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Unpaired Multi-Domain Causal Representation Learning Nils Sturma¹, Chandler Squires², Mathias Drton¹, Caroline Uhler²



Setup and Graphical Perspective "Integrate data from different modalities to identify a shared causal representation." Latent: $(Z_h)_{h \in \mathcal{H}}$, where $Z = AZ + \varepsilon$. **Observed:** $X^e \in \mathbb{R}^{d_e}$, where $X^e = G^e \cdot Z_{S_e}$. $\mathcal{H} \supseteq S_e = \mathcal{L} \cup I_e =$ "shared" and "domain-specific" *m*-domain graph: • Nodes $\mathcal{H} \cup V_1 \cup \cdots \cup V_m$, where $|V_e| = d_e$. • Edges in \mathcal{H} encode sparsity in A (acyclic). • Edges from \mathcal{H} to V_e encode sparsity in G^e . • Causal representation: Structural causal model among Z; • No edges from domain-specific to shared latents. **Joint Distribution** Let G be the "large" mixing matrix, that is, $G_{V_e,S_e} = G^e$. **Goal: Identifiability** of shared causal representation in a **linear** setup. X^1 $= G \cdot Z = G \cdot (I - A)^{-1} \cdot \varepsilon =$ $\mathbf{x} X^m$ $B_{V_m,\mathcal{L}}$ • Sufficient and necessary conditions for identifiability of joint distribution. **Approach/ Algorithm:** • Sufficient conditions for identifiability of the shared causal structure. 1. Linear ICA in each domain. 2. Identify shared columns and shared ε_i by matching distributions. 3. Reconstruct B up to unknown (block)-permutation of the columns. **Assumptions: 1)** Error distributions P_i of ε_i are **non-symmetric** and **pairwise different** Example: $(P_i \neq P_j \text{ and } P_i \neq -P_j \ \forall i, j \in \mathcal{H})$. Additionally: non-degenerate, mean Single-cell data in zero, unit variance and independent. biology. 2) The matrix G_{V_e,S_e} is of full column rank for each $e = 1, \ldots, m$. **Theorem:** "B and $P = (P_h)_{h \in \mathcal{H}}$ are identifiable up to signed blockpermutation." ¹Technical University of Munich; Munich Center for Machine Learning ² LIDS, Massachusetts Institute of Technology; Broad Institute of MIT and Harvard MCML MDS





