covariate X) should have

Validity : zero when $Y \perp X \mid Z$.

Sensitivity : able to detect nonlinear effects and interactions.

Interpretability : interpretable and ready for scientists and practitioners' use.

A desirable inferential procedure for the MOVI should be



Accurate

Introduction	Main Methodology	Genomic Application	Summary O	Références
Motivation				

Confidence intervals on the parameters ;What if no parametric assumption?

How to define a good measure of variable importance (MOVI)?

How to provide inference for it?

A desirable MOVI (of the covariate X) should have

Validity : zero when $Y \perp X \mid Z$.

Sensitivity : able to detect nonlinear effects and interactions.

Interpretability : interpretable and ready for scientists and practitioners' use.

A desirable inferential procedure for the MOVI should be

- General
- Accurate
- Robust

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Literature	review			

- Parametric approaches : Bühlmann et al. (2013), Zhang and Zhang (2014), Javanmard and Montanari (2014), Bühlmann et al. (2015), Dezeure et al. (2017), Zhang and Cheng (2017), Van de Geer et al. (2014), Nickl et al. (2013), Sur and Candès (2019), Zhao et al. (2020) ...
- Projection approaches : Buja et al. (2015, 2019a,b), Rinaldo et al. (2019), Lee et al. (2016), Taylor et al. (2014), Berk et al. (2013), Buja and Brown (2014).
- Random parameters : Lei et al. (2018), Fisher et al. (2018), Watson and Wright (2019), Rinaldo et al. (2019).
- Semi-parametric approaches : Robins et al. (2008, 2009); Li et al. (2011); Robins et al. (2017); Newey and Robins (2018), Shah and Peters (2018).
- A very recent MOVI : Azadkia and Chatterjee (2019).
- Same MOVI as us : Williamson et al. (2017).

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \mid Z\right])^2 \right] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \mid X, Z\right])^2 \right]$$

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}[Y \mid X, Z] \stackrel{a.s.}{=} \mathbb{E}[Y \mid Z]$$

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Definition (mMSE Gap)

The minimum mean squared error (mMSE) gap for variable X is defined as

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \,|\, X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \,|\, Z\right]$$

Predictive : immediate from above.

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \,|\, X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \,|\, Z\right]$$

- Predictive : immediate from above.
- Variance decomposition : $\mathcal{I}^2 = \operatorname{Var} (\mathbb{E} [Y | X, Z]) \operatorname{Var} (\mathbb{E} [Y | Z]).$

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \,|\, X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \,|\, Z\right]$$

- Predictive : immediate from above.
- Variance decomposition : $\mathcal{I}^2 = \operatorname{Var} (\mathbb{E} [Y | X, Z]) \operatorname{Var} (\mathbb{E} [Y | Z]).$

• **Causal**:
$$\mathcal{I}^2 = \frac{1}{2} \mathbb{E}_{x_1, x_2} \stackrel{i.i.d.}{\sim} P_{X|Z} \left[(\mathbb{E}[Y | X = x_1, Z] - \mathbb{E}[Y | X = x_2, Z])^2 \right].$$

Introduction	Main Methodology	Genomic Application	Summary	Références
00000				

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \,|\, X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \,|\, Z\right]$$

- Predictive : immediate from above.
- Variance decomposition : $\mathcal{I}^2 = \operatorname{Var} (\mathbb{E} [Y | X, Z]) \operatorname{Var} (\mathbb{E} [Y | Z]).$
- Causal: $\mathcal{I}^2 = \frac{1}{2} \mathbb{E}_{x_1, x_2} \stackrel{i.i.d.}{\sim} P_{X|Z} \left[(\mathbb{E}[Y | X = x_1, Z] \mathbb{E}[Y | X = x_2, Z])^2 \right].$

• Compact form :
$$\mathcal{I}^2 = \mathbb{E} \left[\operatorname{Var} \left(\mathbb{E} \left[Y \, | \, X, Z \right] \, | \, Z \right) \right].$$

Introduction	Main Methodology	Genomic Application	Summary	Références
	●00000			

Introduction	Main Methodology	Genomic Application	Summary	Références
	•00000			

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \mid Z\right])^2 \right] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \mid X, Z\right])^2 \right]$$

Introduction	Main Methodology	Genomic Application	Summary	Références
	●00000			

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \mid X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \mid Z\right]$$

Introduction	Main Methodology	Genomic Application	Références
	00000		

Definition (mMSE Gap)

The minimum mean squared error (mMSE) gap for variable X is defined as

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}[Y \mid X, Z] \stackrel{a.s.}{=} \mathbb{E}[Y \mid Z]$$

Predictive : immediate from above.

Introduction	Main Methodology	Genomic Application	Références
	00000		

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \,|\, X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \,|\, Z\right]$$

- Predictive : immediate from above.
- Variance decomposition : $\mathcal{I}^2 = \operatorname{Var} (\mathbb{E} [Y | X, Z]) \operatorname{Var} (\mathbb{E} [Y | Z]).$

Introduction	Main Methodology	Genomic Application	Summary	Références
	00000			

Definition (mMSE Gap)

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \,|\, X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \,|\, Z\right]$$

- Predictive : immediate from above.
- Variance decomposition : $\mathcal{I}^2 = \operatorname{Var} (\mathbb{E} [Y | X, Z]) \operatorname{Var} (\mathbb{E} [Y | Z]).$

• **Causal**:
$$\mathcal{I}^2 = \frac{1}{2} \mathbb{E}_{x_1, x_2} \stackrel{i.i.d.}{\sim} P_{X|Z} \left[(\mathbb{E}[Y | X = x_1, Z] - \mathbb{E}[Y | X = x_2, Z])^2 \right].$$
Introduction	Main Methodology	Genomic Application	Summary	Références
	●00000			

Our target MOVI : the mMSE gap

Definition (mMSE Gap)

The minimum mean squared error (mMSE) gap for variable X is defined as

$$\mathcal{I}^2 = \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, Z
ight])^2
ight] - \mathbb{E}\left[(Y - \mathbb{E}\left[Y \,|\, X, Z
ight])^2
ight].$$

$$\mathcal{I}^{2} = 0 \iff \mathbb{E}\left[Y \,|\, X, Z\right] \stackrel{a.s.}{=} \mathbb{E}\left[Y \,|\, Z\right]$$

- Predictive : immediate from above.
- Variance decomposition : $\mathcal{I}^2 = \operatorname{Var} (\mathbb{E} [Y | X, Z]) \operatorname{Var} (\mathbb{E} [Y | Z]).$
- Causal: $\mathcal{I}^2 = \frac{1}{2} \mathbb{E}_{x_1, x_2} \stackrel{i.i.d.}{\sim} P_{X|Z} \left[(\mathbb{E}[Y | X = x_1, Z] \mathbb{E}[Y | X = x_2, Z])^2 \right].$

• Compact form :
$$\mathcal{I}^2 = \mathbb{E} \left[\operatorname{Var} \left(\mathbb{E} \left[Y \, | \, X, Z \right] \, | \, Z \right) \right].$$

Introduction	Main Methodology O●OOOO	Genomic Application	Summary O	Références
How to do) inference on \mathcal{T} ?			

True regression function $\mu^{\star}(x, z) := \mathbb{E}[Y | X = x, Z = z]$

Introduction	Main Methodology ○●○○○○	Genomic Application	Summary O	Références
How to do	inference on \mathcal{T} ?			

True regression function $\mu^{\star}(x, z) := \mathbb{E}\left[Y \mid X = x, Z = z\right]$

$$\Rightarrow \mathcal{I}^2 = \mathbb{E}\left[\operatorname{Var}(\mu^{\star}(X, Z) \,|\, Z)\right] = \mathbb{E}\left[\left(\mu^{\star}(X, Z) - \mathbb{E}\left[\mu^{\star}(X, Z) \,|\, Z\right]\right)^2\right]$$

Challenges :

Introduction 00000	Main Methodology	Genomic Application	Summary O	Références
How to do	inference on \mathcal{T} ?			

True regression function $\mu^{\star}(x, z) := \mathbb{E}\left[Y \mid X = x, Z = z\right]$

$$\Rightarrow \ \mathcal{I}^2 = \mathbb{E}\left[\operatorname{Var}(\mu^\star(X,Z) \,|\, Z)\right] = \mathbb{E}\left[(\mu^\star(X,Z) - \mathbb{E}\left[\mu^\star(X,Z) \,|\, Z\right])^2\right]$$

Challenges :

- \blacksquare μ^{\star} unknown.
- Nonlinearity in the above functional.

Introduction	Main Methodology	Genomic Application	Summary O	Références
How to do	inference on \mathcal{T} ?			

True regression function $\mu^*(x, z) := \mathbb{E}[Y | X = x, Z = z]$

$$\Rightarrow \ \mathcal{I}^2 = \mathbb{E}\left[\operatorname{Var}(\mu^{\star}(X,Z) \,|\, Z)\right] = \mathbb{E}\left[(\mu^{\star}(X,Z) - \mathbb{E}\left[\mu^{\star}(X,Z) \,|\, Z\right])^2\right]$$

Challenges :

- \blacksquare μ^* unknown.
- Nonlinearity in the above functional.

Possible solution : assume we have a good estimator μ of μ^* ?

Introduction	Main Methodology ○●○○○○	Genomic Application	Summary O	Références
How to do inference on \mathcal{T} ?				

True regression function $\mu^{\star}(x, z) := \mathbb{E}[Y | X = x, Z = z]$

$$\Rightarrow \ \mathcal{I}^2 = \mathbb{E}\left[\operatorname{Var}(\mu^{\star}(X,Z) \,|\, Z)\right] = \mathbb{E}\left[(\mu^{\star}(X,Z) - \mathbb{E}\left[\mu^{\star}(X,Z) \,|\, Z\right])^2\right]$$

Challenges :

- \blacksquare μ^* unknown.
- Nonlinearity in the above functional.

Possible solution : assume we have a good estimator μ of μ^* ?

Our approach : construct a lower confidence bound (LCB) for \mathcal{I} via floodgate, i.e.

Introduction	Main Methodology	Genomic Application	Références
	000000		
How to do	τ		

How to do interence on *L* ?

True regression function $\mu^{\star}(x, z) := \mathbb{E}[Y | X = x, Z = z]$

$$\Rightarrow \ \mathcal{I}^2 = \mathbb{E}\left[\operatorname{Var}(\mu^{\star}(X,Z) \,|\, Z)\right] = \mathbb{E}\left[(\mu^{\star}(X,Z) - \mathbb{E}\left[\mu^{\star}(X,Z) \,|\, Z\right])^2\right]$$

Challenges :

 \blacksquare μ^* unknown.

Nonlinearity in the above functional.

Possible solution : assume we have a good estimator μ of μ^* ?

Our approach : construct a lower confidence bound (LCB) for \mathcal{I} via floodgate, i.e.

construct a functional f such that

 $f(\mu) \leq \mathcal{I}$ for any μ .

Introduction	Main Methodology	Genomic Application	Références
	000000		
How to do	τ		

How to do interence on \mathcal{L} ?

True regression function $\mu^{\star}(x, z) := \mathbb{E}[Y | X = x, Z = z]$

$$\Rightarrow \ \mathcal{I}^2 = \mathbb{E}\left[\operatorname{Var}(\mu^{\star}(X, Z) \,|\, Z)\right] = \mathbb{E}\left[(\mu^{\star}(X, Z) - \mathbb{E}\left[\mu^{\star}(X, Z) \,|\, Z\right])^2\right]$$

Challenges :

 \blacksquare μ^* unknown.

Nonlinearity in the above functional.

Possible solution : assume we have a good estimator μ of μ^* ?

Our approach : construct a lower confidence bound (LCB) for \mathcal{I} via floodgate, i.e.

construct a functional f such that

 $f(\mu) \leq \mathcal{I}$ for any μ .

• know how to obtain LCB $L(\mu)$ of $f(\mu)$ for any μ .

Introduction	Main Methodology	Genomic Application	Summary	Références
	00000			
How to do	information τ			

How to do inference on \mathcal{I} ?

True regression function $\mu^{\star}(x, z) := \mathbb{E}[Y | X = x, Z = z]$

$$\Rightarrow \ \mathcal{I}^2 = \mathbb{E}\left[\operatorname{Var}(\mu^*(X, Z) \mid Z)\right] = \mathbb{E}\left[\left(\mu^*(X, Z) - \mathbb{E}\left[\mu^*(X, Z) \mid Z\right]\right)^2\right]$$

Challenges :

- \blacksquare μ^* unknown.
- Nonlinearity in the above functional.

Possible solution : assume we have a good estimator μ of μ^* ?

Our approach : construct a lower confidence bound (LCB) for \mathcal{I} via floodgate, i.e.

construct a functional f such that

 $f(\mu) \leq \mathcal{I}$ for any μ .

- know how to obtain LCB $L(\mu)$ of $f(\mu)$ for any μ .
- (Ideally) the functional *f* also satisfies $f(\mu^*) = \mathcal{I}$.

Introduction	Main Methodology	Genomic Application	Summary O	Références
Floodgate	LCB			
Our choi	ce of functional : $f(\mu) :=$	$\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{\star}(X,Z),\mu(X,Z) \mid Z)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}(\mu(X,Z) \mid Z)\right]}}$		

Introduction 00000	Main Methodology ○○●○○○	Genomic Application O	Summary O	Références
Floodgat	e LCB			
5				
Our ch	noice of functional : $f(\mu) :=$	$\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{\star}(X,Z),\mu(X,Z)\mid Z)\right]}{\sqrt{1-1}}$		
		$\sqrt{\mathbb{E}}[\operatorname{Var}(\mu(X, Z) \mid Z)]$		
Lemm	a (Zhang and Janson (2020)))		
For on	$u_{\mu\nu}$ such that $f(u)$ aviate f	$(u) < T$ and $f(u^*) = T$		
FUI all	y μ such that $I(\mu)$ exists, $I(\mu)$	$(\mu) \leq \mathcal{I}$ and $I(\mu) = \mathcal{I}$.		

Introdu 0000	oction	Main Methodology	Genomic Application O	Summary O	Références
Flo	odgate LCI	3			
	Our choice of	functional : $f(\mu) :=$	$=\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{\star}(X,Z),\mu(X,Z)\mid Z)\right]}{\sqrt{\mathbb{E}[\operatorname{Var}(\mu(X,Z)\mid Z)]}}$		
	Lemma (Zhar	ng and Janson (202	0))		
	For any μ suc	that f(μ) exists, f	$\mathcal{I}(\mu) \leq \mathcal{I} \text{ and } f(\mu^{\star}) = \mathcal{I}.$		

Ingredients of our model-X inferential procedure :

Introdu 0000		Main Methodology	Genomic Application O	Summary O	References
Flo	odgate LC	3			
	Our choice of	functional : $f(\mu) := \frac{\mathbb{E}[C]}{\Gamma}$	$\frac{\operatorname{ov}(\mu^{\star}(X,Z),\mu(X,Z) \mid Z)]}{\sqrt{\mathbb{E}[\operatorname{Var}(\mu(X,Z) \mid Z)]}}$		
	Lemma (Zhan	ng and Janson (2020))			
	For any μ suc	h that f(μ) exists, f(μ)	$\leq \mathcal{I}$ and $f(\mu^{\star}) = \mathcal{I}$.		
	Ingredients of	our model-X inferential	procedure :		

1 $(Y_i, X_i, Z_i)_{i=1}^n$.

Introduction 00000	Main Methodology ○○●○○○	Genomic Application O	Summary O	Références
Eloodaata				
Floougale	LUD			
Our choi	ce of functional : $f(\mu) :=$	$\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{\star}(X,Z),\mu(X,Z)\mid Z)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}(\mu(X,Z)\mid Z)\right]}}$		
Lemma (Zhang and Janson (202	0))		
For any _I	μ such that f(μ) exists, f	$(\mu) \leq \mathcal{I} \text{ and } f(\mu^{\star}) = \mathcal{I}.$		
Ingredier $(Y_i,$	nts of our model-X infere $X_i, Z_i)_{i=1}^n$.	ntial procedure :		

00000		Genomic Application O	o	References
Floodgat	e LCB			
Our ch	noice of functional : $f(\mu) :=$	$\frac{\mathbb{E}[\operatorname{Cov}(\mu^{*}(X,Z),\mu(X,Z) \mid Z)]}{\sqrt{\mathbb{E}[X,\mu(X,Z),\mu(X,Z) \mid Z)]}}$		
		$\sqrt{\mathbb{E}[\operatorname{Var}(\mu(X, Z) \mid Z)]}$		
Lemm	a (Zhang and Janson (2020)))		
For an	by μ such that $f(\mu)$ exists, $f(\mu)$	$(\mu) < \mathcal{I}$ and $f(\mu^{\star}) = \mathcal{I}$.		
Ingrod	lights of our model. V inform	ntial procedure :		
ingreu		mai procedure.		

1 $(Y_i, X_i, Z_i)_{i=1}^n$.

2 μ (can be fitted from a separate dataset e.g. sample splitting).

I Assume $P_{X|Z}$ known (also have robustness analysis and assumption relaxation).

OCOCO	Main Methodology	Genomic Application	O	References
Floodgate	LCB			
Our choic	se of functional : $f(\mu) :=$	$\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{*}(X,Z),\mu(X,Z)\mid Z)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}(\mu(X,Z)\mid Z)\right]}}$		
Lemma (2	Zhang and Janson (2020)))		
For any μ	such that $f(\mu)$ exists, f	$(\mu) \leq \mathcal{I} \text{ and } \mathbf{f}(\mu^{\star}) = \mathcal{I}.$		
Ingredien $(Y_i, .$	ts of our model-X infere $X_i, Z_i)_{i=1}^n$.	ntial procedure :		

3 Assume $P_{X|Z}$ known (also have robustness analysis and assumption relaxation).

 $f(\mu) = \frac{\mathbb{E}\left[Y(\mu(X,Z) - \mathbb{E}\left[\mu(X,Z) \mid Z\right]\right)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}\left(\mu(X,Z) \mid Z\right)\right]}} = \frac{\text{a linear functional of } P_{(Y,X,Z)}}{\sqrt{\text{a linear functional of } P_Z}}$

OCOCO	Main Methodology	Genomic Application	O	References
Floodgate	LCB			
Our choic	se of functional : $f(\mu) :=$	$\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{*}(X,Z),\mu(X,Z)\mid Z)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}(\mu(X,Z)\mid Z)\right]}}$		
Lemma (2	Zhang and Janson (2020)))		
For any μ	such that $f(\mu)$ exists, f	$(\mu) \leq \mathcal{I} \text{ and } \mathbf{f}(\mu^{\star}) = \mathcal{I}.$		
Ingredien $(Y_i, .$	ts of our model-X infere $X_i, Z_i)_{i=1}^n$.	ntial procedure :		

3 Assume $P_{X|Z}$ known (also have robustness analysis and assumption relaxation).

$$f(\mu) = \frac{\mathbb{E}\left[Y(\mu(X, Z) - \mathbb{E}\left[\mu(X, Z) \mid Z\right]\right)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}\left(\mu(X, Z) \mid Z\right)\right]}} = \frac{\text{a linear functional of } P_{(Y, X, Z)}}{\sqrt{\text{a linear functional of } P_Z}}$$

By Delta method, we can construct CLT-based LCB for $f(\mu) : L_n^{\alpha}(\mu)$ (with confidence level α).

OCOCO	Main Methodology	Genomic Application	O	References
Floodgate	LCB			
Our choic	se of functional : $f(\mu) :=$	$\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{*}(X,Z),\mu(X,Z)\mid Z)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}(\mu(X,Z)\mid Z)\right]}}$		
Lemma (2	Zhang and Janson (2020)))		
For any μ	such that $f(\mu)$ exists, f	$(\mu) \leq \mathcal{I} \text{ and } \mathbf{f}(\mu^{\star}) = \mathcal{I}.$		
Ingredien $(Y_i, .$	ts of our model-X infere $X_i, Z_i)_{i=1}^n$.	ntial procedure :		

3 Assume $P_{X|Z}$ known (also have robustness analysis and assumption relaxation).

$$f(\mu) = \frac{\mathbb{E}\left[Y(\mu(X, Z) - \mathbb{E}\left[\mu(X, Z) \mid Z\right]\right)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}\left(\mu(X, Z) \mid Z\right)\right]}} = \frac{\text{a linear functional of } P_{(Y, X, Z)}}{\sqrt{\text{a linear functional of } P_Z}}$$

- By Delta method, we can construct CLT-based LCB for $f(\mu) : L_n^{\alpha}(\mu)$ (with confidence level α).
- under certain fitted models, compute $\mathbb{E}\left[\mu(X,Z) \mid Z\right]$, $\operatorname{Var}\left(\mu(X,Z) \mid Z\right)$ analytically.

OCOCO	Main Methodology	Genomic Application	O	References
Floodgate	LCB			
Our choic	the of functional : $f(\mu) :=$	$\frac{\mathbb{E}\left[\operatorname{Cov}(\mu^{\star}(X,Z),\mu(X,Z)\mid Z)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}(\mu(X,Z)\mid Z)\right]}}$		
Lemma (Zhang and Janson (2020	0))		
For any μ	μ such that f(μ) exists, f	$(\mu) \leq \mathcal{I}$ and $f(\mu^{\star}) = \mathcal{I}$.		
Ingredien $(Y_i,$	ts of our model-X infere $X_i, Z_i)_{i=1}^n$.	ntial procedure :		

3 Assume $P_{X|Z}$ known (also have robustness analysis and assumption relaxation).

$$f(\mu) = \frac{\mathbb{E}\left[Y(\mu(X, Z) - \mathbb{E}\left[\mu(X, Z) \mid Z\right]\right)\right]}{\sqrt{\mathbb{E}\left[\operatorname{Var}\left(\mu(X, Z) \mid Z\right)\right]}} = \frac{\text{a linear functional of } P_{(Y, X, Z)}}{\sqrt{\text{a linear functional of } P_Z}}$$

- By Delta method, we can construct CLT-based LCB for $f(\mu) : L_n^{\alpha}(\mu)$ (with confidence level α).
- under certain fitted models, compute $\mathbb{E}[\mu(X,Z) | Z]$, $Var(\mu(X,Z) | Z)$ analytically.
- Generally, draw $\tilde{X}^{(k)}$, $k = 1, \dots, K$ from $P_{X|Z}$, conditionally independently of X, Y then plug-in the Monte Carlo estimators.

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Asymptoti	c validity			

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and $\mu(X, Z)$, we have

 $\mathbb{P}\left(L_n^{\alpha}(\mu) \leq \mathcal{I}\right) \geq 1 - \alpha - O(n^{-1/2}).$

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Asymptoti	c validity			

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and $\mu(X, Z)$, we have

$$\mathbb{P}\left(L_n^{\alpha}(\mu) \leq \mathcal{I}\right) \geq 1 - \alpha - O(n^{-1/2}).$$

Point-wise result : the convergence rate result builds on recent Berry-Esseen type bounds for Delta method (Pinelis et al., 2016).

Introduction	Main Methodology	Genomic Application O	Summary O	Références
Asymptoti	ic validity			

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and $\mu(X, Z)$, we have

$$\mathbb{P}\left(L_n^{\alpha}(\mu) \leq \mathcal{I}\right) \geq 1 - \alpha - O(n^{-1/2}).$$

- Point-wise result : the convergence rate result builds on recent Berry-Esseen type bounds for Delta method (Pinelis et al., 2016).
- Constant in $O(n^{-1/2})$ has complicated dependence on μ and $P_{(Y,X,Z)}$.

Introduction	Main Methodology	Genomic Application	Summary	Références
	000000			

Asymptotic validity

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and $\mu(X, Z)$, we have

$$\mathbb{P}\left(L_n^{\alpha}(\mu) \leq \mathcal{I}\right) \geq 1 - \alpha - O(n^{-1/2}).$$

- Point-wise result : the convergence rate result builds on recent Berry-Esseen type bounds for Delta method (Pinelis et al., 2016).
- Constant in $O(n^{-1/2})$ has complicated dependence on μ and $P_{(Y,X,Z)}$.
- Invariance of the floodgate procedure : e.g. $\mu(x, z) = ax + g(z)$, constant only depends on sign(a) and bivariate distribution of

$$\left(Y, \frac{X - \mathbb{E}[X \mid Z]}{\sqrt{\operatorname{Var}(X - \mathbb{E}[X \mid Z])}}\right)$$

Introduction	Main Methodology	Genomic Application	Summary	Références
	000000			

Asymptotic validity

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and $\mu(X, Z)$, we have

$$\mathbb{P}\left(L_n^{\alpha}(\mu) \leq \mathcal{I}\right) \geq 1 - \alpha - O(n^{-1/2}).$$

- Point-wise result : the convergence rate result builds on recent Berry-Esseen type bounds for Delta method (Pinelis et al., 2016).
- Constant in $O(n^{-1/2})$ has complicated dependence on μ and $P_{(Y,X,Z)}$.
- Invariance of the floodgate procedure : e.g. $\mu(x, z) = ax + g(z)$, constant only depends on sign(a) and bivariate distribution of

$$\left(Y, \frac{X - \mathbb{E}[X \mid Z]}{\sqrt{\operatorname{Var}(X - \mathbb{E}[X \mid Z])}}\right)$$

Suggests floodgate may be robust to μ and high-dimensionality.

Introduction	Main Methodology	Genomic Application	Summary	Références
	000000			

Statistical accuracy

^{1.} through the best element of its equivalent class \mathcal{S}_{μ} in terms of MSE

Introduction	Main Methodology 0000●0	Genomic Application O	Summary O	Références
Statistical acc	uracy			

$$\mathcal{S}_{\mu} = \{ oldsymbol{c} \mu(x,z) + oldsymbol{g}(z) : oldsymbol{c} > 0, oldsymbol{g} : \mathbb{R}^{oldsymbol{
ho}} oldsymbol{
ightarrow} \mathbb{R} \}.$$

^{1.} through the best element of its equivalent class \mathcal{S}_{μ} in terms of MSE

Introduction	Main Methodology ○○○○●○	Genomic Application	Summary O	Références
Statistical accuracy				

$$S_{\mu} = \{ c\mu(x,z) + g(z) : c > 0, g : \mathbb{R}^{p} \rightarrow \mathbb{R} \}.$$

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and noises, for μ_n with well-behaved moments,

$$\mathcal{I} - L_n^{\alpha}(\mu_n) = O_p\left(\inf_{\mu \in S_{\mu_n}} \mathbb{E}\left[(\mu(X, Z) - \mu^*(X, Z))^2\right] + n^{-1/2}\right).$$

^{1.} through the best element of its equivalent class \mathcal{S}_{μ} in terms of MSE

Introduction	Main Methodology ○○○○●○	Genomic Application	Summary O	Références
Statistical accuracy				

$$\mathcal{S}_{\mu} = \{ \mathcal{C}\mu(x,z) + g(z) : c > 0, g : \mathbb{R}^{p} \to \mathbb{R} \}.$$

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and noises, for μ_n with well-behaved moments,

$$\mathcal{I} - L_n^{\alpha}(\mu_n) = O_p\left(\inf_{\mu \in S_{\mu_n}} \mathbb{E}\left[(\mu(X, Z) - \mu^*(X, Z))^2\right] + n^{-1/2}\right).$$

Inferential accuracy is directly related to the MSE of μ_n ¹

^{1.} through the best element of its equivalent class \mathcal{S}_{μ} in terms of MSE

Introduction	Main Methodology ○○○○●○	Genomic Application O	Summary O	Références
Statistical a	ccuracy			

$$S_{\mu} = \{ c\mu(x,z) + g(z) : c > 0, g : \mathbb{R}^{p} \rightarrow \mathbb{R} \}.$$

Theorem (Zhang and Janson (2020))

Under mild moment conditions on Y and noises, for μ_n with well-behaved moments,

$$\mathcal{I} - L_n^{\alpha}(\mu_n) = O_p\left(\inf_{\mu \in S_{\mu_n}} \mathbb{E}\left[(\mu(X, Z) - \mu^*(X, Z))^2\right] + n^{-1/2}\right).$$

Inferential accuracy is directly related to the MSE of μ_n ¹

Good predictive performance \implies Good inferential accuracy

^{1.} through the best element of its equivalent class S_{μ} in terms of MSE

Introduction	Main Methodology	Genomic Application	Summary	Références
	000000			

Robustness

Suppose $P_{X|Z}$ unknown, we instead use its estimate $Q_{X|Z}^{(n)}$ to run floodgate.

Theorem (Zhang and Janson (2020))

Under moment conditions on Y and noises, for μ_n with well-behaved moments under both the true distribution and the specified one, we have

$$\mathbb{P}\left(L_n^{\alpha}(\mu_n) \leq \mathcal{I} + \Delta_n\right) \geq 1 - \alpha - O(n^{-1/2}),\tag{1}$$

where

$$\Delta_n \leq c_1 \sqrt{\mathbb{E}\left[\chi^2\left(P_{X|Z} \mid \mid Q_{X|Z}^{(n)}\right)\right]} - c_2 \mathbb{E}\left[\left(\bar{\mu}_n(X,Z) - \mu^*(X,Z)\right)^2\right]$$
(2)

where $\bar{\mu}_n$ is a particular representative of S_{μ_n} and $\chi^2(\cdot || \cdot)$ denotes the χ^2 divergence.

^{2.} When $\mathcal{I} > 0$

Introduction	Main Methodology	Genomic Application	Summary	Références
	000000			

Robustness

Suppose $P_{X|Z}$ unknown, we instead use its estimate $Q_{X|Z}^{(n)}$ to run floodgate.

Theorem (Zhang and Janson (2020))

Under moment conditions on Y and noises, for μ_n with well-behaved moments under both the true distribution and the specified one, we have

$$\mathbb{P}\left(L_n^{\alpha}(\mu_n) \leq \mathcal{I} + \Delta_n\right) \geq 1 - \alpha - O(n^{-1/2}),\tag{1}$$

where

$$\Delta_n \leq c_1 \sqrt{\mathbb{E}\left[\chi^2\left(P_{X|Z} \mid \mid Q_{X|Z}^{(n)}\right)\right]} - c_2 \mathbb{E}\left[\left(\bar{\mu}_n(X,Z) - \mu^*(X,Z)\right)^2\right]$$
(2)

where $\bar{\mu}_n$ is a particular representative of S_{μ_n} and $\chi^2(\cdot || \cdot)$ denotes the χ^2 divergence.

$P_{X|Z}$ is better estimated than $\mathbb{E}[Y|X,Z] \Longrightarrow$ ² Floodgate is robust

2. When $\mathcal{I} > 0$

Introduction	Main Methodology	Genomic Application	Summary	Références
00000	000000	•	0	

Application to genomic study of platelet count



FIGURE – Colored Chicago plot* with the color of each point representing the floodgate LCB for the importance of a group of SNPs on Chromosome 12 in the UK Biobank data at different resolutions (y-axis). Bottom plot shows a zoomed-in region of strong importance.

* Sesia, M., Katsevich, E., Bates, S., Candès, E., & Sabatti, C. (2020). Multi-resolution localization of causal variants across the genome. Nature communications, 11(1), 1-10.

Introduction	Main Methodology	Genomic Application O	Summary •	Références
Takeaways				

Floodgate : a new inferential approach for variable importance.

- Focus on an interpretable, sensitive and nonparametric measure of variable importance : the mMSE gap.
- Provide valid and robust lower confidence bounds for the mMSE gap.
- Allow flexible regression algorithms, good predictive performance leads to good inferential accuracy.

See more extensions in our paper :

- **I** Co-sufficient floodgate relaxes the assumptions to only knowing a model for $P_{X|Z}$
- 2 Floodgate for a different measure of variable importance.
- Inference on group variable importance.
- **I** Transporting floodgate inference to a different covariate distribution.
- 5 Adjusting for multiplicity and selection effects.

Zhang, Lu, and Lucas Janson. "Floodgate : inference for model-free variable importance." arXiv preprint arXiv:2007.01283 (2020).

ntroduction	Main Methodology	Genomic Application	Références
00000			

Azadkia, M. and Chatterjee, S. (2019). A simple measure of conditional dependence. arXiv preprint arXiv :1910.12327.

Berk, R., Brown, L., Buja, A., Zhang, K., Zhao, L., et al. (2013). Valid post-selection inference. <u>The Annals of Statistics</u>, 41(2) :802–837.

Bühlmann, P. et al. (2013). Statistical significance in high-dimensional linear models. Bernoulli, 19(4) :1212–1242.

Bühlmann, P., van de Geer, S., et al. (2015). High-dimensional inference in misspecified linear models. <u>Electronic Journal of Statistics</u>, 9(1):1449–1473.

Buja, A., Berk, R. A., Brown, L. D., George, E. I., Pitkin, E., Traskin, M., Zhao, L., and Zhang, K. (2015). Models as approximations-a conspiracy of random regressors and model deviations against classical inference in regression. <u>Statistical Science</u>, page 1.

Buja, A. and Brown, L. (2014). Discussion :" a significance test for the lasso". <u>The</u> Annals of Statistics, 42(2) :509–517.

Buja, A., Brown, L., Berk, R., George, E., Pitkin, E., Traskin, M., Zhang, K., Zhao, L., et al. (2019a). Models as approximations i : Consequences illustrated with linear regression. Statistical Science, 34(4) :523–544.

Buja, A., Brown, L., Kuchibhotla, A. K., Berk, R., George, E., Zhao, L., et al. (2019b). Models as approximations ii : A model-free theory of parametric regression. Statistical Science, 34(4) :545–565.

Dezeure, R., Bühlmann, P., and Zhang, C.-H. (2017). High-dimensional simultaneous inference with the bootstrap. <u>Test</u>, 26(4) :685–719.

Introduction	Main Methodology	Genomic Application		Références
00000	000000	0	0	

- Fisher, A., Rudin, C., and Dominici, F. (2018). Model class reliance : Variable importance measures for any machine learning model class, from the "rashomon" perspective. arXiv preprint arXiv :1801.01489, 68.
- Javanmard, A. and Montanari, A. (2014). Confidence intervals and hypothesis testing for high-dimensional regression. <u>The Journal of Machine Learning Research</u>, 15(1):2869–2909.
- Lee, J. D., Sun, D. L., Sun, Y., Taylor, J. E., et al. (2016). Exact post-selection inference, with application to the lasso. <u>The Annals of Statistics</u>, 44(3) :907–927.
- Lei, J., G'Sell, M., Rinaldo, A., Tibshirani, R. J., and Wasserman, L. (2018). Distribution-free predictive inference for regression. <u>Journal of the American</u> Statistical Association, 113(523) :1094–1111.
- Li, L., Tchetgen, E. T., van der Vaart, A., and Robins, J. M. (2011). Higher order inference on a treatment effect under low regularity conditions. <u>Statistics & probability letters</u>, 81(7) :821–828.
- Newey, W. K. and Robins, J. R. (2018). Cross-fitting and fast remainder rates for semiparametric estimation. arXiv preprint arXiv :1801.09138.
- Nickl, R., Van De Geer, S., et al. (2013). Confidence sets in sparse regression. <u>The</u> Annals of Statistics, 41(6) :2852–2876.
- Pinelis, I., Molzon, R., et al. (2016). Optimal-order bounds on the rate of convergence to normality in the multivariate delta method. <u>Electronic Journal of Statistics</u>, 10(1):1001–1063.
- Rinaldo, A., Wasserman, L., G'Sell, M., et al. (2019). Bootstrapping and sample splitting for high-dimensional, assumption-lean inference. <u>The Annals of Statistics</u>, 47(6):3438–3469.

Introduction	Main Methodology	Genomic Application		Références
00000	000000	0	0	

- Robins, J., Li, L., Tchetgen, E., van der Vaart, A., et al. (2008). Higher order influence functions and minimax estimation of nonlinear functionals. In <u>Probability and</u> <u>statistics : essays in honor of David A. Freedman</u>, pages 335–421. Institute of Mathematical Statistics.
- Robins, J., Tchetgen, E. T., Li, L., and van der Vaart, A. (2009). Semiparametric minimax rates. <u>Electronic journal of statistics</u>, 3 :1305.
- Robins, J. M., Li, L., Mukherjee, R., Tchetgen, E. T., van der Vaart, A., et al. (2017). Minimax estimation of a functional on a structured high-dimensional model. <u>The</u> <u>Annals of Statistics</u>, 45(5) :1951–1987.
- Shah, R. D. and Peters, J. (2018). The hardness of conditional independence testing and the generalised covariance measure. <u>arXiv preprint arXiv :1804.07203</u>.
- Sur, P. and Candès, E. J. (2019). A modern maximum-likelihood theory for high-dimensional logistic regression. <u>Proceedings of the National Academy of</u> <u>Sciences</u>, 116(29) :14516–14525.
- Taylor, J., Lockhart, R., Tibshirani, R. J., and Tibshirani, R. (2014). Exact post-selection inference for forward stepwise and least angle regression. <u>arXiv preprint</u> arXiv :1401.3889, 7 :10–1.
- Van de Geer, S., Bühlmann, P., Ritov, Y., Dezeure, R., et al. (2014). On asymptotically optimal confidence regions and tests for high-dimensional models. <u>The Annals of Statistics</u>, 42(3) :1166–1202.
- Watson, D. S. and Wright, M. N. (2019). Testing conditional predictive independence in supervised learning algorithms. arXiv preprint arXiv :1901.09917.
| Introduction | Main Methodology | Genomic Application | | Références |
|--------------|------------------|---------------------|---|------------|
| 00000 | 000000 | 0 | 0 | |
| | | | | |

Williamson, B. D., Gilbert, P. B., Simon, N., and Carone, M. (2017). Nonparametric variable importance assessment using machine learning techniques. <u>UW</u> Biostatistics Working Paper Series. Working Paper 422.

Zhang, C.-H. and Zhang, S. S. (2014). Confidence intervals for low dimensional parameters in high dimensional linear models. Journal of the Royal Statistical Society : Series B (Statistical Methodology), 76(1) :217–242.

Zhang, L. and Janson, L. (2020). Floodgate : Inference for model-free variable importance. <u>arXiv preprint arXiv :2007.01283</u>.

Zhang, X. and Cheng, G. (2017). Simultaneous inference for high-dimensional linear models. Journal of the American Statistical Association, 112(518) :757–768.

Zhao, Q., Sur, P., and Candes, E. J. (2020). The asymptotic distribution of the mle in high-dimensional logistic models : Arbitrary covariance. <u>arXiv preprint</u> <u>arXiv :2001.09351</u>.