TOPOLOGY INFEERENCE: ESCAPING THE SPATIAL INDEPENDENCE STRAIGHTJACKET

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MULTICAST TOMOGRAPHY
DEFINITIONS AND NOTATION

- Tree $T = (V, L)$.
- Nodes $V$ labelled $0, \ldots, n$.
- $m$ receivers $R$ at leaves of tree.
**PROBING**

Probes $i=0,1,2,...$

$$0 \rightarrow Z_k(i) \rightarrow X_k(i) \rightarrow X_R$$
**PROBING**

Probes $i=0,1,2,...$

$$X_k(i) = X_{f(k)}(i)Z_k(i)$$

$X_R$
PROBING

- View as vector-valued stochastic process

\[ Z(i) = [Z_1(i), \ldots, Z_n(i)] . \]

- Tree-geometry: node/path state fixed by states of ancestor links:

\[ X_k(i) = \prod_{j \in 0 \rightarrow k} Z_j(i) . \]
• View as vector-valued stochastic process

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• Tree-geometry: node/path state fixed by states of ancestor links:

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**Goal: Topology from Tomography**

• Deduce the topology \( T \) from the distribution of \( X_R = (X_k(i))_{k \in R} \).
• First assume infinite data, address identifiability.
• Then consider inference with finite data.
PREVIOUSLY

SPATIAL AND TEMPORAL INDEPENDENCE (CLASSICAL ASSUMPTIONS)

- Link processes $Z_k(i)$ mutually independent.
- Each an i.i.d. random sequence: $\Pr(Z_k(i) = 1) = l_k$. 
PREVIOUSLY

SPATIAL AND TEMPORAL INDEPENDENCE (CLASSICAL ASSUMPTIONS)

- Link processes $Z_k(i)$ mutually independent.
- Each an i.i.d. random sequence: $\Pr(Z_k(i) = 1) = l_k$.
- Assume $l_k < 1$, else unidentifiable.
**Shared Path to Branch Point**

The diagram illustrates a tree-like structure with nodes labeled as `b(i,j)`, `i`, and `j`. The nodes represent different points in a network, with arrows indicating connections. The text `b(i,j)` likely refers to a specific branch point in the network. The diagram suggests a model where nodes share a common path, possibly indicating a model of spatial dependence or identifiable joint (JI) models. The context of the diagram is related to finding siblings within the network, which might involve statistical or algorithmic methods for identifying related nodes or paths.
**SHARED TRANSMISSION**

- Function of two nodes, \( i, j \):

\[
S(i, j) = \frac{\Pr(X_i = 1)\Pr(X_j = 1)}{\Pr(X_i = 1, X_j = 1)}.
\]

- Under spatial independence

\[
S(i, j) = \Pr(X_b = 1).
\]
**SHARED TRANSMISSION**

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  S(i, j) = \frac{\Pr(X_i = 1)\Pr(X_j = 1)}{\Pr(X_i = 1, X_j = 1)}.
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- Under spatial independence

  \[
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  \]

- Use/need pairwise only $\Rightarrow$ still feasible with finite data.
CHOOSING SIBLINGS

SHARED TRANSMISSION DECREASES DOWN THE TREE

- If \( b(i, j) \) under \( b(i, k) \) then \( S(i, j) < S(i, k) \).
CERTAIN PATERNITY

- Pair(s) of nodes in $B$ with lowest shared transmission are siblings.
- If $J \subset B$ has $S(i, j)$ minimal for each pair $i, j \in B$ then $J$ are siblings.
**Shared Transmission for Virtual Nodes**

- Nodes created by merging siblings are “virtual”.
- Will correspond to real nodes if algorithm successful.
- But how to calculate Shared Transmission for $j \in B \setminus R$?
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- But how to calculate Shared Transmission for $j \in B \setminus R$?
- Define “virtual” losses for $j$ as the sequence

$$\tilde{X}_j = \begin{cases} 
1 & \text{if } X_k = 1 \text{ for any } k \in d(j) \cap R \\
0 & \text{otherwise,}
\end{cases}$$

since know $X_j = 1$ if a transmission seen at any descendant.
**Shared Transmission for Virtual Nodes**

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since know \( X_j = 1 \) if a transmission seen at any descendant.
- Shared transmission defined analogously:

\[
\tilde{S}(i,j) = \frac{\Pr(\tilde{X}_i = 1) \Pr(\tilde{X}_j = 1)}{\Pr(\tilde{X}_i = 1, \tilde{X}_j = 1)}
\]

- \( \tilde{S}(i,j) = S(i,j) \) under classical assumptions!
Red nodes are the working set $B$. 
**Shared Loss Topology Discovery – SLTD**

1. **Input:** Set of receivers $R$; distribution $f_R$, $X_R(i)$.
2. **Variables:** Nodes $V$, Links $L$, Root nodes $B$, $\tilde{X}(i)$.
3. **Initialize:** $V \leftarrow R$; $L \leftarrow \emptyset$; $B \leftarrow R$; $\tilde{X}_R(i) \leftarrow X_R(i)$.
4. while $|B| > 1$ do
5. Calculate $S^* = \max_{\{j,k\} \subset B} \tilde{S}_{j,k}$;
6. Find largest $J \subset B$: $\forall \{j,k\} \subset J$, $\tilde{S}_{j,k} = S^*$;
7. if exists some $i \not\in J, j \in J : \tilde{S}_{i,j} = S^*$ then
8. return $\emptyset$; # sibling set not transitive!
9. else
10. Create new node $v$, set $\tilde{X}_v = \bigvee_{j \in J} \tilde{X}_j$;
11. $V \leftarrow V \cup v$;
12. $L \leftarrow L \cup \bigcup_{j \in J} (v,j)$;
13. $B \leftarrow (B \setminus J) \cup v$;
14. end if
15. end while
16. Create root node 0;
17. $V \leftarrow V \cup 0$;
18. $L \leftarrow L \cup (0,B)$; # $|B| = 1$ here
19. **Output:** $T = (V,L)$;
CHARACTERIZING THE LINK PROCESSES

SPATIAL STRUCTURE

- Assume $\mathbf{Z}(i) = [Z_1(i), \ldots, Z_n(i)]$ stationary and ergodic.
- Spatial dependency captured by the marginal $\mathbf{Z} = [Z_1, \ldots, Z_n]$.
- Induces the path-passage marginal $\mathbf{X} = [X_1, \ldots, X_n]$.
- We are interested in $f_{\mathbf{X}_R}$.
Characterizing the Link Processes

Spatial Structure

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Link Joint Distribution

- Characterise joint distribution $f_{\mathbf{Z}}$ using probabilities

$$\Pr(\mathbf{Z} = \mathbf{r}) = \Pr(Z_1 = r_1, Z_2 = r_2, \ldots, Z_n = r_n),$$

one for each link passage pattern $\mathbf{r} = [r_1, \ldots, r_n] \in \{0, 1\}^n$.
- These sum to 1, so $2^n - 1$ degrees of freedom.
- In contrast: classical case is much simpler, $n$ degrees of freedom.
MODELS versus Topology

**MODELS**

- A topology $T$ with a joint distribution $f_Z$ is a *model* $M = (T, f_Z)$.
- A model $M$ induces a joint distribution $f_R(M)$ on the vector observable $X_R$.
- $T(M)$ is the tree component of the model $M$.
- Goal: to determine $T(M)$ from $f_R(M)$.
Two models $M_1$ and $M_2$ are measurement equivalent if $f_R(M_1) = f_R(M_2)$.

**Example 1:**

Classical with $l_k = 0.9$ for all $k \in V$. 
Two models $M_1$ and $M_2$ are *measurement equivalent* if $f_R(M_1) = f_R(M_2)$.

**Example 1:**

Both models have
\[
\begin{align*}
\Pr(X_1 = 1) &= 0.9^3 \\
\Pr(X_2 = 1) &= 0.9^3 \\
\Pr(X_3 = 1) &= 0.9^2 \\
\Pr([X_1, X_2] = 1_2) &= 0.9^4 \\
\Pr([X_1, X_3] = 1_2) &= 0.9^4 \\
\Pr([X_2, X_3] = 1_2) &= 0.9^4 \\
\Pr(X_R = 1_3) &= 0.9^5.
\end{align*}
\]
MEASUREMENT EQUIVALENCE

Two models $M_1$ and $M_2$ are measurement equivalent if $f_R(M_1) = f_R(M_2)$.

**Example 1:**

Classical with $l_k = 0.9$ for all $k \in V$.

\[
\Pr(Z = z) = \begin{cases} 
0 & \text{if } [z_1, z_2, z_3] = [1, 1, 0] \\
0.9^3 0.1^2 + 0.9^2 - 0.9^3 & \text{if } z = [1, 0, 1, 0, 1] \\
0.9 \sum_i z_i 0.1^5 - \sum_i z_i & \text{otherwise.}
\end{cases}
\]
TOPOLOGY IDENTIFIABILITY

EXAMPLE 1 LESSONS

- Example 1 gave two models with same \( f_R(M) \), different \( T(M) \).
- So in that case, \( T \) is not identifiable.
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- Must restrict $\mathcal{M}$ if we hope to identify $T$ for each $M \in \mathcal{M}$. 
Example 1 Lessons

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- So in that case, $T$ is not identifiable.
- Must restrict $M$ if we hope to identify $T$ for each $M \in \mathcal{M}$.

Topological Determinism

- A class $\mathcal{M}$ is Topologically Determinate if $\exists M_1, M_2 \in \mathcal{M}$ with
  - $f_R(M_1) = f_R(M_2)$, and
  - $T(M_1) \neq T(M_2)$.
- i.e., models with same $f_R$ have same $T$. 
**GOALS (INFINITE DATA CASE)**

- Find “large”, natural Topologically Determinate class(es) $\mathcal{M}$.
- Find algorithm guaranteed to recover $T(M)$ for all $M \in \mathcal{M}$.
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**Example: Classical Models $\mathcal{M}_C$**

- Classical models are Topologically Determinate.
- SLTD works for them.
- In fact, one model per $f_R(M)$, so one model per $T$. 
NEW CLASSES

\[ \mathcal{M}_{\text{AJIE}} \supseteq \mathcal{M}_{\text{CE}} \supseteq \mathcal{M}_{\text{AJI}} \supseteq \mathcal{M}_{\text{C}} \supseteq \mathcal{M}_{\text{JI}} \]
**DIMENSIONS OF NEW CLASSES**

<table>
<thead>
<tr>
<th>Model Class</th>
<th>Dimension</th>
<th>Dimension</th>
<th>Dimension</th>
<th>Dimension</th>
<th>Dimension</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\mathcal{M}_{C,T}$</td>
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<td>6</td>
<td>9</td>
<td>14</td>
<td>29</td>
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<td>15</td>
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<tr>
<td>$\mathcal{M}_{AJIE,T}$</td>
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<td>57</td>
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</tr>
<tr>
<td>$\mathcal{M}_T$</td>
<td>15</td>
<td>63</td>
<td>511</td>
<td>16383</td>
<td>536870911</td>
</tr>
</tbody>
</table>

**TABLE**: Examples of model class dimensions.
**Classically Equivalent Models: $\mathcal{M}_{CE}$**

**Definition**

$M_1 \in \mathcal{M}_{CE}$ iff $\exists M_2 \in \mathcal{M}_C$ with $f_R(M_1) = f_R(M_2)$ and $T(M_1) = T(M_2)$.

These are models that appear classical.
**CLASSICALLY EQUIVALENT MODELS: \( \mathcal{M}_{\text{CE}} \)**

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These are models that appear classical.

**SLTD STILL WORKS!**

- SLTD returns \( T(M) \) correctly for every \( M \in \mathcal{M}_{\text{CE}} \).
  - Returns topology as though \( M \) is classical.
  - \( \therefore \) Returns correct topology.
- So \( \mathcal{M}_{\text{CE}} \) is Topologically Determinate.
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These are models that appear classical.

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  - Returns topology as though \( M \) is classical.
  - \( \therefore \) Returns correct topology.
- So \( \mathcal{M}_{CE} \) is Topologically Determinate.

**Extension trick works in general**

- Can apply for any algorithm and class it works on.
COMMENTS ON $\mathcal{M}_{CE}$

**STRENGTHS**

- $\mathcal{M}_C \subset \mathcal{M}_{CE}$.
- Much larger than $\mathcal{M}_C$.
- Can contain complex spatial dependencies.
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**DRAWBACKS**

- Not constructive.
- Depends on receiver positions.
COMMENTS ON $\mathcal{M}_{CE}$

**STRENGTHS**

- $\mathcal{M}_C \subset \mathcal{M}_{CE}$.
- Much larger than $\mathcal{M}_C$.
- Can contain complex spatial dependencies.

**DRAWBACKS**

- Not constructive.
- Depends on receiver positions.
- Need a model class that:
  - Is not based on receiver positions.
  - Reflects properties of real networks.
PAINLESS GENERALITY

RECALL

- \( X_k = \prod_{i \in (0 \rightarrow k)} Z_k \).
PAINLESS GENERALITY

RECALL

• \( X_k = \prod_{i \in (0 \rightarrow k)} Z_k \).

DEPENDENCY OF HIDDEN Z

• If \( X_i = 0 \) then for all \( k \) below \( i \), \( X_k = 0 \).
PAINLESS GENERALITY

RECALL

- \( X_k = \prod_{i \in (0 \rightarrow k)} Z_k \).

DEPENDENCY OF HIDDEN \( Z \)

- If \( X_i = 0 \) then for all \( k \) below \( i \), \( X_k = 0 \).
- If \( X_{f(i)} = 0 \) then changing the value of \( Z_i \) won’t change the output.
- This suggests a way of adding dependency without affecting \( f_R(M) \).
**Model Principles**

**How does dependency arise?**

- Links touch at routers, influenced by router traffic and dynamics
  – suggests dependencies between siblings.
- Distant links unlikely to affect each other except via tree.
  – suggests ruling out ‘action at a distance’.
MODEL PRINCIPLES

HOW DOES DEPENDENCY ARISE?

- Links touch at routers, influenced by router traffic and dynamics – suggests dependencies between siblings.
- Distant links unlikely to affect each other except via tree. – suggests ruling out ‘action at a distance’.

TRANSLATION TO MODEL PRINCIPLES

- Locally: most general possible dependency between adjacent links.
- Globally: only necessary dependency over non-adjacent links.
**Jump Independence**

**Definition (Jump Independent Models)**

A model with links \( L \) and receivers \( R \) is *Jump Independent* if for all \( k \in V \setminus R \), all \( J \subset V \) with \( J \cap d(k) = \emptyset \), \( X_{c(k)} \) is conditionally independent of \( X_J \) given \( X_k = 1 \).
DEFINITIONS

DEFINITION (SUBTREE INDUCED BY U)

Let \( M(T,f_Z) \in \mathcal{M}_{JI} \) with \( T = (V,L) \). Let \( U \subset V \). Then define the subtree induced by \( U \) as

\[
T(U) = \bigcup_{i \in U} \{0 \to i\}
\]

and \( R(U) \) as the leaves of \( T(U) \).

DEFINITION (\( \rho \)-VALUES)

Define sibling passage probabilities:

\[
\rho_J = \Pr(\cap_{j \in D}\{X_j = 1\} | X_{f(D)} = 1)
\]

for each set of siblings \( D \).
**FUNDAMENTAL PROPERTY OF JI MODELS**

**Lemma (Fundamental Property of JI Models)**

Let $M(T, f_Z) \in \mathcal{M}_{JI}$. Then

$$\Pr(\bigcap_{k \in U} \{X_k = 1\}) = \prod_{i \in T(U) \setminus R(U)} \rho_c(i) \cap T(U)$$

for every $U \subset V$. 
Example: \( U = \{2, 5, 6\} \)
\[
\Pr(X_2 = 1, X_5 = 1, X_6 = 1) = \rho_1 \cdot \rho_{2,3} \cdot \rho_{4,5} \cdot \rho_6
\]
For $i, j \in V$, 

$$
S_{i,j} = \Pr(X_b = 1) \cdot \frac{\rho_1 \rho_2}{\rho_{1,2}}
$$

$$
= \left( \prod_{k \in 0 \rightarrow b} \rho_k \right) \cdot \frac{\rho_1 \rho_2}{\rho_{1,2}}
$$

**Shared Transmission**

- a function
- of the shared path and the two children at the branch point.
For $i,j \in V$,

$$S_{i,j} = \Pr(X_b = 1) \cdot \frac{\rho_1 \rho_2}{\rho_{1,2}}$$

$$= (\prod_{k \in 0 \to b} \rho_k) \cdot \frac{\rho_1 \rho_2}{\rho_{1,2}}$$

Shared Transmission a function of the shared path and the two children at the branch point.
**Binary JI Models**

**Measurement Equivalence**

- Assume $M_1 \in \mathcal{M}_{JI}$ and $M_2 \in \mathcal{M}_C$ with $T(M_1) = T(M_2)$.
- Solve for $l_i$ from $M_2$ in terms of $\rho_J$ from $M_1$.

$$l_i = \begin{cases} 
\frac{\rho_{i,s}(i)}{\rho_s(i)}, & \text{if } i \in R \\
\rho_i \cdot \frac{\rho_{c_1}(i) \rho_{c_2}(i)}{\rho_{c_1}(i,c_2)(i)}, & \text{if } i = 1 \\
\frac{\rho_{i,s}(i)}{\rho_s(i)} \cdot \frac{\rho_{c_1}(i) \rho_{c_2}(i)}{\rho_{c_1}(i,c_2)(i)}, & \text{otherwise.}
\end{cases}$$
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    \end{cases}
\]

**Obtain (Binary) Examples of Models in CE**

- If $l_i < 1$, must be the marginal link passage parameter of the CE model.
- Insight: siblings dependencies compensated by change in transmission on path to father.
IDENTIFIABILITY FAILURE: INVISIBLE PATHS

LEMMA

Let $i, j, k$ be three distinct receivers in a Jump Independent model such that $b(i, k)$ is below $b(i, j)$. Then $S(i, k) = S(j, k)$ if and only if $b(i, j) \rightarrow b(i, k)$ is invisible.
IDENTIFIABILITY FAILURE: INVISIBLE PATHS

**Augmented Path**

- An augmented path \( g(g_1, g_2) \rightarrow h(h_1, h_2) \) is a path \( g \rightarrow h \) together with \( g_1, g_2 \in c(g), \ h_1, h_2 \in c(h) \) such that \( g_1 \in g \rightarrow h \).
IDENTIFIABILITY FAILURE: INVISIBLE PATHS

INVISIBLE PATH

- An augmented path is invisible if

\[ \frac{\rho_{g_1} \rho_{g_2}}{\rho_{g_1,g_2}} = \left( \prod_{i \in g \rightarrow h} \rho_i \right) \frac{\rho_{h_1} \rho_{h_2}}{\rho_{h_1,h_2}}. \]
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• For Binary models this reduces to:

\[ \prod_{i \in g \rightarrow h} l_i = 1. \]

• Analogue of \( l_k \neq 1 \) from classical.
IDENTIFIABILITY FAILURE: LOCAL STRUCTURE

LOCAL LIMITATIONS ON ANY SIBLING SET $J$

- **Internally agreeing** if $S_{i,j} = S_{k,l}$ $\forall i,j,k,l \in J$ with $i \neq j$, $k \neq l$.
- **Internally disagreeing** if $S_{i,j} \neq S_{k,l}$ $\forall i,j,k,l \in J$ with $\{i,j\} \neq \{k,l\}$. 
IDENTIFIABILITY FAILURE: LOCAL STRUCTURE

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ROLES

- Disagreeing is the generic/general case.
- Agreeing includes classical.
**AGREEABLE JI MODELS**

**Definition (AGREEABLE JI MODELS ($\mathcal{M}_{\text{AJI}}$))**

An AJI model is a model $M \in \mathcal{M}_{\text{JI}}$ which satisfies:

1. (internally consistent) Each sibling set $J$ is agreeing or disagreeing.
2. (no invisible paths) No augmented paths in $M$ are invisible.
AGREEABLE JI MODELS

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ROLE OF RESTRICTIONS

- Condition (i) prevents sibling sets from looking like they aren’t.
- Condition (ii) prevents groups of non-siblings from looking like they are siblings.
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Including ‘agreeing’ in (i) a big headache, but important!
A PROPERTY OF SIBLINGS IN JI MODELS

Lemma (Siblings Agree Externally)

Let $M \in \mathcal{M}_{JI}$. If two nodes $i, j$ are members of a sibling set $J$, and $k \in R$ such that $(0 \to k) \cap J = \emptyset$, then $S_{i,k} = S_{j,k}$.


**SEEKING CERTAIN PATERNITY**

**TRY TO INVERT SIBLING PROPERTY**

- Define agreement set of $i, j \in V$

\[ A_{i,j} = \{ k \in R : S(i, k) = S(j, k), k \neq i, j \}. \]

- Agreement sets used to compare ‘world view’ of candidate siblings.
**FINDING COMPLETE SIBLING SETS**

**Definition (Externally-agreeing sets)**

Call $D \subset R$ an *externally-agreeing set* (EAS) if $|D| \geq 3$ and $A_{i,j} = R \setminus D$ for all $i, j \in D$. 
**Finding Complete Sibling Sets**

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Call $D \subset R$ an *externally-agreeing set* (EAS) if $|D| \geq 3$ and $A_{i,j} = R \setminus D$ for all $i, j \in D$.

**Definition (All-agreeing sets)**

Call $D \subset R$ with $|D| \geq 2$ an *all-agreeing set* (AAS) if $A_{i,j} = R \setminus \{i, j\}$ for all $i, j \in D$.

Subsets of an all-agreeing set are also all-agreeing. Call an all-agreeing set $D$ a *maximal all-agreeing set* (MAAS) if it is not a proper subset of another one.
**Finding Complete Sibling Sets**

**Lemma (Finding disagreeing sibling sets)**

Consider $M \in \mathcal{M}_{\text{AJI}}$ with receiver nodes $R$. A set $D \subset R$ with $|D| \geq 3$ is an disagreeing sibling set if and only if it is an EAS.
**Finding Complete Sibling Sets**

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**Lemma (Finding agreeing sibling subsets)**

Consider $M \in \mathcal{M}_{\text{AJI}}$ with receiver nodes $R$. A set $D \subset R$ with $|D| \geq 2$ is a subset of an agreeing sibling set if and only if it is an AAS.

- The MAAS are the maximal agreeing sibling subsets.
- Some/all of these may still have hidden siblings.
**Proposition (Certain Paternity II)**

Assume an $M \in \mathcal{M}_{\text{AJI}}$ model. Then at least one available sibling set can be identified without error.

**Proof**

- Find all the EAS and AASes
Case 1: At least one EAS exists

Select any of them.
CASE 2: no EAS exists

Select a MAAS which is a sibling set (can test if one below another).
SLTD2

Similar to SLTD, but agreement set based.
SLTD2

Similar to SLTD, but agreement set based.

**Theorem (Correctness of SLTD2 on \( \mathcal{M}_{\text{AJI}} \))**

Let \( M = (T, f_Z) \in \mathcal{M}_{\text{AJI}} \). Then SLTD2 returns \( T \).
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**Proof**

- Find sibling set using Certain Paternity.
- \( S(i, j) = \tilde{S}(i, j) \) for \( M \in \mathcal{M}_{\text{JI}} \).
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**Proof**

- Find sibling set using Certain Paternity.
- $S(i, j) = \tilde{S}(i, j)$ for $M \in \mathcal{M}_{\text{JI}}$.
- So each iteration will be correct.
- Hence recover $T$ at termination.
AJIE MODELS

- Defined analogously to $M_{CE}$, but start with $M_{AJI}$ instead of $M_{C}$. 
AJIE MODELS

- Defined analogously to $\mathcal{M}_{CE}$, but start with $\mathcal{M}_{AJI}$ instead of $\mathcal{M}_{C}$.
- $\mathcal{M}_{CE} \subset \mathcal{M}_{AJIE}$, since $\mathcal{M}_{C} \subset \mathcal{M}_{AJI}$.
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- $\mathcal{M}_{CE} \subset \mathcal{M}_{AJIE}$, since $\mathcal{M}_{C} \subset \mathcal{M}_{AJI}$.
- SLTD2 succeeds on all topologies in $\mathcal{M}_{AJIE}$. 
RELATIONSHIPS BETWEEN CLASSES

\[ M_{\text{AJIE}} \]

\[ M_{\text{CE}} \]

\[ M_{\text{AJI}} \]

\[ M_{\text{JI}} \]

\[ M_{\text{C}} \]
### Dimensions of Classes

<table>
<thead>
<tr>
<th>Model Class</th>
<th>dim($\mathcal{M}_{C,T}$</th>
<th>dim($\mathcal{M}_{CE,T}$)</th>
<th>dim($\mathcal{M}_{JI,T}$)</th>
<th>dim($\mathcal{M}_{AJI,T}$)</th>
<th>dim($\mathcal{M}_{AJIE,T}$)</th>
<th>dim($\mathcal{M}_T$)</th>
</tr>
</thead>
<tbody>
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<td>536613988</td>
<td>15</td>
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<tr>
<td>$\mathcal{M}_{AJI,T}$</td>
<td>15</td>
<td>56</td>
<td>478</td>
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<td>536613988</td>
<td>15</td>
</tr>
<tr>
<td>$\mathcal{M}_{AJIE,T}$</td>
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<td>57</td>
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<tr>
<td>$\mathcal{M}_T$</td>
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<td>511</td>
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<td>536870911</td>
<td>15</td>
</tr>
</tbody>
</table>

**Table**: Examples of model class dimensions.
INFINITE DATA SUMMARY

PREVIOUS WORK

- Classical model: full spatial independence of tree loss process.
- Algorithm SLTD to recover topology in this case.
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- Define class $\mathcal{M}_{JI}$ with physically motivated structure.
- Find TD class $\mathcal{M}_{AIJ}$ with $\dim(\mathcal{M}_{AIJ}) = \dim(\mathcal{M}_{JI})$. 
Infinite Data Summary

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- Break spatial independence assumptions.
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- Define class $\mathcal{M}_{\text{JI}}$ with physically motivated structure.
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- New algorithm SLTD2 recovers topology for all $M \in \mathcal{M}_{\text{AJI}}$. 
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- Classical model: full spatial independence of tree loss process.
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- Break spatial independence assumptions.
- Define more general class $\mathcal{M}_{CE}$ such that SLTD still works.
- General result for extending class while keeping algorithm.

- Define class $\mathcal{M}_{JI}$ with physically motivated structure.
- Find TD class $\mathcal{M}_{AJI}$ with $\dim(\mathcal{M}_{AJI}) = \dim(\mathcal{M}_{JI})$.
- New algorithm SLTD2 recovers topology for all $M \in \mathcal{M}_{AJI}$.
- Also recovers topology for all $M \in \mathcal{M}_{AJIE}$.
CHALLENGES FOR FINITE DATA

- Underlying $S_{ij}$ not known, only estimated.
- Failure of exact $S_{ij}$ equality underlying agreement set definition.
- Random topology selection in $\mathcal{M}_{\text{AJI}}$, with degree constraints.
- Random model selection, with loss constraints.
- Sensible error metric on trees.
A SLTD Based Algorithm

Modified Iteration

- Estimate shared transmission over all pairs
  \[ \hat{S}_{ij} = \frac{\sum X_i/n_p \sum X_j/n_p}{\sum X_iX_j/n_p}. \]
  
- Merge \( i, j \) into \( J^* = (ij) \) with minimal \( \hat{S}_{ij} \).
- Merge additional receivers \( k \) in \( J^* \) obeying (we use \( \beta = 0.002 \))
  \[ \hat{S}_{(ij)k} \leq (1 + \beta)\hat{S}^*. \]

Straightforward because key steps based on inequality of \( \hat{S}_{ij} \).
MEASURING APPROXIMATE AGREEMENT

THREE STEPS TO MEASURE AGREEMENT OF J TO A

(i) shared passage measure $p_{k;ij}$ ($|J| = 2$ and $|A| = 1$);
(ii) agreement set measure $g_{ij}(A)$ ($|J| = 2$ and $|A| \geq 1$);
(iii) sibling set measure $r_A(J)$ ($|J| \geq 2$ and $|A| \geq 1$).
MEASURING APPROXIMATE AGREEMENT

STEP (I): SHARED PASSAGE MEASURE $p_{k;ij}$  

(\mid J \mid = 2 \text{ AND } \mid A \mid = 1)

Let $p_{k|i} = \Pr(X_k = 1|X_i = 1)$.

From the definition, $S_{ik} = S_{jk}$ equivalent to $p_{k|i} = p_{k|j}$.
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From the definition, $S_{ik} = S_{jk}$ equivalent to $p_{k|i} = p_{k|j}$.

Estimate $p_{k|i}$ by

$$\hat{p}_{k|i} = \frac{\sum (X_k X_i)}{n_i}.$$
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STEP (I): SHARED PASSAGE MEASURE $p_{k;ij}$  
($|J| = 2$ AND $|A| = 1$)

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Estimate $p_{k|i}$ by

$$\hat{p}_{k|i} = \sum (X_kX_i)/n_i.$$  

Null hypothesis: $p_{k|i} = p_{k|j}$.

Under H0 $\hat{p}_{k|} = (n_i\hat{p}_{k|i} + n_j\hat{p}_{k|j})/(n_i + n_j)$

Test statistic: $T_{ij}(k) = \frac{\hat{p}_{k|i} - \hat{p}_{k|j}}{\sqrt{\frac{n_i+n_j}{n_in_j}\hat{p}_{k|}(1 - \hat{p}_{k|})}}$

with corresponding (Gaussian based) $p$-value $p_{ij} \in [0, 1]$.

Higher $p_{ij} \implies$ higher agreement.
**MEASURING APPROXIMATE AGREEMENT**

**STEP (II): AGREEMENT SET MEASURE** $g_{ij}(A)$  
($|J| = 2$ AND $|A| \geq 1$)

Let $A \subset B \setminus \{i,j\}$, and select a significance level $\alpha$. 

Note the good proportion, $g_p$, of the $p(k)$ obeying $p(k) > \alpha$, $k \in A$. 

(Avoids using $p$-value as a weight – bad idea)

Note worst agreement: $g_w = \min_{k \in A} p(k)$. 

(for $g_p$ and $g_w$, higher values $\Rightarrow$ closer agreement)

Define $g_{ij}(A) = g_p$, using $g_w$ to break ties. 

In other words, agreement follows the worst case in $A$. 

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**Step (iii): Sibling Set Measure** $r_A(J)$ \hfill ($|J| \geq 2$ AND $|A| \geq 1$)

Assume $A \subset B \setminus J$.

To define $r_A(J)$, must combine the values of $g_{ij}(A)$ for all $\{i,j\} \in J$. 

Notes:

- $r_A(J) = g(A)$ whenever $|J| = 2$ such as in binary trees.
- Typically $A = B \setminus J$ in which case we write simply $r(J)$. 

Measuring Approximate Agreement

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Define $r_A(R) \in [0, 1]$ as the smallest such average.

(signature of bad leaves won’t be diluted)
Measuring Approximate Agreement

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Inspired by SLTD2, tries to use $r(J)$ to identify the MAAS and EAS.
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LOCATING AN EAS

Infeasible to search for highest $r(J)$ at each iteration – too many $J$. 

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Infeasible to search for highest $r(J)$ at each iteration – too many $J$.

**Greedy alternative:** construct a subset of $J$’s likely to contain the EASes

- Set seed $J_1 = \{i,j\}$, record $r(J_1)$.
- $J_2 = J_1 \cup \{k_d\}$, where $k_d \in B \setminus J_1$ is the leaf that **minimizes** $r_{\{k\}}(J_1)$ – invite most disagreeable member outside of $J$ to join $J$.
- For each of $\binom{m}{2}$ seeds, get a sequence of $|B| - 1$ candidates EAS $J$ sets.
- Select $J^*$ with the highest agreement $r(J)$.
- Termination step: (needed since above gives $|J| \leq |B| - 1$)
  
  Set $J = B$ if $|J^*| = |B| - 1$, AND if $r(J) > \alpha$ for all $J$ of size $|J| = |B| - 1$. 


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LOCATING A COMPLETE MAAS

Try to assemble set with highest internal agreement based on sibling transitivity.

- Order all seed $J$’s according to their $r(J)$: $r(J_1) \leq r(J_2) \leq r(J_3) \leq$ etc.
- Initialize $J^* = J_1$.
- If $J^* \cap J_2 \neq \emptyset$, set $J^* = J^* \cup J_2$ and continue, else stop.
Inspired by SLTD2, tries to use $r(J)$ to identify the MAAS and EAS.

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**Finally:** from candidate EAS and MAAS, select one with highest $r(J)$.
Want to constrain maximum node degree $d_{\text{max}}$:

- gives spectrum of error modes.
- includes binary special case.
**RANDOM TOPOLOGY GENERATION**

Want to constrain maximum node degree \( d_{\text{max}} \):
- gives spectrum of error modes.
- includes binary special case.

**Generation Method:**
- Pseudo-uniform bottom up algorithm with \( d_{\text{max}} \) constraint.
- Working on fast approach for true uniform generation.
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**Test cases**

<table>
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<tr>
<th>$d_{\text{max}}$</th>
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<th>7</th>
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<td></td>
<td></td>
<td>✓</td>
</tr>
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</table>

**Table:** The $(m, d_{\text{max}})$ used in model generation.
**Random Spatial Dependence Generation**

Want to sample from $\mathcal{M}_{\text{AJJ}}(T)$. 
Want to sample from $\mathcal{M}_{\text{AJI}}(T)$.
Main task is to select the joint sibling distributions.
Need to add constraints to allow scenario control.
**RANDOM SPATIAL DEPENDENCY GENERATION**

Want to sample from $\mathcal{M}_{\text{AJI}}(T)$.

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Need to add constraints to allow scenario control.

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– Select loss marginal targets for each sibling set.
– Express constraints as a matrix equation defining a subset of $\mathcal{M}_{\text{JI}}$.
– Use MCMC (R.L. Smith ’84) method to sample uniformly.
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Compose sibling set samples according to global JI model rules.
Resulting model-sample is in $\mathcal{M}_{\text{AJI}}(T)$ with probability 1.
Tree Distance / Error

Want to define distance between $T_1 = (V_1, L_1)$ and $T_2 = (V_2, L_2)$, sharing the same labelled receivers $R$, with $m = |R|$. 
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(leaf based equivalent tree description)

Let $V_{1\setminus 2} = \{v \in V_1 | \nexists u \in V_2 \text{ with } R(v) = R(u)\}$.

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**Definition:**

$$\text{dist}(T_1, T_2) = |V_{1\setminus 2}| + |V_{2\setminus 1}|$$

This is a true distance metric, taking values in $\{0, 1, \ldots, 2(m - 2)\}$. 
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**Error:**

$$e_T = \text{dist}(T, \hat{T})$$
PERFORMANCE UNDER ‘GENTLE MODELS’

Low Loss Regime: \( \rho_i \in [0.9, 0.99] \) for each node \( i \).

(errors averaged over 200 random models for each fixed \( T \), and 6000 probes)
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(errors averaged over 200 random models for each fixed \( T \), and 6000 probes)

**Binary trees: samples** **Classically Equivalent** \( \implies \) SLTD, TrueTree legal.

If \( d_{\text{max}} > 2 \): TrueTree legal (model in \( M_{\text{AJI}} \)), but SLTD behaviour undefined.
**PERFORMANCE UNDER ‘GENTLE MODELS’**

**Low Loss Regime:** \( \rho_i \in [0.9, 0.99] \) for each node \( i \).
PERFORMANCE ON DISRUPTIVE MODELS

Low Hot Spot scenario: single model with negative dependency.

(errors averaged over 200 random models for each fixed $T$, and 6000 probes)
**PERFORMANCE ON DISRUPTIVE MODELS**

**Low Hot Spot scenario:** single model with negative dependency.

![Graph showing performance comparison between SLTD and TrueTree](image)

(errors averaged over 200 random models for each fixed $T$, and 6000 probes)

SLTD has worst possible $e_T = 2$ in 100% of cases.
TrueTree has $e_T = 0$ in 100% of cases.
Agreement sets great in theory, tricky in practice, but can be done.

*TrueTree*
- gives comparable results to SLTD on gentle loss.
- can handle disruptive loss.
- outperforms SLTD when loss higher.

More work to be done, but promise of SLTD2 on rich class of spatial models can be realized.