Multi-task group Lasso for Genome Wide Association Studies in admixed populations

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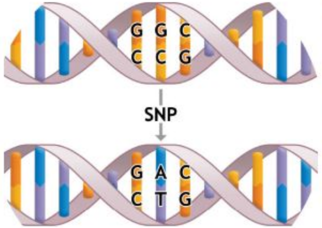
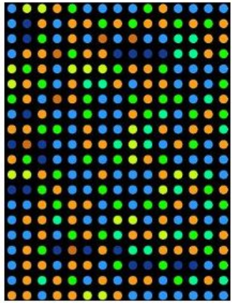
Genome Wide Association Studies





Goal: Find association between the genotype and the phenotype.

- The genotype: Single Nucleotide Polymorphism (SNP) arrays.
- The phenotype:
  - Quantitative: BMI, weight, height, etc.
  - Qualitative: Case-control study

Challenges in GWAS analysis

- **Microarray data: SNP arrays**

Curse of dimensionality (p>>N): $p \approx 10^5 - 10^7\ ,\ N \approx 10^2 - 10^4$

01

Single marker analysis

Testing each SNP individually

02

Population stratification

Difference in allele frequencies between subpopulations

03

Linkage disequilibrium

Dependence relationship between two alleles at two different loci

04

Computational limitations

For complex methods:

- Memory errors
- Very slow

05

Lack of stability

Susceptibility to small perturbations in the data set

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From GWAS to Machine Learning

- **Single-marker analysis:**

Given a phenotype y, $\mathbf{X}$ is the genotype matrix:

For each feature $\mathbf{X}_j$, we fit a **single-predictor** equation $\mathbf{y} = \beta_0 + \beta_j \mathbf{X}_j + \varepsilon \Rightarrow$ **p-value from a t-test** against an intercept-only model $H_0 = \{\beta_j = 0\}$.

- **Multi-variate approach:** Feature selection based on regularization

- Regularization: adding a penalty term

$$\underset{\beta \in \mathbb{R}^p}{\operatorname{argmin}} \underbrace{\mathscr{L}\left(y, \beta X_j\right)}_{\text{loss}} + \underbrace{\lambda \Omega\left(\beta_1, \beta_2, \ldots, \beta_j\right)}_{\text{regularization term}}$$

- Lasso: shrinkage and feature selection (L1-regularization)

$$\underset{\beta \in \mathbb{R}^p}{\operatorname{argmin}} \underbrace{\mathscr{L}\left(y, \beta X_j\right)}_{\text{loss}} + \lambda \underbrace{\sum_{j=1}^{p} \left|\beta_j\right|}_{\text{sparsity}}$$

- Group lasso: allow predefined groups of covariates to be jointly selected

$$\underset{\beta \in \mathbb{R}^p}{\operatorname{argmin}} \underbrace{\mathscr{L}\left(y, \beta X_j\right)}_{\text{loss}} + \lambda \underbrace{\sum_{g \in \mathscr{G}} \sqrt{p_g} \left\|\beta_g\right\|_2}_{\text{sparsity at the group level}}$$

where β is a $p \times 1$ vector corresponds to the SNP effects

Ω is the regularizer

λ is the penalization term

where $\mathscr{G}$ is the set of groups

β_g is β restricted to the SNPs in g

$\sqrt{p_g}$ scales the penalization factor according to the group size

From GWAS to Machine Learning

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$$\underset{\beta\in\mathbb{R}^p}{\operatorname{argmin}}\,\underbrace{\mathcal{L}\left(y,\beta X_j\right)}_{\text{loss}}+\underbrace{\lambda\sum_{g\in\mathcal{G}}\sqrt{p_g}\left\|\beta_g\right\|_2}_{\text{sparsity at the group level}}$$

- **Multi-task lasso:** allows fitting multiple regression problems jointly

$$\underset{\beta\in\mathbb{R}^{T\times p}}{\operatorname{argmin}}\,\underbrace{\sum_{t=1}^{T}\frac{1}{n_t}\sum_{m=1}^{n_t}\mathcal{L}\left(y^{(tm)},\left(\beta_0^{(t)}+\sum_{j=1}^{p}\beta_j^{(t)}X_j^{(tm)}\right)\right)}_{\text{loss}}+\lambda\underbrace{\sum_{j=0}^{p}\sum_{t=1}^{T}\left|\beta_j^{(t)}\right|}_{\text{task sharing}}$$

where β is a $p\times 1$ vector corresponds to the SNP effects

Ω is the regularizer

λ is the penalization term

where $\mathcal{G}$ is the set of groups

β_g is β restricted to the SNPs in g

$\sqrt{p_g}$ scales the penalization factor according to the group size

where T is the number of tasks to learn the training set

$\left\{\left(x_{tm},y_{tm}\right)\text{ for }t=1..T\text{ and }m=1..n_t\right\}$

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Population stratification

Population stratification refers to the presence of differences in allele frequencies between subpopulations due to different ancestry.

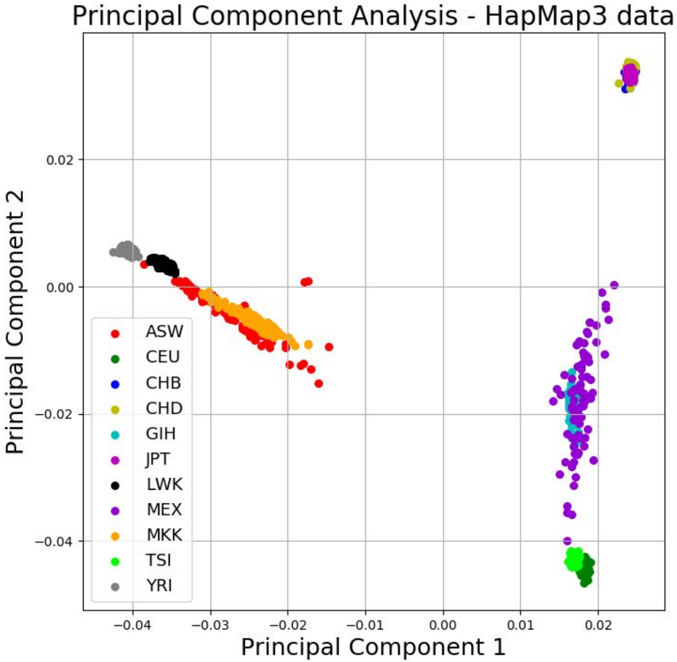
- **State-of-the art adjustment methods**
  - PCA-based methods

    Include Principal components (PCs) as covariates

    - Logistic Regression + Top PCs[1,2]
    - EIGENSTRAT[3]: multi-linear regression + 10 PCs

  - Linear mixed models

    Fast-LMM[4]



[1] Need et al.,A genome-wide investigation of snps and cnvs in schizophrenia. 2009, *PLoS Genet*.

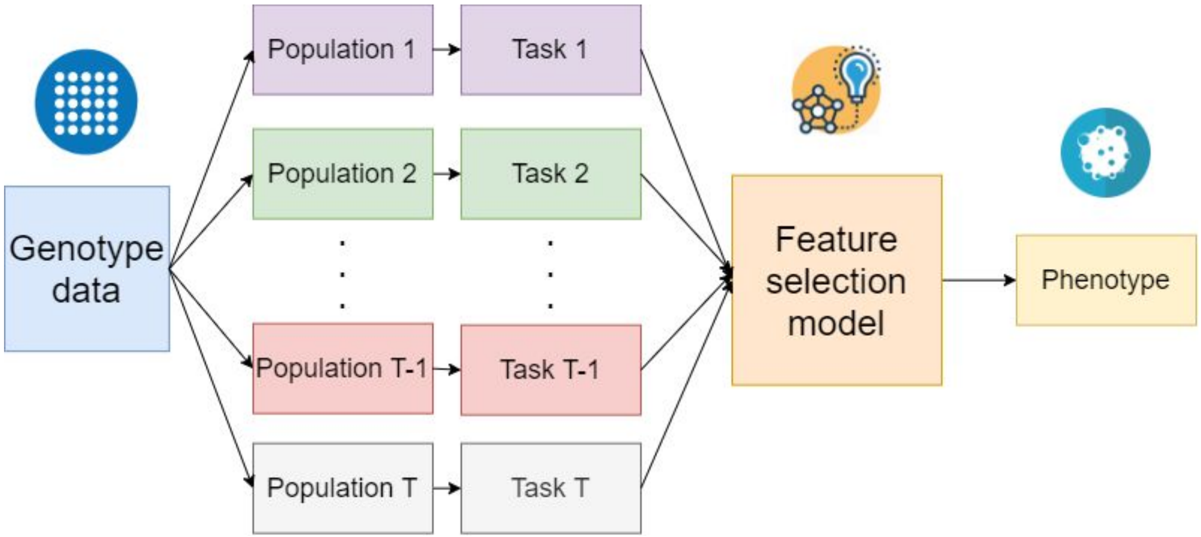
[2] Zeggini et al., Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. 2008, *Nat Genet*.

[3] Price et al.,Principal components analysis corrects for stratification in genome-wide association studies. *Nat Genet.*

[4] Lippert et al., FaST linear mixed models for genome-wide association studies. 2011. *Nat Methods.*

Population stratification

- **Proposed adjustment method**: subpopulations assignment in multitask framework



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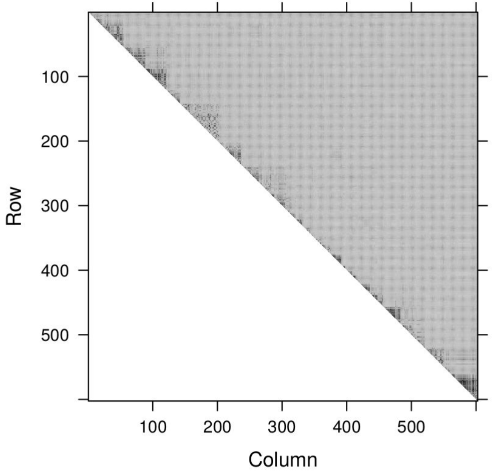
Linkage Disequilibrium groups clustering

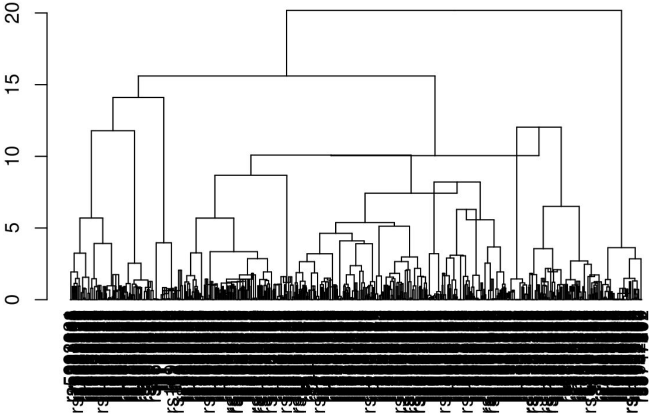
Linkage Disequilibrium (LD):

- Tendency of alleles to be transmitted together, more often that expected by chance alone.
- Usually caused by close proximity of genes in the same chromosome.

Hierarchical clustering approach[1]

Performing a **spatially-constrained hierarchical clustering**





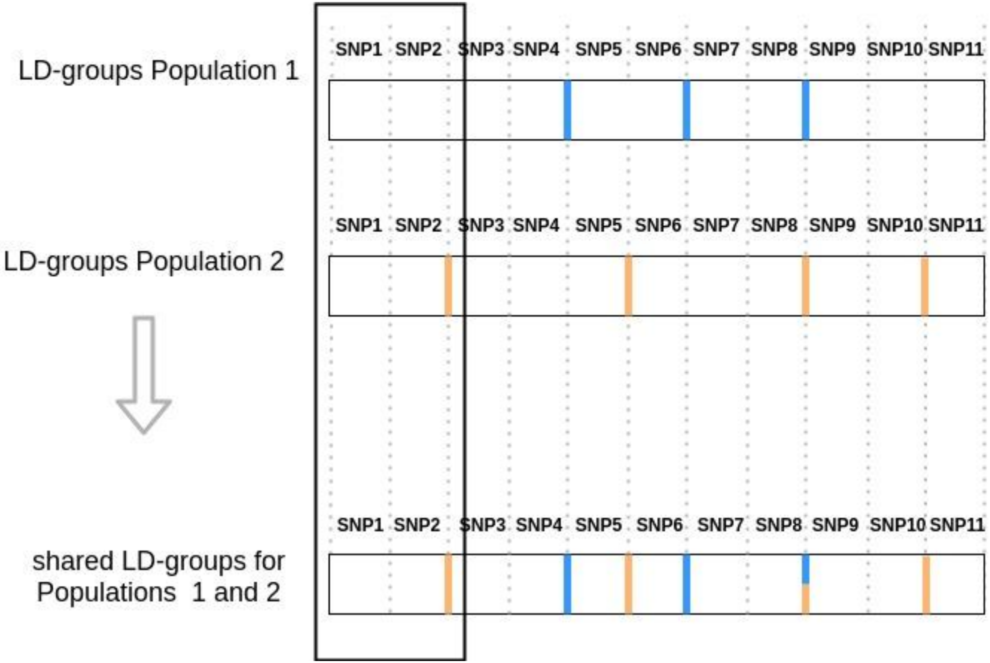
⇒ Selection on the **LD-group level** instead of single-SNP level.

[1] Ambroise et al.., Adjacency-constrained hierarchical clustering of a band similarity matrix with application to genomics. 2019. arXiv:1902.01596v1 [math.ST].

Linkage Disequilibrium groups clustering

- **Choice of LD-groups**

Linkage disequilibrium is different in different populations


LD-groups Population 1
SNP1 SNP2 SNP3 SNP4 SNP5 SNP6 SNP7 SNP8 SNP9 SNP10 SNP11
LD-groups Population 2
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shared LD-groups for Populations 1 and 2
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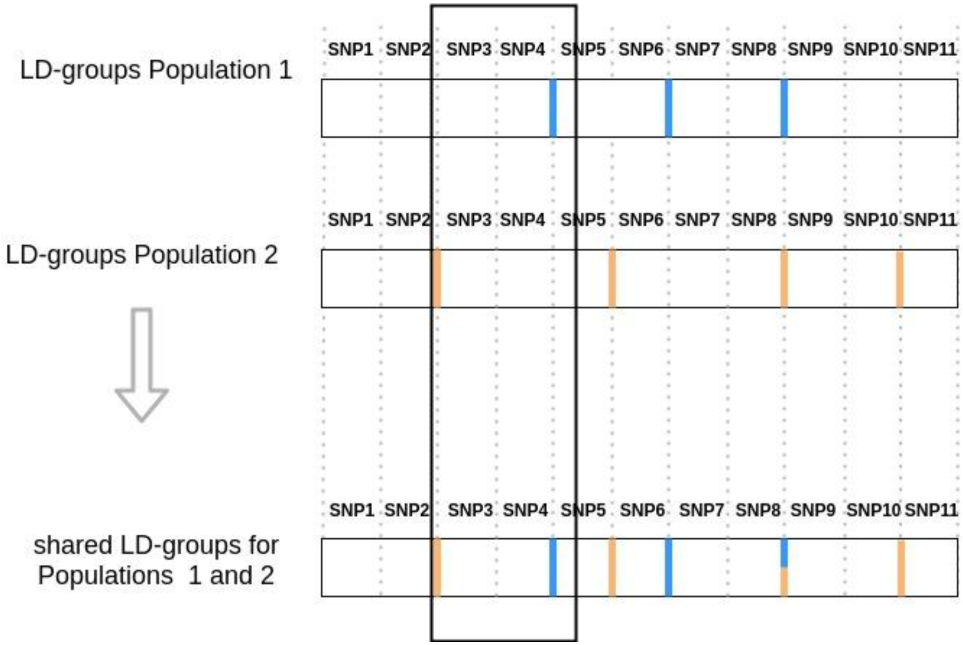
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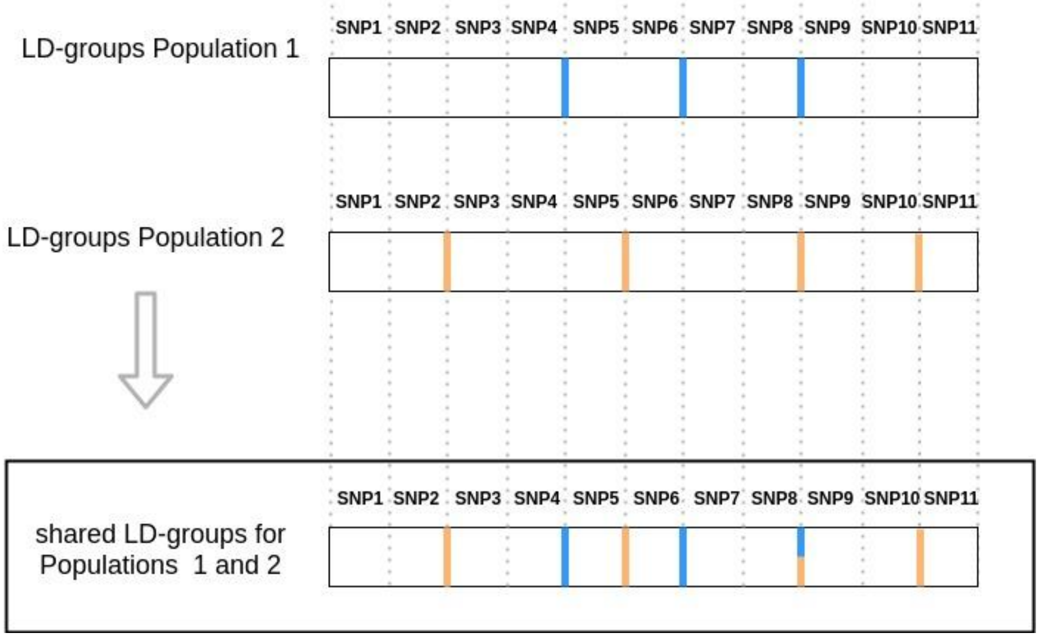
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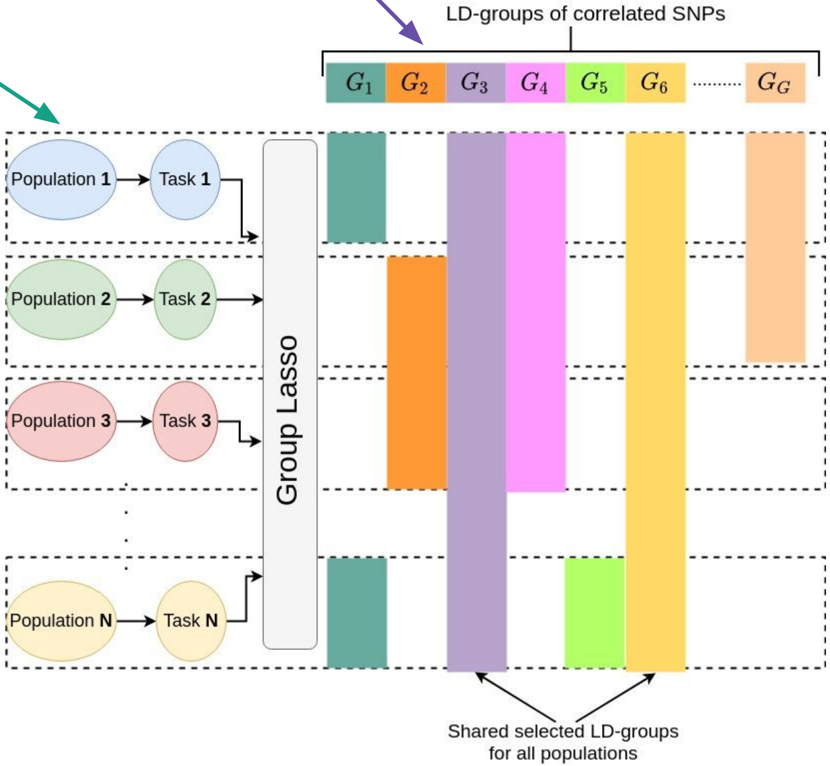
Multitask group Lasso for Genome Wide Association studies in admixed populations

Multitask group Lasso where **tasks** correspond to **subpopulations** and **groups** correspond to **LD-groups** of strongly correlated SNPs

$$\min_{\beta\in\mathbb{R}^{T\times(p+1)}} \underbrace{\sum_{t=1}^{T} \frac{1}{n_t}\sum_{m=1}^{n_t} \mathscr{L}\left(y^{(tm)}, \left(\beta_0^{(t)} + \sum_{j=1}^{p} \beta_j^{(t)} x_j^{(tm)}\right)\right)}_{\textbf{loss for each task}} + \lambda \underbrace{\boxed{\sum_{g=1}^{G}}\boxed{\sum_{t=1}^{T}}\sqrt{p_g}\left\|\beta_g^{(t)}\right\|_2}_{\textbf{sparsity at the LD-group level across tasks}}$$

where

- $\beta^{(t)} \in \mathbb{R}^{p+1}$ is a task-specific vector of regression coefficients
- $\mathscr{L}$ is the loss function (quadratic or logistic regression)
- B_g is a $T \times p_g$ matrix of the regression coefficients, across all tasks T, for the SNPs of LD-group g
- λ is the penalization parameter
- $\sqrt{p_g}$ scales the penalization factor according the group size



⇒ Selection of LD-groups associated with **the phenotype** **across all tasks/populations**, or **specifically for some tasks/populations**

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Gap Safe screening rules

Gap Safe Screening rules[1]: eliminates features with associated coefficients are proved to be zero at the optimum in order to obtain **more speed up** and to **avoid memory errors**.

Ignoring some variables by exploiting geometric properties of the dual formulation of the following optimization problem:

$$\widehat{\beta}^{(\lambda)} \in \underset{\beta \in \mathbb{R}^p}{\operatorname{argmin}} P_\lambda(\beta), \text{ for } P_\lambda(\beta) := F(\beta) + \lambda\Omega(\beta) := \sum_{i=1}^{n} f_i\left(x_i^\top \beta\right) + \lambda\Omega(\beta)$$

where $f_i : \mathbb{R} \mapsto \mathbb{R}$ *are convex and differentiable functions and* $\Omega : \mathbb{R}^p \mapsto \mathbb{R}_+$ *is a group-decomposable norm:* $\Omega(\beta) = \sum_{g \in \mathcal{G}} \Omega_g(\beta_g)$
with Ω_g *a norm of* $\mathbb{R}^{n_g}$

For group Lasso: the data fitting term is $F(\beta) = \frac{\mathcal{L}\left(y, \beta X_j\right)}{2}$,

The *L1/L2-norm* is defined by $\Omega(\beta) = \Omega_w(\beta)$:

$$\Omega_w(\beta) := \sum_{g \in \mathcal{G}} w_g \|\beta_g\|_2 \quad \text{and} \quad \Omega_w^D(\xi) := \max_{g \in \mathcal{G}} \frac{\|\xi_g\|_2}{w_g}$$

where $w = (w_g)_{g \in \mathcal{G}}$ *are weights satisfying* $w_g > 0$ *for all* $g \in \mathcal{G}$ *and* $\Omega_w^D(\xi)$ *is the dual norm along the regularization path.*

[1] Ndiaye et al.,Gap Safe Screening Rules for Sparsity Enforcing Penalties. 2017, *Journal of Machine Learning Research 18*.

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Stability Selection

Stability selection[1]**:** **bootstrap aggregation** procedure where feature selection is performed repeatedly on bootstrap subsamples, and the results of all repetitions are aggregated. It allows a **precise statement** of the significance of the selected features set and **reduce false positives**.

Procedure:

- Identify $S = \left\{k : \beta_k \neq 0\right\}$ a set of non-zero inputs of a sparse parameter vector β of observed data (X, y)
- Feature selection is performed on randomly $|\mathrm{I}| = \frac{n}{2}$ of observations, where $\mathrm{I} \subset \{1, \ldots, n\}$
- Selection Path: Probability of the selection of a feature $k \in \{1, \ldots, p\}$

$$\pi_k^\lambda = Pr^*\left[k \in \widehat{S}^\lambda(I)\right],$$ where $\widehat{S}^\lambda(\mathrm{I}) \subset \{1, \ldots, p\}$ denotes the selected features by a subsample I

⇒ Captures random selection within feature selection algorithms

- For a chosen cut-off $\frac{1}{2} \leq \pi_{thre} \leq 1$, the set of stable features is:

$$\widehat{S}^{stable} = \left\{k : \pi_k^\lambda \geq \pi_{thre}\right\}$$

⇒ Only variables that are selected consistently across all the random halves remain.

[1] Meinshausen et al,. Stability selection. 2010. *Journal of the Royal Statistical Society Series B-Statistical Methodology*.

Multitask group Lasso implementation

- Datasets

Realistic simulated data using GWAsimulator[1]

- **Dimension:** 4,000 samples x 1,400,000 SNPs
- **Populations:** 2000 European (CEU), 2000 African (YRI)
- **Phenotype:** 1100 CEU cases, 900 CEU controls, 900 YRI cases, 1100 controls.
- **Disease loci:** chromosomes: **2** (located on 1,000-50,000 SNPs), **12** (located on 10-40,000 SNPs), **19** (1000-50,000 SNPs), **21** (10-10,000 SNPs) and **22** (10-2000 SNPs)

Real data: DRIVE Breast Cancer OncoArray[2]

- **Dimension:** 28,281 samples x 528,620 SNPs
- **Phenotype:** 13,846 cases and 14,435 controls
- **Populations:** USA – Uganda – Nigeria – Cameroon – Australia – Denmark

[1] Li et al., GWAsimulator: a rapid whole-genome simulation program. 2008 *Bioinformatics, Volume 24, Issue 1, 1 January 2008, Pages 140–142.*

[2] DRIVE: "General Research Use" datasets in DRIVE Breast Cancer OncoArray Genotypes, available from dbGaP (study accession: phs001265.v1.p1 GRU), accessed under project #17707.

Multitask group Lasso implementation

- Quality control and preprocessing
  - MAF < 5%
  - HWE-P-Value < 0.0001
  - Remove samples with missing case/control criterion
  - Sex check
  - Remove samples and/or variants with high genotypic missing rate
  - Imputation of missing values: IMPUTE2

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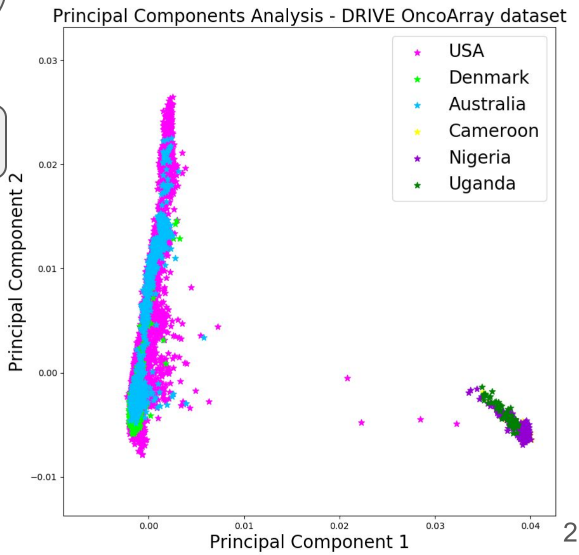
- Subpopulations definition

  Assign subpopulations in Multitask framework according to PCA patterns



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- Evaluation of Multi-task group Lasso
  - **Validation using simulated data**

    Generate simulations with specified multi locus disease model in specified regions

    ⇒ Compute **false positives rate**

  - **Estimation of the stability of the selection** [1,2]

    $$Stability = \widehat{\Phi}(s_1, s_2, \dots s_M) = \frac{1}{M(M-1)} \sum_{i} \sum_{j \neq i} sim(s_i, s_j)$$

  - **Comparison with the state-of-the art methods**

[1] Kuncheva et Al., A stability index for feature selection. 2008, *IASTED International Conference on Artificial Intelligence and Applications*.

[2] Nogueira et Al., On the Stability of Feature Selection Algorithms. 2018, *Journal of Machine Learning Reasearch 18.*

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  - **Comparison with the state-of-the art methods**

1. Lasso **after PCA adjustment** for population stratification at the **SNP level**
2. **Group Lasso after PCA adjustment** for population stratification at **LD-groups level**
3. **Separate group Lasso** for each subpopulation at **LD-groups level**
4. **Separate Lasso** for each subpopulation at **the SNP level**

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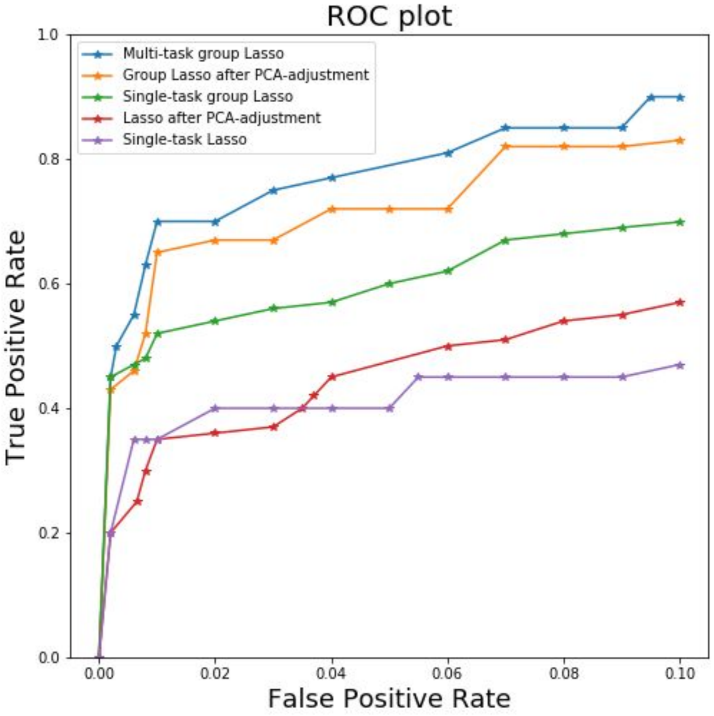
  - **Comparison with the state-of-the art methods**
  - **Computational time**

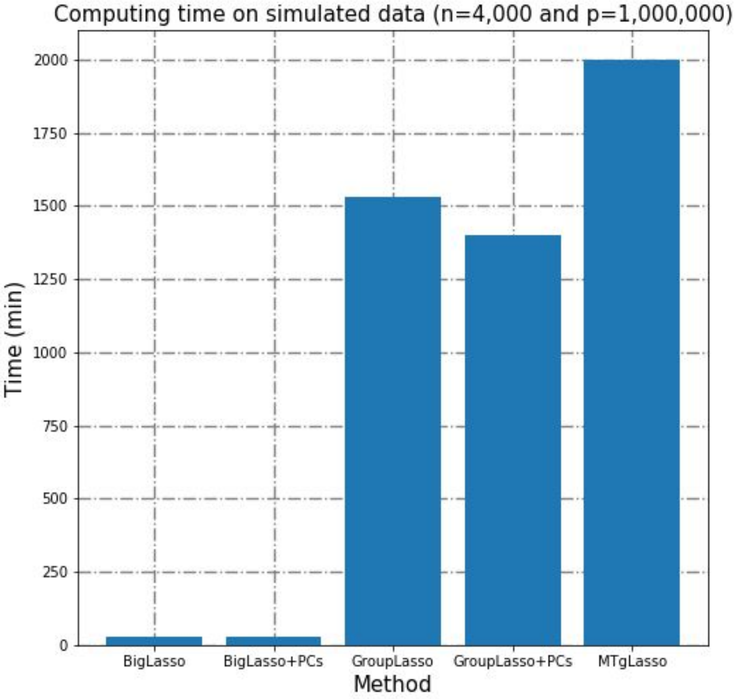
[1] Kuncheva et Al., A stability index for feature selection. 2008, *IASTED International Conference on Artificial Intelligence and Applications*.

[2] Nogueira et Al., On the Stability of Feature Selection Algorithms. 2018, *Journal of Machine Learning Reasearch 18.*

Results of Multitask group Lasso and comparison

Multitask group Lasso outperforms the state-of-the-art methods on simulated data



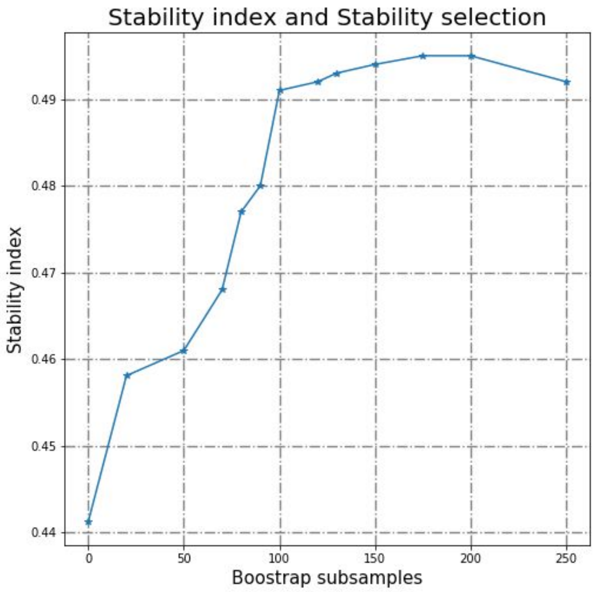


Multitask group Lasso results and comparison

Multitask group Lasso is **more stable** than the state-of-the-art methods.

Simulated data: n=4,000 ; p=1,000,000 ; LD-groups number = 35,792 groups

Methods	Number of selected features/groups	Stability index	Selection level
Multi-task group Lasso (100 boostraps)	5,623	0.4912	LD-groups level
Group Lasso after PCs adjustment	6,054	0.4134	LD-groups level
Single task group Lasso	4,836	0.3398	LD-groups level
Lasso after PCs adjustment	158,856	0.2368	Single-SNP level
Single task Lasso	168,158	0.1742	Single-SNP level



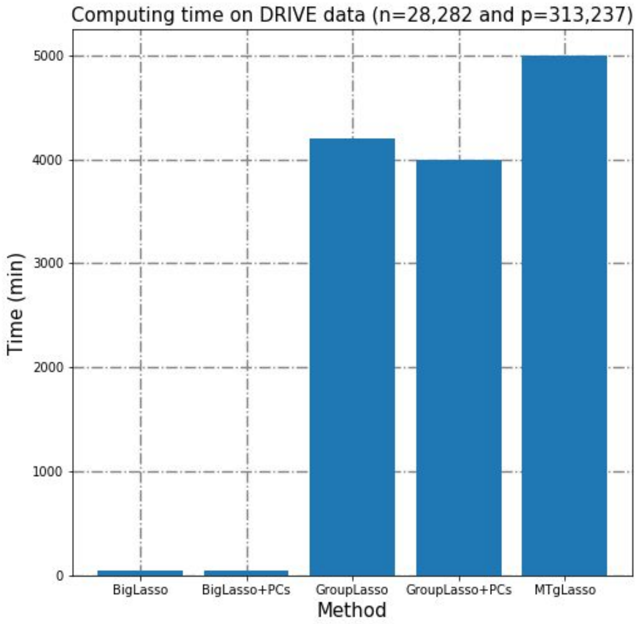
⇒ The feature selection at the LD-groups level alleviate the curse of dimensionality and the lack of stability.

Multitask group Lasso results and comparison

Multitask group Lasso is **more stable** than the state-of-the-art methods.

Real data: DRIVE Breast Cancer OncoArray[1] n=28,282 ; p=313,237 ; LD-groups number = 17,782 groups

Methods	Number of selected features/groups	Stability index	Selection level
Multi-task group Lasso (100 boostraps)	62	0.4312	LD-groups level
Group Lasso after PCs adjustment	59	0.3234	LD-groups level
Single task group Lasso	58	0.2498	LD-groups level
Lasso after PCs adjustment	874	0.2068	Single-SNP level
Single task Lasso	789	0.1581	Single-SNP level



[1] DRIVE: "General Research Use" dataset in DRIVE Breast Cancer OncoArray Genotypes, available from dbGaP (study accession: phs001265/GRU), accessed under project #17707.

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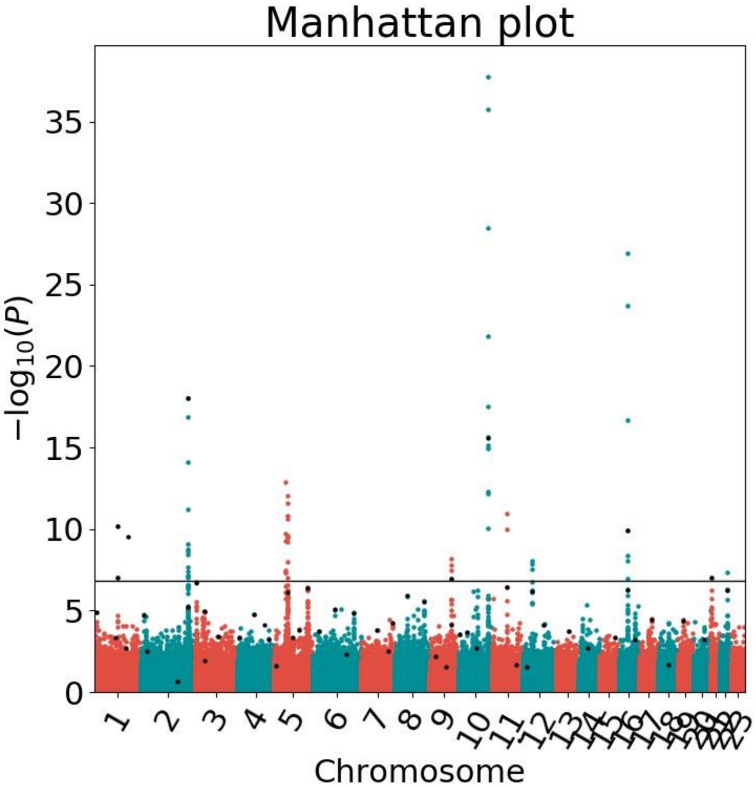

Black dots corresponds to Multitask group Lasso **discoveries** (one SNP per LD-group is represented in the Manhattan plot)

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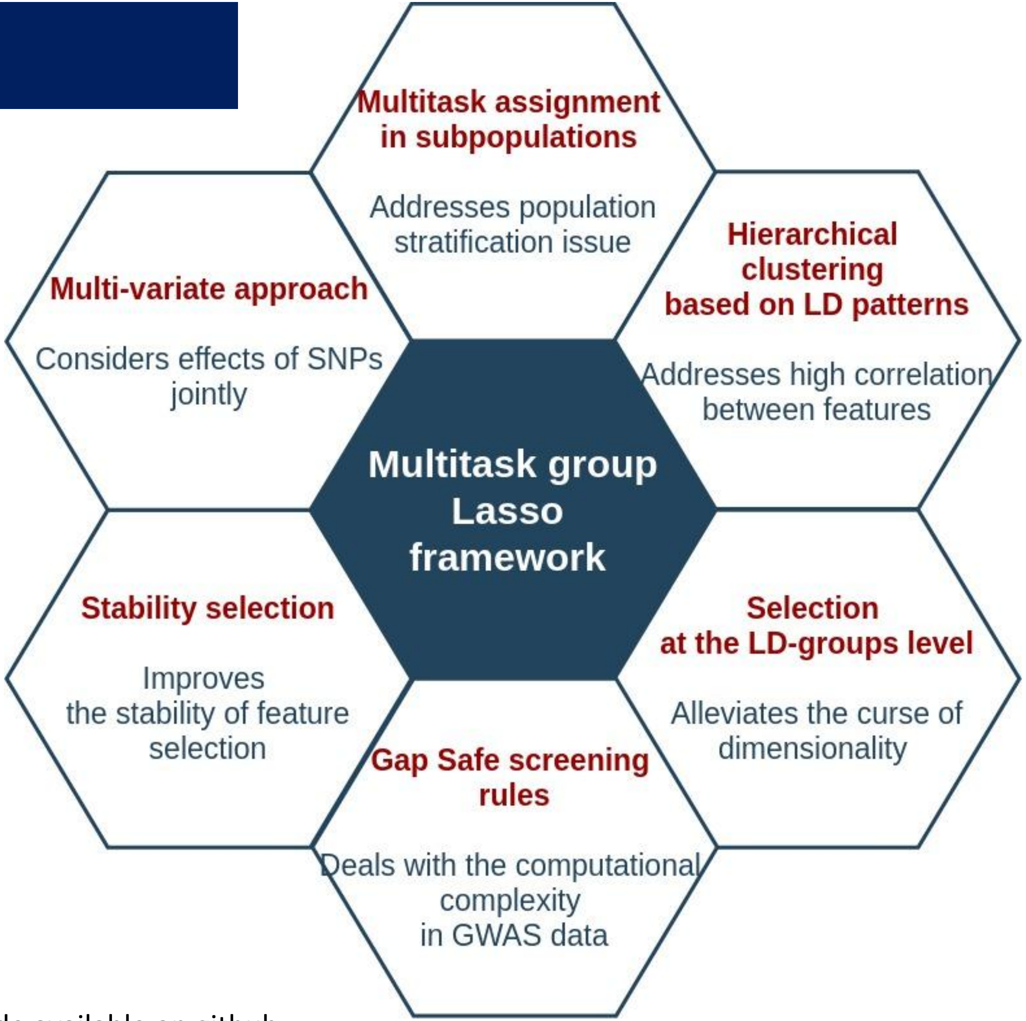
Conclusion



Multitask group Lasso framework

Multitask assignment in subpopulations

Addresses population stratification issue

Hierarchical clustering based on LD patterns

Addresses high correlation between features

Selection at the LD-groups level

Alleviates the curse of dimensionality

Gap Safe screening rules

Deals with the computational complexity in GWAS data

Stability selection

Improves the stability of feature selection

Multi-variate approach

Considers effects of SNPs jointly

Software: Python code will be made available on github.

Acknowledgements

- CBIO (Mines ParisTech)

- GWAS team

- U900 (Institut Curie)

- This work was supported in part by Agence Nationale de la Recherche (ANR-18-CE45-0021-01 and ANR19-P3IA-0001)

CBIO is hiring...

Postdoc openings on GWAS & ML at CBIO! Talk to Chloé

Thank you

Poster session

29th July 15:20 à 16:20