Scaling up the LASSO with interaction features

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DNA sequences



Response to treatment? Disease risk? Drug assimilation rate? Ancestry?

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DNA sequences





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DNA sequences

Single Nucleotide Polyphormisms (SNPs)





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DNA sequences

	<i>s</i> ₁ –	$ s_2$	$ s_3$	$ S_4$	$-s_{5}$	 y
$P_1 \ldots$	1	0	1	0	0	 1
$P_2 \ldots$	0	1	0	0	0	 X
$P_3 \ldots$	1	0	1	0	0	 X
$P_4 \ldots$	0	0	0	0	0	 1
<i>P</i> ₅	0	0	0	0	0	 1
$P_6 \ldots$	1	1	0	1	1	 X
P_7	1	1	1	1	1	 X
<i>P</i> ₈	0	1	0	0	1	 1
	↑	\uparrow	\uparrow	↑	\uparrow	

Single Nucleotide Polyphormisms (SNPs)





Query Orug assimilation rate? Ancestry?

. . .

Motivating example

The LASSO is commonly used to predict y:



The penalty forces only a few features to be selected in the model, for ex:

$$y = w_1^* X_{s_1} + w_4^* X_{s_4} + w_5^* X_{s_5}$$

We would like to also consider second order interaction effects of the form:

$$\boldsymbol{X}_{j} \odot \boldsymbol{X}_{k}, \quad (j,k) \in \llbracket 1, p
rbracket^{2}$$

where \odot is the Hadamard product (=entrywise product).

Typically, we would like to be able to learn a model such as:

$$y = w_1^* X_{s_1} + w_4^* X_{s_4} + w_5^* X_{s_5} + w_{1,2}^* X_{s_1} \odot X_{s_2}$$

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Why is it interesting?



Marine Le Morvan (Mines Paristech)

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Why is it difficult?

The number of interactions terms is equal to:

$$D=\frac{p(p-1)}{2}$$

If p = 100.000, then $D = 5 \times 10^9$. Classical LASSO solvers will be too slow.



This work aims at providing a framework to fit sparse linear models with second order interaction terms when the data is binary.

Problem formulation



• We will indifferently use $X_j \odot X_k$ and $X_j X_k$.

Primal problem

$$\min_{(\boldsymbol{w},b)\in\mathbb{R}^D\times\mathbb{R}}g_{\lambda}(\boldsymbol{w},b) = \frac{1}{n}\|\boldsymbol{y} - \boldsymbol{Z}\boldsymbol{w} - b\|_2^2 + \lambda \|\boldsymbol{w}\|_1$$
(1)

Dual problem

$$\max_{\boldsymbol{\theta}\in\mathbb{R}^n} f_{\lambda}(\boldsymbol{\theta}) = \frac{1}{2} \|\boldsymbol{y}\|_2^2 - \frac{1}{2} \|\boldsymbol{\theta} - \boldsymbol{y}\|_2^2 \text{ s.t. } \begin{cases} |(\boldsymbol{X}_j \boldsymbol{X}_k)^T \boldsymbol{\theta}| \le \lambda & (j,k) \in [\![1,p]\!]^2 \\ \mathbf{1}^T \boldsymbol{\theta} = \mathbf{0} \end{cases}$$
(2)

- Safe Pattern Pruning (SPP) (Nakagawa et al., 2016)
- SPP relies on safe screening rules. Given primal and dual feasible solutions, safe screening rules identify features which are guaranteed not be active at the optimum.
- The idea of SPP is to leverage **the tree structure of interactions features**, and propose a screening rule applicable to entire branches.



WHInter

• Limitations:

- \checkmark SPP does not allow to prune enough branches, especially when *n* increases.
- \checkmark The size of the safe set can be big (for medium values of λ)
- A dual feasible point is expensive to compute.

• We propose WHInter:

- ✓ Working set strategy.
- ✓ New branch pruning strategy for the identification of the active set.
- Efficient computation of branch bounds using a Maximum Inner Product Search (MIPS) framework for binary data.

WHInter achieves a speed ups of up to one order of magnitude compared to SPP.

Input: $\boldsymbol{X} \in [\![0,1]\!]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



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Initialize \mathcal{M}_{λ} .

Input: $\boldsymbol{X} \in [\![0,1]\!]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



Initialize \mathcal{M}_{λ} . Pre-solve and initialize ϕ .

$$\boldsymbol{w}, \boldsymbol{b} \leftarrow \operatorname*{argmin}_{(\boldsymbol{w}, \boldsymbol{b}) \in \mathbb{R}^{D} \times \mathbb{R}} \frac{1}{n} \| \boldsymbol{y} - \boldsymbol{Z}_{\mathcal{M}_{\lambda}} \boldsymbol{w} - \boldsymbol{b} \|_{2}^{2} + \lambda \| \boldsymbol{w} \|_{1}$$
$$\boldsymbol{\phi} \leftarrow \boldsymbol{y} - \boldsymbol{Z}_{\mathcal{M}_{\lambda}} \boldsymbol{w} - \boldsymbol{b}$$

Problem formulation



• The KKT conditions state that:

$$\forall (j,k) \in \llbracket 1, p \rrbracket^2, \quad \left| (\boldsymbol{X}_j \boldsymbol{X}_k)^T \boldsymbol{\theta}^* \right| \in \begin{cases} \{\lambda\} \text{ if } \boldsymbol{w}_{j,k}^* \neq 0\\ [-\lambda, \lambda] \text{ if } \boldsymbol{w}_{j,k}^* = 0 \end{cases}$$
(3)

We will say that the constraint relative to $X_j X_k$ is violated whenever $|(X_j X_k)^T \theta| > \lambda$

• The primal and dual optimal variables (w*, b*) and θ * are related as follows:

$$\boldsymbol{\theta}^* = \boldsymbol{y} - \boldsymbol{Z} \boldsymbol{w}^* - \boldsymbol{b}^*$$

Input: $\boldsymbol{X} \in [0, 1]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



Identify violated constraints and update working set. Compute the bound $\eta(\phi, \mathbf{X}_j)$. We define $\eta(\phi, \mathbf{X}_j)$ as an upper bound on $\max_{\mathbf{X}_k: \mathbf{X}_j \mathbf{X}_k \notin \mathcal{M}_\lambda} | (\mathbf{X}_j \mathbf{X}_k)^T \phi|$.

If $\eta(\phi, \mathbf{X}_i) \leq \lambda$, then we know that all features in the branch respect the optimality conditions.

Input: $\boldsymbol{X} \in [\![0,1]\!]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



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We define $\eta(\phi, X_j)$ as an upper bound on

$$\max_{\boldsymbol{X}_k:\,\boldsymbol{X}_j\boldsymbol{X}_k\notin\mathcal{M}_\lambda}\Big|\big(\boldsymbol{X}_j\boldsymbol{X}_k\big)^{\mathsf{T}}\,\boldsymbol{\phi}\Big|.$$

$$\eta(\phi, X_1) < \lambda$$

Input: $\boldsymbol{X} \in [\![0,1]\!]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



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$$\eta(\phi, X_2) \geq \lambda$$

Input: $\boldsymbol{X} \in [0, 1]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



Identify violated constraints and update working set. Compute the bound $\eta(\phi, X_i)$. We define $\eta(\phi, \mathbf{X}_j)$ as an upper bound on $\max_{\mathbf{X}_k: \mathbf{X}_j \mathbf{X}_k \notin \mathcal{M}_\lambda} | (\mathbf{X}_j \mathbf{X}_k)^T \phi|$.

$\eta(\phi, X_3) \geq \lambda$

Input: $\boldsymbol{X} \in [\![0,1]\!]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



Identify violated constraints and update working set. Compute the bound $\eta(\phi, \mathbf{X}_j)$.

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$$\eta(\phi, X_4) < \lambda$$

Input: $\boldsymbol{X} \in [0, 1]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



Identify violated constraints and update working set. Compute the bound $\eta(\phi, \mathbf{X}_j)$.

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$$\sup_{\substack{\substack{d \in \mathcal{M}_{\lambda}}}} \left| \left(\boldsymbol{X}_{j} \boldsymbol{X}_{k} \right)^{T} \boldsymbol{\phi} \right|.$$

done

Input: $\boldsymbol{X} \in [0, 1]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



Identify violated constraints and update working set. If $\eta(\phi, \mathbf{X}_j) \ge \lambda$, compute $\mathbf{m}_j(\phi)$ and update \mathcal{M}_{λ} .

$$\boldsymbol{m}_{j}(\boldsymbol{\phi}) = \max_{\boldsymbol{X}_{k}:\,\boldsymbol{X}_{j}\boldsymbol{X}_{k}\notin\mathcal{M}_{\lambda}} \left| \left(\boldsymbol{X}_{j}\boldsymbol{X}_{k} \right)^{\mathsf{T}} \boldsymbol{\phi} \right|, \quad \mathcal{M}_{\lambda} \leftarrow \mathcal{M}_{\lambda} \cup \left\{ \boldsymbol{X}_{j}\boldsymbol{X}_{k}: \left| \left(\boldsymbol{X}_{j}\boldsymbol{X}_{k} \right)^{t} \boldsymbol{\phi} \right| \geq \lambda \right\}$$

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 $\left| \left(\boldsymbol{X}_{2} \boldsymbol{X}_{4} \right)^{T} \boldsymbol{\phi} \right| < \lambda$

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Input: $\boldsymbol{X} \in [0, 1]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



Solve subproblem restricted to \mathcal{M}_λ Update residuals

$$\boldsymbol{w}, \boldsymbol{b} \leftarrow \operatorname*{argmin}_{(\boldsymbol{w}, \boldsymbol{b}) \in \mathbb{R}^{D} \times \mathbb{R}} \frac{1}{n} \| \boldsymbol{y} - \boldsymbol{Z}_{\mathcal{M}_{\lambda}} \boldsymbol{w} - \boldsymbol{b} \|_{2}^{2} + \lambda \| \boldsymbol{w} \|_{1}$$
$$\boldsymbol{\phi} \leftarrow \boldsymbol{y} - \boldsymbol{Z}_{\mathcal{M}_{\lambda}} \boldsymbol{w} - \boldsymbol{b}$$

Input: $\boldsymbol{X} \in [0, 1]^{n \times p}, \quad \boldsymbol{y} \in \mathbb{R}^n$



- 1: Initialize \mathcal{M}_{λ} . Pre-solve and initialize ϕ .
- 2: repeat:
- 3: **for** each branch *j* **do**:

- 4: Compute the bound $\eta(\phi, \mathbf{X}_j)$.
- 5: If $\eta(\dot{\phi}, X_j) \ge \lambda$, compute $m_j(\phi)$ and update \mathcal{M}_{λ} .
- 6: Solve subproblem
- 7: until no violated constraint remains.

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• Suppose the current residual is ϕ . For each branch $j \in [\![1, p]\!]$, we want a bound $\eta(\phi, \mathbf{X}_j)$ such that:

$$\boldsymbol{m}_{j}(\boldsymbol{\phi}) = \max_{\boldsymbol{X}_{k}: \, \boldsymbol{X}_{j} \boldsymbol{X}_{k} \notin \mathcal{M}_{\lambda}} \left| (\boldsymbol{X}_{j} \boldsymbol{X}_{k})^{T} \boldsymbol{\phi} \right| \leq \eta(\boldsymbol{\phi}, \boldsymbol{X}_{j})$$

• One possibility is to use the following bound (as in Nakagawa et al.):

$$\begin{split} \boldsymbol{m}_{j}(\boldsymbol{\phi}) &\leq \max_{\boldsymbol{x} \in [0,1]^{n}} \left| \left(\boldsymbol{X}_{j} \odot \boldsymbol{x} \right)^{T} \boldsymbol{\phi} \right| \\ &= \max \left(\sum_{i: \phi_{i} > 0} \boldsymbol{X}_{ij} \phi_{i}, -\sum_{i: \phi_{i} < 0} \boldsymbol{X}_{ij} \phi_{i} \right) \\ &= \zeta(\boldsymbol{\phi}, \boldsymbol{X}_{j}) \end{split}$$

- ✓ can be computed very efficiently.
- \checkmark but becomes too loose when *n* increases, leading to only few branches pruned.

Branch Bounds

• Suppose the current residual is ϕ . Suppose we have already computed $m_j(\phi^{prev}) = \max_{\boldsymbol{X}_k: \, \boldsymbol{X}_j \boldsymbol{X}_k \notin \mathcal{M}_\lambda} \left| (\boldsymbol{X}_j \boldsymbol{X}_k)^T \phi^{prev} \right|$ We propose the following bound:

$$\begin{split} \boldsymbol{m}_{j}(\phi) &= \max_{\boldsymbol{x} \in \mathcal{D}e(\boldsymbol{X}_{j})} \left| \boldsymbol{x}^{T} \phi \right| \\ &= \max_{\boldsymbol{x} \in \mathcal{D}e(\boldsymbol{X}_{j})} \left| \boldsymbol{x}^{T} \phi^{prev} + \boldsymbol{x}^{T} \left(\phi - \phi^{prev} \right) \right| \\ &\leq \max_{\boldsymbol{x} \in \mathcal{D}e(\boldsymbol{X}_{j})} \left| \boldsymbol{x}^{T} \phi^{prev} \right| + \max_{\boldsymbol{x} \in \mathcal{D}e(\boldsymbol{X}_{j})} \left| \boldsymbol{x}^{T} \left(\phi - \phi^{prev} \right) \right| \\ &\leq \boldsymbol{m}_{j}(\phi_{prev}) + \max_{\boldsymbol{x} \in [0,1]^{n}} \left| (\boldsymbol{X}_{j} \odot \boldsymbol{x})^{T} \left(\phi - \phi^{prev} \right) \right| \\ &= \boldsymbol{m}_{j}(\phi_{prev}) + \max \left(\sum_{i:\phi_{i} > \phi_{i}^{prev}} \boldsymbol{X}_{ij} \left(\phi_{i} - \phi_{i}^{prev} \right), - \sum_{i:\phi_{i} < \phi_{i}^{prev}} \boldsymbol{X}_{ij} \left(\phi_{i} - \phi_{i}^{prev} \right) \right) \\ &= \eta(\phi, \boldsymbol{X}_{j}) \end{split}$$

• We leverage previously computed maximum inner products and the fact that residuals along the regularization path are correlated.

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Branch Bounds

• Suppose the current residual is ϕ . Suppose we have already computed $\boldsymbol{m}_{j}(\phi^{\text{prev}}) = \max_{\boldsymbol{X}_{k}: \boldsymbol{X}_{j} \boldsymbol{X}_{k} \notin \mathcal{M}_{\lambda}} \left| (\boldsymbol{X}_{j} \boldsymbol{X}_{k})^{T} \phi^{\text{prev}} \right|$ We propose the following bound:

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• We leverage previously computed maximum inner products and the fact that residuals along the regularization path are correlated.

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$$\eta(\phi, \mathbf{X}_{j}, \alpha) = |\alpha| \mathbf{m}_{j} + max \left(\sum_{i:\phi_{i} > \alpha \phi_{i}^{\textit{prev}}} \mathbf{X}_{ij} \left(\phi_{i} - \alpha \phi_{i}^{\textit{prev}}\right), - \sum_{i:\phi_{i} < \alpha \phi_{i}^{\textit{prev}}} \mathbf{X}_{ij} \left(\phi_{i} - \alpha \phi_{i}^{\textit{prev}}\right) \right)$$



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$$\eta(\phi, \mathbf{X}_{j}, \alpha) = |\alpha| \mathbf{m}_{j} + max \left(\sum_{i:\phi_{i} > \alpha \phi_{i}^{\textit{prev}}} \mathbf{X}_{ij} \left(\phi_{i} - \alpha \phi_{i}^{\textit{prev}}\right), - \sum_{i:\phi_{i} < \alpha \phi_{i}^{\textit{prev}}} \mathbf{X}_{ij} \left(\phi_{i} - \alpha \phi_{i}^{\textit{prev}}\right) \right)$$



Branch Bounds: Optimisation

$$\eta(\phi, \mathbf{X}_{j}, \alpha) = |\alpha| \mathbf{m}_{j} + \max\left(\sum_{i:\phi_{i} > \alpha \phi_{i}^{prev}} \mathbf{X}_{ij} \left(\phi_{i} - \alpha \phi_{i}^{prev}\right), -\sum_{i:\phi_{i} < \alpha \phi_{i}^{prev}} \mathbf{X}_{ij} \left(\phi_{i} - \alpha \phi_{i}^{prev}\right)\right)$$

How to choose α ?

- Option 1: $\alpha^* = \operatorname*{argmin}_{\alpha \in \mathbb{R}} \eta(\phi, X_j, \alpha)$
 - $\checkmark \eta$ is a piecewise continuous function which is convex in α .
 - $\checkmark \eta$ can be minimized in $\mathcal{O}(n_j \log n_j)$ operations.

• Option 2: $\alpha_{\ell 2} = \frac{\phi^T \phi^{prev}}{\|\phi^{prev}\|_2^2}$

- $\checkmark \alpha_{\ell 2}$ minimizes $\|\phi \alpha \phi^{\text{prev}}\|_2^2$.
- $\checkmark \alpha_{\ell 2}$ can be obtained in $\mathcal{O}(n_j)$ operations.



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- 2: repeat:
- 3: **for** each branch *j* **do**:

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- 3: **for** each branch *j* **do**:

- 4: Compute the bound $\eta(\phi, X_j)$.
- 5: If $\eta(\phi, X_j) \ge \lambda$, compute $m_j(\phi)$ and update \mathcal{M}_{λ} .
- 6: Solve subproblem
- 7: until no violated constraint remains.

- Whenever $\eta(\phi, \mathbf{X}_j, \alpha^*) \ge \lambda$, then there is a chance that branch *j* contains a feature which is violated for the current residual ϕ . In this case we need to:
 - ✓ identify all violated features.
 - ✓ compute:

$$\boldsymbol{m}_{j} = \max_{\boldsymbol{X}_{k}: \boldsymbol{X}_{j} \boldsymbol{X}_{k} \notin \mathcal{M}_{\lambda}} \left| \left(\boldsymbol{X}_{j} \odot \boldsymbol{X}_{k} \right)^{T} \boldsymbol{\phi} \right|$$

which naively requires computing all inner products.

• We note that **m**_i can be rewitten as:

$$\boldsymbol{m}_{j} = \max_{\boldsymbol{X}_{k}: \boldsymbol{X}_{j} \boldsymbol{X}_{k} \notin \mathcal{M}_{\lambda}} \left| \boldsymbol{X}_{k}^{\mathsf{T}} \left(\boldsymbol{X}_{j} \odot \boldsymbol{\phi} \right) \right|$$

This is (almost) a Maximum Inner product Search (MIPS) problem with query vector $\mathbf{X}_j \odot \phi$ and database or probe vectors $\{\mathbf{X}_k, k \in [\![1, p]\!] : \mathbf{X}_j \mathbf{X}_k \notin \mathcal{M}_\lambda\}$.

- Relevant work in the data mining literature (far from exhaustive):
 - ✓ State-of-the-art exact MIPS algorithm:
 - Christina Teflioudi and Rainer Gemulla. "Exact and Approximate Maximum Inner Product Search with LEMP". . In: TODS (2016)
 - ✓ All pairs similarity search algorithm:

Roberto J. Bayardo, Yiming Ma, and Ramakrishnan Srikant. "Scaling up all pairs similarity search". In: Proc. 16th Int. Conf. World Wide Web - WWW '07 (2007), p. 131

- We borrow the idea of computing inner products on restricted sets of dimensions, and bounding the part of the inner product on the remaining dimensions.
- We implement this idea in the case of our particular setting where:
 - ✓ queries are sparse vectors of the form: $X_j \odot \phi$, and ϕ can have both positive and negative entries.
 - ✓ probes are binary vectors.

Input: $\boldsymbol{Q} = \{\boldsymbol{X}_j : \eta(\phi, \boldsymbol{X}_j) \ge \lambda\} \in [0, 1]^{n \times q}, \quad \boldsymbol{P} \in [0, 1]^{n \times p}, \quad \phi \in \mathbb{R}^n$

Param: $n_c \in \mathbb{N}$

Output: $m \in \mathbb{R}^q$ and $k \in \mathbb{R}^q$.

- 1: Reorder the dimensions $1 \dots n$ such that $|\phi|$ is sorted in descending order.
- 2: Reorder the vectors \boldsymbol{P}_j in \boldsymbol{P} in increasing order of $nnz(\boldsymbol{P}_j)$.
- 3: Initialize the best inner products $\pmb{m} \in \mathbb{R}^q$ for each query.

We note $\mathcal{N}_j \subset \llbracket 1, n \rrbracket$ the set of non zero entries of X_j .

- 4: for $j \in [\![1, q]\!]$ do # Compute $r^+ \in \mathbb{R}^n$ and $r^- \in \mathbb{R}^n$ the partial inner product upperbour
 - 5: for $i \in \mathcal{N}_i$ do

6:
$$\mathbf{r}_i^+ = \sum_{m>i; m:\phi_m>0} \mathbf{X}_{mj} \phi_m$$
 and $\mathbf{r}_i^- = \sum_{m>i; m:\phi_m<0} \mathbf{X}_{mj} \phi_m$

7: **for** $k \in [\![1, p]\!]$ **do**

8: d = 0 (inner product initialization); c = 0 (counter initialization);

9: for $i \in \mathcal{N}_i$ do

10:
$$d = d + \mathbf{Q}_{ij}\mathbf{P}_{ik}\phi_i; \quad c = c+1.$$

- 11: **if** *c* mod *n_c* == 0 **then**
- 12: if $(d + r_i^+) < \min(m_i, \lambda)$ and $|(d + r_i^-)| < \min(m_j, \lambda)$ then go to next probe.
- 13: if $m_j < d < \lambda$ then set $m_j = d$ and $k_j = k$
- 14: **if** $d \ge \lambda$ **then** add $X_j X_k$ to \mathcal{M}_λ

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4: for $j \in \llbracket 1, q \rrbracket$ do

Compute $\mathbf{r}^+ \in \mathbb{R}^n$ and $\mathbf{r}^- \in \mathbb{R}^n$ the partial inner product upperbounds.

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Param: $n_c \in \mathbb{N}$

Output: $m \in \mathbb{R}^q$ and $k \in \mathbb{R}^q$.

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• We propose WHInter:

- ✓ Working set strategy.
- ✓ New branch pruning strategy for the identification of the active set.
- ✓ Efficient computation of branch bounds using a Maximum Inner Product Search (MIPS) framework for binary data.

• Evaluation of WHInter on:

- ✓ Simulated datasets.
- Real toxicogenetics dataset.

- We simulate X ∈ [[0, 1]]^{n×p} where X_{ik} ~ Bernoulli (q_k), and q_k ~ Unif (0.1, 0.5) for different combinations of n and p.
- We randomly pick a set S of 100 features (among original and interaction ones).
- The associated weights are drawn from a standard gaussian distribution.

• We set $\phi = \mathbf{Z}_{S} \mathbf{w}$

We choose 100 values of λ logarithmically spaced in [λ_{max}, 0.01λ_{max}]. We stop the algirithm as soon as more than 150 features are selected in the model.

LASSO Simulations

n = 1000 fixed, p varied.



LASSO Simulations

p = 1000 fixed, n varied.



LASSO Simulations

n = 1000, p = 10000.



- We consider the SNPs from chromosomes 1 and 19 of 620 lymphoblastoid cell lines, represented by X¹ ∈ [[0, 1]]^{620×102196} and X¹⁹ ∈ [[0, 1]]^{620×28418}.
- The response $y \in \mathbb{R}^{620}$ is the cytotoxicity (EC10) of a chemical compound.
- Correction for population structure was applied as in Price et al (2006).

	Chr	omosom	e 19	Chromosome 1			
Method	Preproc	Path	Tot. time	Preproc	Path	Tot. time	
	(min)	(min)	(min)	(ĥ)	(h)	(h)	
$\eta(\alpha_{l2}) + MIPS$	13	13	26	2.5	1.4	3.9	
$\eta(\alpha^*) + MIPS$	13	13	26	2.5	1.2	3.7	
$\eta(\alpha = 1) + MIPS$	13	22	35	2.5	2.9	5.4	
$\eta(\alpha_{l2}) + naive$	13	23	36	2.5	2.5	5	
$\dot{\zeta} + \dot{M}IPS$	7	84	91	1.2	13.5	14.7	
$\dot{\zeta} + naive$	7	109	116	1.2	17.2	18.4	
SPP	7	173	180	1.2	25.2	26.4	

Thank you for your attention.



- Roberto J. Bayardo, Yiming Ma, and Ramakrishnan Srikant. "Scaling up all pairs similarity search". In: *Proc. 16th Int. Conf. World Wide Web WWW '07* (2007), p. 131.

- Olivier Fercoq, Alexandre Gramfort, and Joseph Salmon. "Mind the duality gap: safer rules for the Lasso". In: *ICML*. 2015, pp. 333–342.
- Kazuya Nakagawa et al. "Safe Pattern Pruning: An Efficient Approach for Predictive Pattern Mining". In: *KDD* (2016). arXiv: 1602.04548.
- Christina Teflioudi and Rainer Gemulla. "Exact and Approximate Maximum Inner Product Search with LEMP". In: *TODS* (2016).