# High-dimensional graphical modeling and causal inference

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### joint work with



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Sara van de Geer

cannot do confirmatory causal inference without randomized intervention experiments...

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but we can do better than proceeding naively

## Goal

in genomics:

if we would make an intervention at a single gene, what would be its effect on a phenotype of interest?

want to infer/predict such effects without actually doing the intervention i.e. from observational data

(from observations of a "steady-state system")

it doesn't need to be genes can generalize to intervention at more than one variable/gene

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### Genomics

1. Flowering of arabidopsis thaliana



phenotype/response variable of interest:

Y = days to bolting (flowering)

"covariates" X = gene expressions from p = 21'326 genes

question: infer/predict the effect of knocking-out/knocking-down (or enhancing) a single gene (expression) on the phenotype/response variable *Y*?

### 2. Gene expressions of yeast



p = 5360 genes phenotype of interest: Y = expression of first gene "covariates" X = gene expressions from all other genes

and then phenotype of interest: Y = expression of second gene "covariates" X = gene expressions from all other genes

and so on

infer/predict the effects of a single gene knock-down on all other genes

 $\rightsquigarrow$  consider the framework of an

intervention effect = causal effect

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Regression - the "statistical workhorse": the wrong approach

we could use linear model (fitted from *n* observational data)

$$Y = \sum_{j=1}^{p} \beta_j X^{(j)} + \varepsilon,$$
  
Var $(X^{(j)}) \equiv 1$  for all  $j$ 

 $|\beta_j|$  measures the effect of variable  $X^{(j)}$  in terms of "association" i.e. change of *Y* as a function of  $X^{(j)}$  when keeping all other variables  $X^{(k)}$  fixed

not very realistic for intervention problem if we change e.g. one gene, some others will also change and these others are not (cannot be) kept fixed Regression – the "statistical workhorse": the wrong approach

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### and indeed:



 $\sim$  can do much better than (penalized) regression

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### and indeed:



→ can do much better than (penalized) regression!

Effects of single gene knock-downs on all other genes (yeast)

(Maathuis, Colombo, Kalisch & PB, 2010)

- *p* = 5360 genes (expression of genes)
- $\bullet$  231 gene knock downs  $\rightsquigarrow 1.2\cdot 10^6$  intervention effects
- the truth is "known in good approximation" (thanks to intervention experiments)

goal: prediction of the true large intervention effects based on observational data with no knock-downs

n = 63 observational data



### DAGs and causal effects

- univariate response Y
- *p*-dimensional covariate X

question:

what is the effect of setting the *j*th component of *X* to a certain value *x*:

$$\operatorname{do}(X^{(j)}=x)$$

 $\rightsquigarrow$  this is a question of intervention type

not the effect of  $X^{(j)}$  on Y when keeping all other variables fixed (regression effect) Reichenbach, 1956; Suppes, 1970; Rubin, 1978; Dawid, 1979; Holland, Pearl, Glymour, Scheines, Spirtes,... ... a substantial machinery... (e.g. Pearl)

two main assumptions

causal influence diagram is a DAG



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relaxation allowing for cycles:

e.g. Hyttinen, Eberhardt & Hoyer (2010, 2012)

there are no hidden (relevant) variables

relaxation including hidden variables:

e.g. Spirtes, Glymour & Scheines (2000); Colombo, Maathuis & Richardson (2012),...

if  $Y, X^{(1)}, \dots, X^{(p)} \sim \mathcal{N}_{p+1}(\mu, \Sigma)$  $\rightsquigarrow$  intervention (or causal) effect is a real-valued parameter

$$\theta_j \equiv \frac{\partial}{\partial x} \mathbb{E}[Y | \operatorname{do}(X^{(j)} = x)]$$
 constant w.r.t. x

and the intervention effect parameter can be characterized as:

for 
$$Y \notin pa(j)$$
:  $\theta_j$  is the regression parameter in  

$$Y = \theta_j X^{(j)} + \sum_{k \in pa(j)} \gamma_k X^{(k)} + \text{error}$$

only need parental set and regression

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j = 2, pa $(j) = \{3, 4\}$ 



### when having no unmeasured confounder (variable):

intervention effect (as defined) = causal effect

causal effect = effect from a randomized trial (but we want to infer it without a randomized study... because often we cannot do it, or it is too expensive)

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Inferring intervention effects from observational distribution

main problem: inferring DAG or parental set(s) from observational data

impossible! can only infer equivalence class of DAGs (several DAGs can encode exactly the same conditional independence relationships)

Example:

 $(X) \longrightarrow (Y)$ 

X causes Y

Y causes X

### a lot of work about identifiability:

Verma & Pearl (1991); Spirtes, Glymour & Scheines (1993); Tian & Pearl (2000–2002); Lauritzen & Richardson (2002); Shpitser & Pearl (2006–2011); vanderWeele & Robins (2007–2011); Drton, Foygel & Sullivant (2011);...

# we cannot estimate causal/intervention effects from observational distribution

but can estimate "informative" lower bounds of causal eff. based on Markov equivalence class of DAGs



(Maathuis, Kalisch & PB, 2009)

R-package: pcalg

what we used in the yeast example to score importance of genes according to size of  $\hat{\alpha}_i$ 



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# Estimation of the Markov equivalence class of DAGs

notation: drop the Y-notation ( $Y = X^{(1)}, X^{(2)}, \dots, X^{(p)}$ )

goal: infer CPDAG (Markov equivalence class of DAGs)





two main approaches:

- multiple testing of conditional (in-)dependences
- score-based methods: MLE as prime example

## Estimation of the Markov equivalence class of DAGs

notation: drop the Y-notation ( $Y = X^{(1)}, X^{(2)}, \dots, X^{(p)}$ )

goal: infer CPDAG (Markov equivalence class of DAGs)  $\sim$  "structure learning"



 $P \Rightarrow \underbrace{\text{CPDAG}(P)}_{\text{equiv. class of DAGs}}$ 

two main approaches:

- multiple testing of conditional (in-)dependences
- score-based methods: MLE as prime example

# Faithfulness assumption

for inferring CPDAG via conditional (in-)dependences ("essentially" necessary for conditional dependence testing approaches)

a distribution P is called faithful to a DAG D if all conditional independences can be inferred from the graph

(can infer some conditional independences from a Markov assumption; but we require here "all" conditional independences)

assuming faithfulness:  $\rightsquigarrow$  can infer the CPDAG from a list of conditional (in-)dependence relations

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### What does it mean?



$$X^{(1)} \leftarrow \varepsilon^{(1)},$$
  

$$X^{(2)} \leftarrow \alpha X^{(1)} + \varepsilon^{(2)},$$
  

$$X^{(3)} \leftarrow \beta X^{(1)} + \gamma X^{(2)} + \varepsilon^{(3)},$$
  

$$\varepsilon^{(1)}, \varepsilon^{(2)}, \varepsilon^{(3)} \text{ i.i.d. } \sim \mathcal{N}(0, 1)$$

enforce marginal independence of  $X^{(1)}$  and  $X^{(3)}$  $\beta + \alpha \gamma = 0$ , e.g.  $\alpha = \beta = 1$ ,  $\gamma = -1$ 

$$\Sigma = \begin{pmatrix} 1 & 1 & 0 \\ 1 & 2 & -1 \\ 0 & -1 & 2 \end{pmatrix}, \ \Sigma^{-1} = \begin{pmatrix} 3 & -2 & -1 \\ -2 & 2 & 1 \\ -1 & 1 & 1 \end{pmatrix}.$$

failure of faithfulness due to cancellation of coefficients

failure of exact faithfulness is "rare" (Lebesgue measure zero)

but for statistical estimation (in the Gaussian case): "often" require strong faithfulness (Robins, Scheines, Spirtes & Wasserman, 2003):

faithfulness &

$$\begin{split} \min \left\{ |\rho(i, j | \mathcal{S})|; \ \rho(i, j | \mathcal{S}) \neq 0, \ i \neq j, \ |\mathcal{S}| \leq d \right\} \geq \tau, \\ \tau \asymp \sqrt{\log(p)/n} \end{split}$$

... strong faithfulness can be rather severe (Uhler, Raskutii, PB & Yu, 2012)

3 nodes, full graph



# unfaithful distributions due to exact cancellation



1.0 lambda=0.1 lambda=0.01 0.9 lambda=0.00 0.8 <sup>2</sup>roportion of unfaithful distributions 0.7 0.6 0.5 0.4 0.3 0.2 0.1 0.0 0.0 0.2 0.8 0.0 10 Probability of an edge P[not strongly faithful]

8 nodes

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Estimating the CPDAG: the PC-algorithm (Spirtes & Glymour, 1991)

- crucial assumption: distribution P (strongly) faithful to the true underlying DAG
- ► less crucial but convenient: Gaussian assumption for X<sup>(1)</sup>,..., X<sup>(p)</sup> → can work with partial correlations
- input:  $\hat{\Sigma}_{MLE}$

but we only need to consider many small sub-matrices of it (assuming sparsity of the graph)

output: based on a clever data-dependent (random)

sequence of multiple tests

estimated CPDAG

Statistical theory for PC-algorithm (Kalisch & PB, 2007; Maathuis, Kalisch & PB, 2009)

*n* i.i.d. observational data points; *p* variables high-dimensional setting where  $p \gg n$ 

assumptions:

- $X^{(1)}, \ldots, X^{(p)} \sim \mathcal{N}_{p}(0, \Sigma)$  Markov and faithful to true DAG
- ▶ high-dimensionality: log(p) ≪ n
- ▶ sparsity: maximal degree  $d = \max_j |\operatorname{ne}(j)| \ll n$
- "coherence": maximal (partial) correlations ≤ C < 1 max{|ρ<sub>i,j|S</sub>|; i ≠ j, |S| ≤ d} ≤ C < 1
  </p>
- ► signal strength/strong faithfulness: min{ $|\rho_{i,j|S}|$ ;  $\rho_{i,j|S} \neq 0$ ,  $i \neq j$ ,  $|S| \leq d$ }  $\gg \sqrt{d \log(p)/n}$

Then, for some suitable tuning param. and  $0 < \delta < 1$ :

$$\mathbb{P}[\widehat{\mathsf{CPDAG}} = \mathsf{true} \ \mathsf{CPDAG}] = 1 - O(\exp(-Cn^{1-\delta}))$$

(Restricted) strong-faithfulness (Uhler, Raskutti, PB & Yu, 2012)

strong-faithfulness: faithfulness &

$$\mathsf{min}\left\{|\rho(i,j|\mathcal{S})|; \ \rho(i,j|\mathcal{S}) \neq \mathsf{0}, \ i \neq j, \ |\mathcal{S}| \leq d\right\} \geq \tau$$

 $\tau \asymp \sqrt{d \log(p)/n}, \ d = \max.$  degree of DAG

sufficient and necessary for PC-/conservative PC-algorithm: restricted strong-faithfulness

1. adjacency strong-faithfulness

$$\min\left\{ ert 
ho(i,jert \mathcal{S})ert; \ 
ho(i,jert \mathcal{S}) 
eq 0, \ ig(i,j) \in oldsymbol{E}, \ ert \mathcal{S} ert \leq oldsymbol{d} 
ight\} \geq au$$

2. orientation strong-faithfulness

$$\min\left\{|\rho(i,j|S)|; \ (i,j,S) \in \operatorname{neigh}\right\} \geq \tau$$

neigh = {(i, j, S); i, j not adjacent, (i, j, k) unshielded triple with i, j not d-separated by S}

goal: understand

 $p(\tau) = \mathbb{P}[\text{failure of } \tau \text{ restricted strong-faithfulness}]$ 

when edge weights  $\beta_{jk}$  (for edge  $j \rightarrow k$ ) i.i.d. Uniform([-1, 1])

results (Uhler, Raskutti, PB & Yu, 2012):

upper bound:

$$\leq C_1 C_2(|E|) \underbrace{\kappa_{\max_{i,j,S} \operatorname{Var}(X^{(i)}|X^{(S)})}_{\max_{i,j,S} \operatorname{Var}(X^{(i)}|X^{(S)})} \tau^k \underbrace{\sum_{i,j,S} \operatorname{deg}(\operatorname{Cov}(X^{(i)}, X^{(j)}|X^{(S)}))}_{\text{often large}}$$

k depends on polynomials character. strict unfaithfulness

### Iower bounds

- for trees
- for cycles
- for bi-partite graphs

Trees:

$$p(\tau) \ge 1 - (1 - \tau)^{p-1}$$

Cycles:

$$p( au) \geq 1 - (1- au)^{3p-2}$$

→ similar regime as trees

Bipartite graphs:

$$p(\tau) \ge 1 - (1 - \tau)^{(p-2)(2^{p-3}+1)}$$

 $\sim$  a "disaster"...!





"most favorable" case: trees

$$p(\tau) \ge 1 - (1 - \tau)^{p-1}$$

with  $\tau = \sqrt{\log(p)/n}$  (for bounded degree trees)  $\rightsquigarrow$ 

 $\mathbb{P}[\tau \text{ restricted strong-faithfulness holds}] \rightarrow 1 \Rightarrow \mathbf{p} = \mathbf{o}(\sqrt{n})$ 

- due to necessity of restricted strong-faithfulness
- assuming framework with i.i.d. sampling of edge weights (Uniform, Gaussian, Laplace,...)

⇒ cannot achieve high-dimensional consistency of PC-algorithm (conditional independence testing approaches) without further conditions

(e.g. saying that non-zero edge weights are "very" large)

Maximum likelihood estimation without requiring strong faithfulness!



Gaussian DAG is Gaussian linear structural equation model:



$$\begin{aligned} X^{(1)} &\leftarrow \varepsilon^{(1)} \\ X^{(2)} &\leftarrow \beta_{21} X^{(1)} + \varepsilon^{(2)} \\ X^{(3)} &\leftarrow \beta_{31} X^{(1)} + \beta_{32} X^{(2)} + \varepsilon^{(3)} \end{aligned}$$

 $X^{(j)} \leftarrow \sum_{k=1}^{p} \beta_{jk} X^{(k)} + \varepsilon^{(j)} \ (j = 1, ..., p), \ \beta_{jk} \neq 0 \Leftrightarrow \text{ edge } k \to j$  $X = BX + \varepsilon, \ \varepsilon \sim \mathcal{N}_{p}(0, \operatorname{diag}(\sigma_{1}^{2}, ..., \sigma_{p}^{2})) \text{ in matrix notation}$ 

$$X = BX + \varepsilon$$

non-zeroes of  $B \Rightarrow$  knowledge of the corresponding DAG

if we would know the order of the variables  $\sim$  (high-dimensional) multivariate regression

but we don't know the order of the variables:

- ► can only identify equivalence class of B's → "obvious"
- ▶ neg. log-likelihood is non-convex fct.(B) → next slides
- learning of ordering has large complexity (in general p!)

$$\hat{B}, \{\hat{\sigma}_j^2\} = \operatorname{argmin}_{B; \ \{\sigma_j^2\}} - \ell(B, \{\sigma_j^2\}; \ \operatorname{data}) + \lambda \underbrace{\|B\|_0}_{\sum_{jk} l(B_{jk} \neq 0)}$$

under the non-convex constraint that *B* corresponds to "no directed cycles"

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non-convex parameter space! (convex relaxation?  $\rightarrow$  see discussion)

### Why $\ell_0$ -penalty?

- ensures the same score for Markov-equivalent structures (this would not be true when using l<sub>1</sub>-norm penalty)
- *l*<sub>0</sub>-penalty leads to decomposable score

score(
$$D, \mathbf{X}$$
) =  $\sum_{j=1}^{p} g_j(\mathbf{X}^{(j)}, \mathbf{X}^{(\mathrm{pa}_D(j))})$ 

 $\sim$  dynamic programming for computation if  $p \approx 20 - 30$  (not easily possible with  $\ell_1$ -norm penalization) recall that the estimation problem is non-convex...

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Statistical properties for  $\ell_0$ -penalized MLE (van de Geer & PB, 2012)

### the target:

 $\ell_0\mbox{-}penalized$  MLE estimates a DAG with fewest edges which represents the true distribution: minimal edges I-MAP

in the Gaussian linear structural eqn. model:  $\operatorname{Cov}(X) = \Sigma = (I - B)^{-1}\Omega(I - B)^{-T}, \Omega = \operatorname{diag}(\sigma_1^2, \dots, \sigma_p^2)$ true  $\Sigma^0$  of data-generating distribution minimal edges I-MAP: a DAG and corresponding  $B^0, \Omega^0$  such that  $\Sigma^0 = (I - B^0)^{-1}\Omega^0(I - B^0)^{-T}$ not unique (in general)



non-faithful distribution where  $Cov(X^{(1)}, X^{(3)}) = 0$ 



no faithfulness required for inferring minimal edges I-MAP  $\rightsquigarrow$  no strong-faithfulness required either

and when assuming faithfulness:

equivalence class of minimal edges I-MAP = (usual) Markov equivalence class

without requiring strong-faithfulness!

main condition required for  $\ell_0$ -penalized MLE: permutation beta-min condition for an ordering of the variables i.e. permutation  $\pi$ :  $\{1, \ldots, p\} \rightarrow \{1, \ldots, p\}$ consider regressions of

 $X_{\pi(j)}$  versus  $X_{\pi(j-1)}, \ldots, X_{\pi(1)}$  (Gram-Schmidt)

 $\sim$  coefficients  $B^0(\pi)$ (for a true ordering  $\pi^0$ :  $B^0(\pi^0)$  is most  $\ell_0$ -sparse)

permutation beta-min condition: for any  $\pi$ , "most of non-zero"  $|B_{jk}^0(\pi)|$  are sufficiently large technically: for any  $\pi$  $(1 - \eta)$   $\underbrace{s(\pi)}_{k(\pi)}$  edges (j, k) with no. of edges in  $B^0(\pi)$  $|B_{jk}^0(\pi)| > \sqrt{\log(p)/n} \underbrace{(\sqrt{p/s_0} \lor 1)}_{typically \simeq 1}/\eta_0$ 

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# example: AR(1) (and AR(k) with fixed k) model satisfy the permutation beta-min condition

AR(1) model is a chain, i.e., a tree with maximal degree = 2  $\rightarrow$  still "bad" in terms of strong faithfulness

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#### Main results (van de Geer & PB, 2012)

assume permutation beta-min condition (and other "mild conditions")

then:

• with high probability: for  $\lambda^2 \simeq \log(p)/n$ 

$$\begin{split} \|\hat{B} - B^0(\hat{\pi})\|_F^2 + \|\hat{\Omega} - \Omega^0(\hat{\pi})\|_F^2 &= O(\lambda^2 s_0)\\ s_0 &= \text{ no. of edges in minimal edges I-MAP} \end{split}$$

number of estimated edges is in the correct order of magnitude

$$\hat{\boldsymbol{s}} \asymp \boldsymbol{s}_0$$

• exact edge recovery of minimal edges I-MAP: our result "essentially requires"  $p = o(\sqrt{n/\log(n)})$ (which is the best case regime for strong faithfulness condition)

no strong faithfulness condition!

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improvement for linear structural equation model with same error variances, for the regime  $p = o(n/\log(n))$ 

$$X^{(j)} \leftarrow \sum_{k \in \operatorname{pa}(j)} B_{jk} + \varepsilon^{(j)}, \operatorname{Var}(\varepsilon^{(j)}) \equiv \omega^2$$
 (i.e.  $\Omega = \omega^2 I$ )

only "standard" beta-min condition instead of permutation beta-min condition: "most of non-zero"  $|B_{jk}^0(\pi^0)|$  are sufficiently large instead for all  $\pi \rightsquigarrow$  only for true ordering  $\pi^0$ 

and we have supporting empirical results to quantify the improvement if error variances are "approximately the same"



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# Route via structural equation models: many interesting extensions

full identifiability (card(Markov equivalence class) = 1): if

► same error variances:  $X^{(j)} \leftarrow \sum_{k \in pa(j)} B_{jk} X^{(k)} + \varepsilon^{(j)}, Var(\varepsilon^{(j)}) \equiv \omega^2$ Peters & PB (2012)

► nonlinear structural equation models with additive noise:
 X<sup>(j)</sup> ← non-linear function f(X<sup>(pa(j))</sup>) + ε<sup>(j)</sup>
 Mooij, Peters, Janzing & Schölkopf (2009-2012)

e.g.  $X^{(j)} \leftarrow \sum_{k \in pa(j)} f_k(X^{(k)}) + \varepsilon^{(j)}$  (additive strctl. eqns.) Nowzohour & PB (in progress)

linear structural eqns. with non-Gaussian errors:
 ..., at least one ε<sup>(j)</sup> non-Gaussian
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### Observational-interventional data

increase identifiability from (randomized) interventional data combination of observational-interventional data is common in e.g. biology

yeast example:

63 observational and 231 interventional data

- MLE for Gaussian observational-interventional data (Hauser & PB, 2012a)
- active learning by choosing sequentially the next best intervention for identifying the true DAG (and solving the Eberhardt conjecture) (Hauser & PB, 2012b)



## Concluding discussion

1. we have achieved some success in biology applications (simple organisms: yeast and arabidopsis thaliana)  $\sim$  but there seems ample room for improvement

2. methods based on inferring conditional independences necessarily require version of strong faithfulness (e.g. PC-algorithm)
 → restrictive in term of dimensionality

3. route via structural equation models does not require strong faithfulness; and "natural restrictions" lead to full identifiability!

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the price to pay with MLE (and other estimators?) for structural equation models: computation!

re-consider (penalized) MLE for linear Gaussian case:

model:
$$X = BX + \varepsilon$$
penalized MLE: $\hat{B}, \hat{\Omega} = \operatorname{argmin}_{B,\Omega} \ell(B, \Omega; \operatorname{data}) + \lambda \operatorname{pen}(B)$ 

under non-convex constraint of no directed cycles



can we do efficient convex relaxation for  $S = \{\Pi(I-B)^{-1}\Omega(I-B)^{-T}\Pi^{T}; \Pi \text{ perm.}, B \text{ lower triang.}, \Omega\}$ 

so far, our solution:

• dynamic programming if p pprox 20 - 30

• greedy equivalence class search if *p* is large (only ad-hoc... but reasonable results) the price to pay with MLE (and other estimators?) for structural equation models: computation!

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- $\bullet$  dynamic programming if  $p\approx 20-30$
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# Thank you!

### R-package: pcalg (Kalisch, Mächler, Colombo, Maathuis & PB, 2012)

References:

- van de Geer, S. and Bühlmann, P. (2012). l<sub>0</sub>-penalized maximum likelihood for sparse directed acyclic graphs. arXiv:1205.5473v1
- Peters, J. and Bühlmann, P. (2012). Identifiability of Gaussian structural equation models with same error variances. arXiv:1205.2536v1
- Uhler, C., Raskutti, G., Bühlmann, P. and Yu, B. (2012). Geometry of faithfulness assumption in causal inference. arXiv:1207.0547v2 (To appear in the Annals of Statistics).
- Kalisch, M., Mächler, M., Colombo, D., Maathuis, M.H. and Bühlmann, P. (2012). Causal inference using graphical models with the R package pcalg. Journal of Statistical Software 47 (11), 1-26.
- Stekhoven, D.J., Moraes, I., Sveinbjörnsson, G., Hennig, L., Maathuis, M.H. and Bühlmann, P. (2011). Causal stability ranking. Bioinformatics 28, 2819-2823.
- Hauser, A. and Bühlmann, P. (2012). Two optimal strategies for active learning of causal models from interventions. Proc. of the 6th European Workshop on Probabilistic Graphical Models (PGM 2012), pp. 123-130, 2012.
- Hauser, A. and Bühlmann, P. (2012). Characterization and greedy learning of interventional Markov equivalence classes of directed acyclic graphs. Journal of Machine Learning Research 13, 2409-2464.
- Maathuis, M.H., Colombo, D., Kalisch, M. and Bühlmann, P. (2010). Predicting causal effects in large-scale systems from observational data. Nature Methods 7, 247-248.
- Maathuis, M.H., Kalisch, M. and Bühlmann, P. (2009). Estimating high-dimensional intervention effects from observational data. Annals of Statistics 37, 3133-3164.

# SEV-method $\rightsquigarrow \hat{D}$ ; completion to Markov-equivalence class $\rightsquigarrow \mathcal{E}(\hat{D})$



performance of  $\mathcal{E}(\hat{D})$  for true CPDAG