# Causal discovery

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IPL

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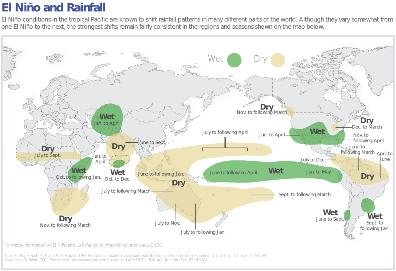

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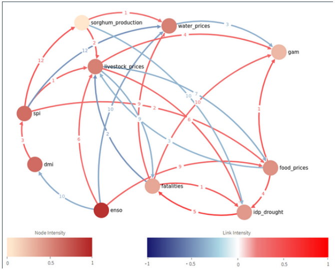

# Causal Discovery

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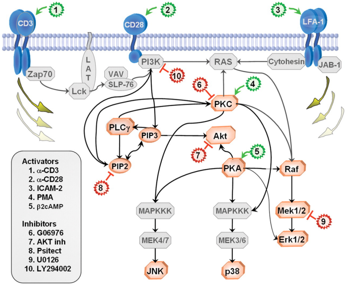
- Which are the causal drivers and the causal relationships involving food insecurity?
- Retrieve the reaction network between genes and proteins from single-cell data



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- it always require assumptions
- can use only observational data, or even interventions
- usually the output is not a complete description of the causal relationships (depends on the assumptions, the type of data etc..)

# Causal discovery methods

- Constrained Based, Score based, Asymmetry based
- Methods for i.i.d. data or for time-series
- Bivariate vs multivariate
- Observational and/or Interventional data

# In this session

- Causal discovery for BN and SCM
- Causal discovery taxonomy
- Some methods
- Examples

We will see only methods that employ observational data ... thus we will need assumptions

# Structural learning for BN

Estimate the structure of a BN from observational data. That is, recovering of $G$ from (i.i.d.) observations sampled from a probability $P$ such that $(G, P)$ is a BN

- it is a model selection problem
- no causality involved (yet)
- Problem: a probability $P$ can be *comaptible* with multiple BN!!

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Using observational data alone, Can we hope to learn something more than the Markov equivalence class?

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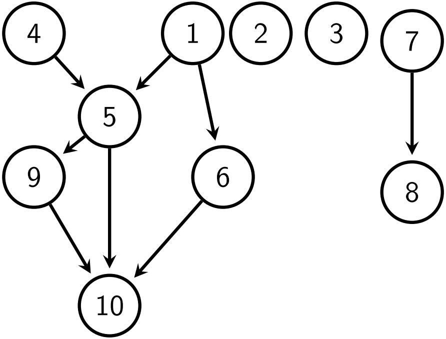


we can represent the Markov equivalence class with a partial directed acyclic graph (PDAG)

# Taxonomy of methods for BN

- Constrained based: PC algorithm

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- Score based or score+search: GES, tabu search, hill-climbing
- hybrid: max-min-hill-climbing (mmhc)

# Constrained based

- Start from the full dependency graph

Glymour et al. [2019], Spirtes et al. [2000]

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# Constrained based

- Start from the full dependency graph
- prune edges by iteratively test (conditional) independences
- use some rules to orient edges
- obtain a PDAG (partial directed acyclic graph) representing the Markov equivalence class

Glymour et al. [2019], Spirtes et al. [2000]

The PC algorithm starts from a fully connected undirected graph and consists of three phases:

1. The *skeleton phase* uses statistical (conditional) independence tests to infer the adjacencies of the underlying causal graph. If two variables $X$ and $Y$ are found to be independent conditional on a (possibly empty) set of variables $\mathbf{Z}$, then the edge between $X$ and $Y$ is removed.
2. The *collider orientation phase* then orients all *collider motifs*, that is, motifs of the form $X \rightarrow Y \leftarrow Z$ where $X$ and $Z$ are non-adjacent. These orientations can be inferred because collider motifs impose a particular pattern of (conditional) (in-)dependencies.
3. The *orientation phase* finally uses graphical rules [Meek, 1995] to infer the orientation of as many remaining unoriented edges as possible using the acyclicity assumption and the fact that all colliders have been found in the previous step.

# Score based

- find the **best scoring graph** with respect to some scoring criteria (e.g. BIC)

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- space of DAGs is huge .... we need heuristic searches
- hill-climbing, tabu search
- GES (greedy equivalent search) in the space of CPDAG (the space of Markov equivalence classes) [under some assumpotions it is proven to recover the true Markov equivalence class]

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- example, Linear non-Gaussian acyclic model (LiNGAM) [Shimizu et al., 2006]

# Time series

- Causal discovery in time series can be *easier* then i.i.d. case
- The *arrow of time* helps in orienting some edges

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- The *arrow of time* helps in orienting some edges
- Granger causality, convergent cross-mapping (CCM), PC-based methods (PCMCI), score-based methods, (VAR)LinGAM, TiMINO, . . .

# Granger causality

## Granger causality

$A(t)$ is linearly Granger-cause of $B(t)$ with respect to a fixed time-lag $m$ if the null hypothesis $\{\alpha_\ell = 0 \,\text{for}\, \ell = 1, \ldots, m\}$ is rejected for the linear AR model

$$B(t) = \sum_{\ell=1}^{m} \beta_\ell B(t-\ell) + \sum_{\ell=1}^{m} \alpha_\ell A(t-\ell) + \beta_0 + \epsilon.$$

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