Matroid Applications in Phylogenetic Algebraic Geometry

Studying the generic identifiability of 2-mixture phylogenetic models via their algebraic matroids.

Miłosz Szymański

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Acknowledgements

1 Introduction

The goal of this project is to investigate the generic identifiability algorithm presented in *Hollering & Sullivant* [1]. In that paper the authors describe how to each variety a corresponding algebraic matroid can be associated, specifically how to each join variety that arises from a phylogenetic mixture model we can associate the corresponding algebraic matroid. The idea is then to study these matroids to deduce generic identifiability of the mixture models. An algorithm is developed which confirms whether two algebraic matroids are different or not, from which we can obtain identifiability results between a pair of mixture models. Using the algorithm, *Hollering & Sullivant* are able to prove generic identifiability of the tree parameters for 2-mixture CFN and K3P models on six leaves, and together with the *Six-To-Infinity* Theorem this allows them to prove identifiability for 2-mixture CFN and K3P models on at least six leaves.

In this paper, we aim to study Algorithm 3.3 in detail by picking an explicit example of a 2-mixture CFN models on six leaves and showing how the algorithm operates explicitly on them. Rather than computing the defining ideals of the join varieties of these models to obtain the algebraic matroids, which would include computationally expensive Groebner basis calculations, we instead use results from matroid theory to obtain related linear matroids. We can then work with these linear matroids to more efficiently establish generic identifiability between two phylogenetic 2-mixture models. *Hollering & Sullivant* also mention a pair of 2-mixture CFN models on six leaves for which the algorithm fails to distinguish the associated matroids, and they conjecture that the associated matroids are actually equal. Time permitting, we would like to investigate more thoroughly why the algorithm breaks down for this pair of models and attempt to calculate the associated algebraic matroids to comment on the conjecture.

2 Preliminaries I: Phylogenetic Models

Before proceeding to more detailed explanations, we should first review some definitions and concepts which come up in the *Hollering & Sullivant* paper.

Definition 1. *Statistical Model* [[2] *Definition 5.1.1*]
*A **statistical model** $\mathcal{M}$ is a collection of probability distributions or density functions. A **parametric statistical model** $\mathcal{M}_\Theta$ is the image of the mapping from a finite-dimensional parameter space $\Theta \subseteq \mathbb{R}^d$ to a space of probability distributions or density functions, i.e.*

$$p_\bullet : \Theta \to \mathcal{M}_\Theta, \ \theta \to p_\theta.$$

Alternatively we may write $\mathcal{M}_\Theta = \{p_\theta : \theta \in \Theta\}$.

Definition 2. *Identifiability.*
*A parametric statistical model $\mathcal{M}_\Theta = \{p_\theta : \theta \in \Theta\}$ is **identifiable** iff the mapping $p_\bullet$ (as in Definition 1) is injective.*

Intuitively, if we are given enough data so that we can estimate a particular probability distribution p_θ arising from an identifiable parametric statistical model, then we can uniquely determine the parameters θ so that $p_\bullet(\theta) = p_\theta$.

Example 3. *Let's consider the parametric statistical model of a Bernoulli random variable. For this example we define $p_\bullet(r) = f(r, k) = r^k(1-r)^{1-k}$, where $k \in \{0, 1\}$. Hence for a specific choice of r (probability of success) we obtain a probability mass function $f(r, k)$. Note that here $\Theta = [0, 1]$, and so we see that the parametric statistical model can also be written as $\mathcal{M}_\Theta = \{f(r, k) : r \in [0, 1]\}$. Moreover, note that this is an identifiable model since if for $r, s \in [0, 1]$ we have $r^k(1-r)^{1-k} = s^k(1-s)^{1-k}$ for all $k \in \{0, 1\}$ then crucially for $k = 1$ we have,*

$$r = r^1(1-r)^0 = f(r, 1) = f(s, 1) = s^1(1-s)^0 = s.$$

Definition 4. *Phylogenetic Tree*
*A **phylogenetic tree** is an n-leaf tree $T = (V, E)$ whose leaves are labelled by the elements of the set $[n]$, where $n \in \mathbb{N}$. That is, if $L \subset V$ denotes the set of leaves then we have a bijection $\phi : [n] \to L$ which effectively labels all elements of L.*
*A **binary** phylogenetic tree T is a phylogenetic tree in which every internal vertex has degree three.*
*A **rooted** phylogenetic tree T is a phylogenetic tree with a distinguished internal vertex, which we typically label as r and refer to as the "root" of the tree.*

In the *Hollering & Sullivant* paper the authors focus there attention on binary phylogenetic trees, and we will do the same in this report.

Definition 5. *Phylogenetic Model*
*A **phylogenetic model** is a Markov Model on a rooted phylogenetic tree T so that to each vertex $v \in V$ we associate a random variable X_v which takes one of possible κ states which we collect into the set C, where $\kappa \in \mathbb{N}$. That is, for each vertex v, $X_v \in C = \{g_1, \dots, g_\kappa\}$ where g_i denotes the i-th state the random variables can take in the Markov model. To each edge $(s, t) = e \in E$ we associate a $\kappa \times \kappa$ transition matrix M_e such that $M_{ij} = \mathbb{P}(X_t = g_j \mid X_s = g_i)$. Finally we attach some distribution to the root of the tree T which we denote as π and we orient the edges so that travelling along an edge always takes us further away from the root r.*

Remark 6. *The entries of the transition matrices M_e and of the root distribution π are commonly referred to as **continuous parameters** and the phylogenetic tree T is commonly referred to as the **tree parameter** of the phylogenetic model. We will also adopt this convention and use these terms to refer to both types of parameters.*

Example 7. *Let's take the tree $T = K_{1,3}$, the claw tree on three leaves, declare the vertex of degree 3 to be the root, and label the leaves by elements of $[3]$. Additionally, let's associate to each vertex $v \in V$ a random variable X_v which takes values in the set $G = \{0, 1\}$, and to each edge $e \in E$ let's associate a 2×2 symmetric transition matrix M_e such that $(M_e)_{00} = e_0$ and $(M_e)_{01} = e_1$, and let's place the uniform distribution on the root r, i.e. $\pi = (1/2, 1/2)$. Then all this information combined defines a phylogenetic model on the claw tree $K_{1,3}$. In fact, this is an example of a group-based model, the CFN-model to be precise, which is a special class of models for which the transition matrices inherit the structure of some underlying group. We will define group-based models formally in due course.*

Phylogenetic models allow us to study the evolutionary relationships between species. Given n species we may propose a certain phylogenetic model comprising of an n-leaf phylogenetic tree T, a root distribution π and transition matrices M_e for each edge e, as a possible model of the evolutionary relationship between the species. We may then write down all the possible probability distributions of genes/amino acids/traits that we would expect to observe amongst the n species assuming that the

phylogenetic model does indeed capture the true nature of the evolutionary history. Comparing this collection of probability distributions to the empirically observed probability distribution allows us to decide whether the proposed model is indeed a good model.

Example 8. *Taking the phylogenetic model from Example 7, we now explain how to express the probability of observing a collection of states at the leaves.*

As the figure above suggests, we adopt the convention that the edges of the phylogenetic model be labelled by lowercase letters from the start of the Latin alphabet, hence given the assumptions presented in Example 7 we may write down the transition matrices as for each edge as,

$$M_a = \begin{pmatrix} a_0 & a_1 \\ a_1 & a_0 \end{pmatrix} \qquad M_b = \begin{pmatrix} b_0 & b_1 \\ b_1 & b_0 \end{pmatrix} \qquad M_c = \begin{pmatrix} c_0 & c_1 \\ c_1 & c_0 \end{pmatrix} \qquad (1)$$

Now, say we wish to calculate $\mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1)$. We begin from the root of the tree and use the law of total probability to condition on the state of X_r which will either be 0 or 1. We can write this as follows:

$$\mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1)$$
$$= \mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1 \mid X_r = 0)\mathbb{P}(X_r = 0)$$
$$+ \mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1 \mid X_r = 1)\mathbb{P}(X_r = 1),$$

next we can use the fact that the changes of states along the edges are independent events to further simplify the above expression,

$$\mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1)$$
$$= \mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1 \mid X_r = 0)\mathbb{P}(X_r = 0)$$
$$+ \mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1 \mid X_r = 1)\mathbb{P}(X_r = 1)$$
$$= \mathbb{P}(X_1 = 0 \mid X_r = 0)\mathbb{P}(X_2 = 0 \mid X_r = 0)\mathbb{P}(X_3 = 1 \mid X_r = 0)\mathbb{P}(X_r = 0)$$
$$+ \mathbb{P}(X_1 = 0 \mid X_r = 1)\mathbb{P}(X_2 = 0 \mid X_r = 1)\mathbb{P}(X_3 = 1 \mid X_r = 1)\mathbb{P}(X_r = 1),$$

and finally we can read of each of the individual transition probabilities in the product off the corresponding transition matrices in Equation 1 and use the root distribution to obtain the probabilities for the root states to obtain,

$$\mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1)$$
$$= \mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1 \mid X_r = 0)\mathbb{P}(X_r = 0)$$
$$+ \mathbb{P}(X_1 = 0, X_2 = 0, X_3 = 1 \mid X_r = 1)\mathbb{P}(X_r = 1)$$
$$= \mathbb{P}(X_1 = 0 \mid X_r = 0)\mathbb{P}(X_2 = 0 \mid X_r = 0)\mathbb{P}(X_3 = 1 \mid X_r = 0)\mathbb{P}(X_r = 0)$$
$$+ \mathbb{P}(X_1 = 0 \mid X_r = 1)\mathbb{P}(X_2 = 0 \mid X_r = 1)\mathbb{P}(X_3 = 1 \mid X_r = 1)\mathbb{P}(X_r = 1)$$
$$= \frac{1}{2}a_0 b_0 c_1 + \frac{1}{2}a_1 b_1 c_0.$$

We will denote this probability as p_{000} and from now on we write $p_{g_i g_j g_k}$ as a shorthand for $\mathbb{P}(X_1 = g_i, X_2 = g_j, X_3 = g_k)$.

Remark 9. *Hopefully the reader can see how the shorthand above can be extended to phylogenetic models on trees with n leaves. From now on we will write $p_{g^{(1)}g^{(2)}\ldots g^{(3)}}$ to denote $\mathbb{P}(X_1 = g^{(1)}, X_2 = g^{(2)}, \ldots, X_n = g^{(n)})$. Note how the superscripts on the g's refer to the state observed at a particular leaf (so $g^{(i)}$ is the state observed at leaf i) rather than denoting a power or anything else.*

We observe that p_{000} is a polynomial in terms of the continuous parameters. Repeating the procedure above for all possible combination of states we may observe at the leaves we get a total of 8 polynomials. The idea behind Phylogenetic Algebraic Geometry is to study the variety defined by the vanishing of these polynomials using techniques from the field of Algebraic Geometry in order to study the phylogenetic model itself. Instead of providing an exposition to the field of Algebraic Geometry, we direct the curious reader to the excellent notes by *Gathmann*[3] which provide a good introduction to, and overview of, the subject.

More precisely, given a phylogenetic model on an n-leaf phylogenetic tree T, we may specify a map $\psi : \Theta_T \to \Delta_{\kappa^n-1}$ from the space of continuous parameters Θ_T to the space of probabilities of all possible combinations of states at the leaves which sit inside the simplex Δ_{κ^n-1}. Note that there are κ^n possible combinations of states at the leaves of the phylogenetic model we may observe, however since these represent probabilities we know that they must sum to one, that is,

$$\sum_{(g^{(1)},\ldots,g^{(n)})\in C^n} p_{g^{(1)},\ldots,g^{(n)}} = 1$$

and hence having determined $\kappa^n - 1$ probabilities we may determine the last remaining probability. We collect the above into a definition:

Definition 10. *Parametrisation Maps & V_T*
Consider a phylogenetic model on an n-leaf phylogenetic tree T, and denote by Θ_T the space of its continuous parameters and let Δ_{κ^n-1} denote the simplex with dimension $\kappa^n - 1$. Then the polynomials $p_{g^{(1)},\ldots,g^{(n)}}$ in terms of the continuous parameters define a polynomial map,

$$\psi_T : \Theta_T \to \Delta_{\kappa^n-1}$$

*which we refer to as the **parametrisation map** of the model. We define $V_T = \overline{\psi(\Theta_T)}$ to be the associated variety obtained by taking the Zariski closure of the image of the map ψ_T. Alternatively we may consider the ideal generated by the polynomials $p_{g^{(1)},\ldots,g^{(n)}}$, denoted I_T, and define $V_T = \mathbb{V}(I_T)$ as the vanishing locus of the ideal I_T. Each point $p \in V_T$ specifies a possible probability distribution of the states observed at the leaves of the model.*

To distinguish which probability distribution can arise from certain phylogenetic models, we may compare the associated varieties see how they differ. The way we distinguish these varieties is through phylogenetic invariants, which we define below.

Definition 11. *Phylogenetic Invariants*
*For a phylogenetic model on a phylogenetic tree T with n leaves, a **phylogenetic invariant** is a polynomial which is in the ideal I_T generated by the polynomials $p_{g^{(1)}\ldots g^{(n)}}$.*

The importance of phylogenetic invariants comes from the fact that they help to distinguish between different types of trees our models contain, i.e. if I have T and T', two potential phylogenetic trees, and the varieties of phylogenetic models defined on those trees are denoted by V_T and $V_{T'}$ respectively,

then if there exists a polynomial f such that it is contained in one vanishing ideal but not both, then $T \neq T'$. After we distinguish the particular tree parameter, (if the model is identifiable given the choice of tree) then by observing enough data we can infer the values of the parameters $\theta \in \Theta$ in the phylogenetic model.

Now we briefly turn our attention to the tree parameters of phylogenetic trees. We wish to succinctly write down the tree parameter T which consists of the tree topology and the leaf-labelling, and the way to do this will involve the notion of a valid split, which we define below.

Definition 12. *(Valid) Splits:* *Given a phylogenetic tree T on n leaves, a split is a set bipartition of the labelling set $[n]$ into two sets A and B, commonly written down as $A|B$. A split $A|B$ is valid (aka compatible) if there exists an edge $e \in E$ such that the two connected components of $T \setminus e$ have leaf-sets A and B. The set of splits of the tree T is denoted by $\Sigma(T)$.*
A split $A|B$ is non-trivial if $A|B$ is a valid split and the associated edge $e \in E$ is an internal edge of the phylogenetic tree T. We will denote the set of all non-trivial splits on the tree T by $\Sigma^*(T)$.

It has been shown in *Sullivant* [2] that the tree parameter of any binary phylogenetic tree is completely recovered from its set of splits. Therefore two phylogenetic models have the same tree parameters T_1 and T_2 if they have the same set of splits. Moreover, since the set of splits of any phylogenetic tree T will contain all possible trivial splits, it suffices to know only the non-trivial splits to recover the tree parameter. Crucially for us, this means that we can label the edges by the splits that they induce.

For example, below is a picture of two trees which have the same set of splits, that being $\Sigma(T) = \{1|23, 2|13, 3|12\}$, and therefore have the same tree parameters:

Remark 13. *Split Notation*
Note that given a split $A|B$, it can be denoted by either specifying the set A, in which case $B = [n]\backslash A$, or specifying the set B, in which case $A = [n]\backslash B$. Since it only suffices to specify one set to denote the split, we adopt the convention of denoting the split by the smallest set in the partition when it's clear from the context what is the set of leaves. Hence the split $14|235$ will be denoted as 14 for example.

Hopefully the reader can see that not every split of the leaf set $[n]$ is a valid split for a given phylogenetic tree T. Furthermore, we could be presented with two splits $A_1|B_1$, $A_2|B_2$ which are valid splits for a pair of trees T_1 and T_2 respectively, however for which there doesn't exist a phylogenetic tree T such that $A_1|B_1, A_2|B_2 \in \Sigma(T)$. Such a pair of splits is *incompatible*, and analogously if such a tree T exists then we call such a pair of splits *compatible*. We capture this concept in the following definition

Definition 14. *Compatible Splits (1)*
Let $A_1|B_1, A_2|B_2$ be two splits of the leaf set $[n]$. If their exists an n-leaf phylogenetic tree T such that $A_1|B_1, A_2|B_2 \in \Sigma(T)$, then $A_1|B_1, A_2|B_2$ are compatible.

There's an analogous definition of split compatibility which is more useful when reasoning about splits of phylogenetic trees, but which might at first seem a bit abstract. This definition is due to *Semple & Steel*, and is given below:

Definition 15. *Compatible Splits (2)*[Definition 3.1.3 [4]]
A pair of splits $A_1|B_1, A_2|B_2$ of the leaf set $[n]$ are compatible if at least one of the sets $A_1 \cap A_2$, $A_1 \cap B_2$, $B_1 \cap A_2$ and $B_1 \cap B_2$ is empty.

In this project we wish to focus on particular class of phylogenetic models called **group-based models**.

Definition 16. *Group-Based Models*
*Let G be a finite abelian group of order κ and T a rooted phylogenetic tree. Then a **group-based model** on T is a phylogenetic Markov model on T with a uniform root distribution such that for each transition matrix M_e, there exists a function $f_e : G \to \mathbb{R}$ such that $(M_e)_{g,h} = f(g - h)$.*

The structure of group-based models allows for a linear change of coordinates using the Discrete Fourier Transform, which transforms ψ_T into a monomial map. This is desired as the associated variety V_T becomes a toric variety, which is easier to work with.

Given a group-based model with underlying group G, the linear change of coordinates is captured through the use of a Hadamard matrix H, which is defined using G and its character group. For more information on this process we refer the curious reader to *Sturmfels & Sullivant*[5] as well as chapter 15 of *Patcher & Sturmfels*[6]. In this paper we focus on the *CFN* and the *Jukes-Cantor* models which have associated groups $\mathbb{Z}_2$ and $\mathbb{Z}_2 \times \mathbb{Z}_2$ respectively. The Hadamard matrices for these models are respectively given by,

$$H_{CFN} = \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix} \qquad\qquad H_{JC} = \begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & 1 & -1 & -1 \\ 1 & -1 & 1 & -1 \\ 1 & -1 & -1 & 1 \end{pmatrix}$$

For each edge $e \in E$ of a group-based model we collect the unique entries of the transition matrices into a $\kappa \times 1$ vector denoted $\underline{e}$ and obtain the transformed Fourier parameters $\epsilon = H\underline{e}$. Likewise we take the root distribution π which is already a $\kappa \times 1$ vector and obtain the transformed Fourier parameters $\rho = H\pi$. We obtain the transformed Fourier coordinates by collecting all the probability coordinates $p_{g^{(1)}\ldots g^{(n)}}$ into a $\kappa^n \times 1$ vector denoted $\underline{p}$ and left multiplying by the matrix H_n which is defined recursively by,

$$H_n = \begin{pmatrix} H_{n-1} & H_{n-1} \\ H_{n-1} & -H_{n-1} \end{pmatrix}, \qquad\qquad H_1 = H,$$

where H is the Hadamard matrix specific to the group G of the group-based model. Hence we obtain $\underline{q} = H_n \underline{p}$, where $\underline{q}$ denotes the $\kappa^n \times 1$ vector of transformed Fourier coordinates, and each entry of this vector is a monomial in terms of the transformed Fourier continuous parameters, denoted $q_{g^{(1)}\ldots g^{(n)}}$, indexed by the states at the leaves of the n-leaf group-based model.

Remark 17. *We have previously mentioned that we can label the edges of a phylogenetic tree by the splits which they induce. We use this fact to introduce a new notation which we will use in this paper. Instead of each edge being labelled by the letters of the Latin alphabet, we fix a single letter from the start of the Latin alphabet, say a, which will refer to the specific phylogenetic tree and each edge of that tree will be denoted by that letter with its induced split in the superscript, e.g. $a^{(1)}$. Note that the use of the brackets in the superscript in order to avoid any confusion with the operation of taking powers. Using this notation, we may write the probability coordinate p_{000} from Example 8 as follows,*

$$p_{000} = \frac{1}{2} a_0^{(1)} a_0^{(2)} a_0^{(3)} + \frac{1}{2} a_1^{(1)} a_1^{(2)} a_1^{(3)}$$

and the Fourier probability coordinate q_{000} of the above will be,

$$q_{000} = \alpha_0^{(1)} \alpha_0^{(2)} \alpha_0^{(3)}$$

Note that we label the DFT-transformed continuous parameters by the letters of the Greek alphabet. Using this notation, for a general group-based model on an n-leaf phylogenetic tree T, the Fourier coordinates can be expressed by,

$$q_{g^{(1)}\ldots g^{(n)}} = \begin{cases} \prod_{A|B \in \Sigma(T)} \alpha_{\sum_{i \in A} g^{(i)}}^{(A|B)} & \text{if } \sum_{i \in [n]} g^{(i)} = 0, \\ 0 & \text{otherwise.} \end{cases}$$

When we talk about multiple trees, for each tree we will pick a different letter from the start of the Latin alphabet and again label the edges using the specific letter with the induced splits in the superscript. In this way the reader can distinguish which tree we're referring to by looking at the letter used in the parametrisation, and distinguish the specific edge by looking at the superscript of the continuous parameter. This will come in use when discussing parametrisations of mixture models.

By definition, group-based models assume a uniform root distribution, and moreover these models impose a structure on the transition matrices which makes them symmetric matrices. These two facts, the uniform root distribution as well as the symmetric structure of the transition matrices allows us to prove the rather remarkable fact that for such models the choice of internal vertex as the root doesn't change the probability coordinate parametrisations. We make this more precise below:

Theorem 1. *Consider a phylogenetic model on an n-leaf rooted phylogenetic tree T with root r, with a uniform root distribution, and such that the transition matrices M_e are symmetric for each edge e. Now consider another phylogenetic model which is a copy of the first model, but with the only change being that we choose a new (not necessarily different) internal vertex r′ as the root. Then the probability coordinates $\underline{p}$ of the first model with root r and the probability coordinates $\underline{p}'$ of the second model with root r′ are equal, i.e. $\underline{p} = \underline{p}'$.*

Proof. Both roots $r, r' \in V(T)$ are inner vertices of the tree T, and since T is a tree we have a unique path from r to r', which we will denote by ϕ. We can write the probabilities $p_{g^{(1)}\ldots g^{(n)}}$ and $p'_{g^{(1)}\ldots g^{(n)}}$ of observing the combined-state $g^{(1)} \ldots g^{(n)}$ in the first and second model respectively in terms of the transition probabilities as follows,

$$p_{g^{(1)}\ldots g^{(n)}} = \sum_{(g^{(r)}, g^{(v_1)}, \ldots g^{(v_{k-1})}) \in C^k} \pi_{g^{(r)}} \prod_{i=1}^{k-1} a_{s(A_i),t(A_i)}^{(A_i)} \prod_{j=1}^{n} a_{s(j),g^{(j)}}^{(j)}, \tag{2}$$

$$p'_{g^{(1)}\ldots g^{(n)}} = \sum_{(g^{(r')}, g^{(v'_1)}, \ldots g^{(v'_{k-1})}) \in C^k} \pi'_{g^{(r')}} \prod_{i=1}^{k-1} b_{s'(A_i),t'(A_i)}^{(A_i)} \prod_{j=1}^{n} b_{s'(j),g^{(j)}}^{(j)}, \tag{3}$$

where $s, s', t, t' : \Sigma(T) \to C$ are injective maps from the set of of the set of splits $\Sigma(T)$ to the set of characters C. More precisely, given a split $A|B \in \Sigma(T)$ we take its associated edge e and define $s(A|B) = g^{(v_i)}$ such that v_i is the source node of the edge e. Likewise, we define $t(A|B) = g^{(v_j)}$ such that v_j is the terminal node of the edge e. One can see that specifying a root in either model specifies an orientation for each edge of the tree, that is specifies for each edge a source node and a terminal node, and hence the maps s and t reflect the orientation induced by choosing r as the root for the tree T and the maps s' and t' reflect the orientation induced by choosing r' as the root for the tree T. Now, the difference between the two models we are considering is that the choices of root may induce possibly different orientations on the inner edges of the tree T. Note that the orientation of

the outer edges is unaffected between the models as in each case, since we're only choosing internal vertices as possible roots, for any leaf we have to travel away from the root to get closer to it. Fixing the states of the k internal nodes of the tree T, we note that for each non-trivial split $A|B \in \Sigma^*(T)$, the corresponding edge will either have the same orientation in both models, or the orientation will be flipped. Hence for each non-trivial split $A|B$, we have that,

$$s(A|B) = s'(A|B) \text{ and } t(A|B) = t'(A|B) \qquad \text{or} \qquad s(A|B) = t'(A|B) \text{ and } t(A|B) = s'(A|B).$$

Therefore for each non-trivial split A, letting $s(A) = v_i$ and $t(A) = v_j$, we have that $b^{(A)}_{s'(A),t'(A)} = \mathbb{P}(X_i = g^{(i)}|X_j = g^{(j)})$ or $b^{(A)}_{s'(A),t'(A)} = \mathbb{P}(X_j = g^{(j)}|X_i = g^{(i)})$ for the previously fixed states $g^{(i)}$ and $g^{(j)}$. Since by hypothesis we know that both models are symmetric, we have that $\mathbb{P}(X_j = g^{(j)}|X_i = g^{(i)}) = \mathbb{P}(X_i = g^{(i)}|X_j = g^{(j)})$, and so we see that changing the orientation of the edge doesn't affect the transition probability as we travel along it. Since this holds for an arbitrary fixed state-combination of the inner vertices, it holds for them all, therefore $a^{(A_i)}_{s(A_i),t(A_i)} = b^{(A_i)}_{s'(A_i),t'(A_i)}$.

Moreover, by hypothesis we know that both models have a uniform root distribution, and so $\pi_{g^{(r)}} = 1/n = \pi_{g^{(r')}}$ for any character $g^{(r)}, g^{(r')} \in C$.

Using both $a^{(A_i)}_{s(A_i),t(A_i)} = b^{(A_i)}_{s'(A_i),t'(A_i)}$ and $\pi_{g^{(r)}} = \pi_{g^{(r')}}$ in Equation 2 we see that $p_{g^{(1)}\ldots g^{(n)}} = p'_{g^{(1)}\ldots g^{(n)}}$. Since the state-combination at the leaves was general, this holds for all state-combinations at the leaves, which implies the result $\underline{p} = \underline{p}'$. $\qquad\square$

Theorem 1 applies to group-based models, and as such we see that the choice of root for these models is arbitrary. To reflect this, we work with phylogenetic models on *unrooted trees*, which we define below:

Definition 18. *Models on Unrooted Tree*
A phylogenetic model on an unrooted n-leaf tree T is a phylogenetic model on a rooting of the tree T which assumes a uniform root distribution and assumes that the transition matrices are symmetric.

Remark 19. *Parametrisations of Unrooted Models*
The idea behind the above definition is that we can take the unrooted tree T and make an arbitrary choice of internal vertex as the root for the phylogenetic model. The additional assumptions imposed on the model of the uniform root distribution and the symmetric structure of the transition matrices guarantees by Theorem 1 that the probability coordinates will indeed by invariant under a different choice of a root for T.

We now turn our attention to mixture models, with the goal of studying 2-mixtures of group-based models.

Definition 20. *Mixture Models*
Consider r phylogenetic models all on n-leaf phylogenetic trees, where $r \in \mathbb{N}$. We collect the r phylogenetic trees into an ordered tuple $\mathbf{T} = (T_1, \ldots, T_r)$, and recall that for each phylogenetic model on tree T_i we have the associated parametrisation map ψ_{T_i}. Let $\Theta_{\mathbf{T}} = \Theta_{T_1} \times \cdots \times \Theta_{T_r} \times \Delta_{r-1}$, and $\lambda = (\lambda_1, \ldots \lambda_r) \in \Delta_{r-1}$ then the parametrisation map of the r-mixture model $\psi_{\mathbf{T}} : \Theta_{\mathbf{T}} \to \Delta_{\kappa^n-1}$ is given by,

$$\psi_{\mathbf{T}}(\theta_1, \ldots, \theta_r, \lambda) = \lambda_1 \psi_{T_1}(\theta_1) + \cdots + \lambda_r \psi_{T_r}(\theta_r),$$

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where we refer to entries of the vector λ as the mixing parameters of the model. Moreover, the associated variety of the mixture model, denoted $V_{\mathbf{T}}$, can be understood as the join of the varieties of the individual models V_{T_i}, that is,

$$V_{\mathbf{T}} = V_{T_1} * \cdots * V_{T_r}$$

Remark 21. *2-mixture models*
In this report we are interested in 2-mixture models, therefore we can specialise Definition 20 to the case when $r = 2$. The parametrisation map can be written down as,

$$\psi_{\mathbf{T}}(\theta_1, \theta_2, \lambda) = \lambda \psi_{T_1}(\theta_1) + (1 - \lambda)\psi_{T_2}(\theta_2)$$

and the variety $V_{\mathbf{T}}$ can be understood as the join of the varieties V_{T_1} and V_{T_2}.

As with any statistical model, we would like to determine under what conditions the 2-mixture phylogenetic models are identifiable. Here we will concern ourselves only with the identifiability of tree parameters, as this is the focus of the *Hollering & Sullivant* paper. Given two 2-mixture phylogenetic models on 2-tuples $\mathbf{T} = (T_1, T_2)$ and $\mathbf{S} = (S_1, S_2)$, it may be the case that the associated varieties do intersect, i.e. $V_{\mathbf{T}} \cap V_{\mathbf{S}} \neq \emptyset$. This means that given a probability distribution $p_\theta \in V_{\mathbf{T}} \cap V_{\mathbf{S}}$, we may not distinguish whether it arose from the model on $\mathbf{T}$ or the model on $\mathbf{S}$, which poses a challenge to the identifiability of the tree parameters. However, if the intersection is *small* enough, then the probability that a random probability distribution will be contained in this problematic intersection of the two varieties becomes vanishingly small. We capture this idea precisely in the following definition,

Definition 22. *Generic Identifiability[[1]]*
*Let $\{M_i\}_{i=1}^k$ be a collection of algebraic models that sit inside the probability simplex Δ_r, then the parameter i is **generically identifiable** if for each 2-subset $\{i_1, i_2\} \subseteq [k]$,*

$$\dim(M_{i_1} \cap M_{i_2}) < \min(\dim(M_{i_1}), \dim(M_{i_2})).$$

With this slightly relaxed notion of identifiability, we are now ready to define what it means for the tree parameters of r-mixture models to be generically identifiable.

Definition 23. *Tree Parameter Generic Identifiability[[7]]*
The tree parameters of the r-tree mixture model are generically identifiable if for any collection of phylogenetic trees $\mathbf{T} = (T_1, \ldots, T_r)$ on the same set of taxa (leaves) and generic choices of parameters $\theta_1, \ldots, \theta_r, \lambda$,

$$\psi_{\mathbf{T}}(\theta_1, \ldots, \theta_r, \pi) = \psi_{\mathbf{T}'}(\theta_1', \ldots, \theta_r', \pi')$$

implies $\mathbf{T} = \sigma \cdot \mathbf{T}'$ for some permutation $\sigma \in \mathfrak{S}_r$.

Note that "generic choices of parameters" refers to randomly choosing the continuous parameters, the idea being that since the intersection of generically identifiable models is a set of Lebesgue measure 0 (this is equivalent to the dimensional strict inequality in Definition 22) then any randomly chosen point in the union of these models should lie outside the intersection with probability 1.

3   Preliminaries II: Matroids

In this section we introduce the theory of matroids, giving an exposition of some basic ideas and discussing results which we'll refer to in later sections. Most of the definitions, results and their proofs, unless otherwise stated, come from *Oxley*[8] and we refer the curious reader there for a great exposition on matroid theory. First, we give a definition of matroids:

Definition 24. *Matroids*
A matroid $\mathcal{M}$ is a pair $(E, \mathcal{I})$ consisting of a finite set E called the groundset, and a collection of subtests $\mathcal{I}$ of E having the following three properties:

1. *$\emptyset \in \mathcal{I}$.*

2. *If $I \in \mathcal{I}$ and $I' \subseteq I$ then $I' \in \mathcal{I}$.*

3. *If I_1 and I_2 are in $\mathcal{I}$ and $|I_1| < |I_2|$, then there exists an element $e \in I_2 \backslash I_1$ such that $I_1 \cup \{e\} \in \mathcal{I}$.*

*Each $I \in \mathcal{I}$ is referred to as an **independent set**, and all subsets $X \subseteq E$ such that $X \notin \mathcal{I}$ are known as dependent sets.*

Definition 25. *Equality & Isomorphism*
Let $\mathcal{M}_1 = (E_1, \mathcal{I}_1)$ and $\mathcal{M}_\in = (E_2, \mathcal{I}_2)$ be two matroids. Then the two matroids are equal, $\mathcal{M}_1 = \mathcal{M}_2$, iff $E_1 = E_2$ and $\mathcal{I}_1 = \mathcal{I}_2$, where both of these equalities are equalities of sets.
The two matroids are isomorphic, $\mathcal{M}_1 \cong \mathcal{M}_2$, iff there exists an isomorphism $\phi : E_1 \to E_2$ such that $I \in \mathcal{I}_1$ iff $\phi(I) \in \mathcal{I}_2$.

The definition above is designed such that isomorphisms of matroids preserve the structure of independent sets, as this is the matroids defining algebraic structure. Now we give some examples to show the difference between the notions of equality and isomorphism.

Example 26. *Let,*

$$E_1 = \{1, 2, 3\},$$
$$E_2 = \{1, 2, 3, 4, 5\}$$
$$E_3 = \{3, 4, 5\}$$
$$\mathcal{I}_1 = \{\emptyset, \{1\}, \{2\}, \{3\}, \{1, 3\}\}$$
$$\mathcal{I}_2 = \{\emptyset, \{1\}, \{4\}, \{3\}, \{1, 3\}, \{1, 4\}, \{3, 4\}, \{1, 3, 4\}\}$$
$$\mathcal{I}_3 = \{\emptyset, \{3\}, \{4\}, \{5\}, \{4, 5\}\}$$

Then by definition it follows that $(E_i, \mathcal{I}_j) = (E_k, \mathcal{I}_l)$ iff $i = k$ and $j = l$, where $1 \leq i, j, k, l \leq 3$. Moreover, we see that $(E_1, \mathcal{I}_1) \cong (E_3, \mathcal{I}_3)$ where the isomorphism of matroids ϕ is given by $\phi(1) = 4$, $\phi(2) = 3$ and $\phi(3) = 5$.

First introduced in *Whitney*[9], matroids are meant to be a generalisation of the idea of linear independence. There are many ways to characterise a matroid which doesn't resort to an exhaustive listing of all independent sets (or equivalently all dependent sets); these include the notions of bases, circuits, and rank, which we define below.

Definition 27. *Bases*
Let $\mathcal{M} = (E, \mathcal{I})$ be a matroid. A maximal independent set B (that is $B \in \mathcal{I}$ and for all $X \subseteq E$ such that $B \subset X$ we have that X is dependent) is called a basis of $\mathcal{M}$. We collect all bases B of $\mathcal{M}$ into the set $\mathcal{B}$. This set has the following two defining properties:

(B1) $\mathcal{B} \neq \emptyset$.

(B2) If $B_1, B_2 \in \mathcal{B}$ and $\exists x \in B_1 \backslash B_2$ then $\exists y \in B_2 \backslash B_1$ such that $(B_1 \backslash \{x\}) \cup \{y\} \in \mathcal{B}$.

The set of bases has the following nice property which we state without proof,

Lemma 2. Let $B_1, B_2 \in \mathcal{B}$ be bases of a matroid $\mathcal{M}$, then $|B_1| = |B_2|$.

Definition 28. *Circuits*
Let $\mathcal{M} = (E, \mathcal{I})$ be a matroid. A minimal dependent set C (that is $C \notin \mathcal{I}$ and for all $X \subseteq E$ such that $X \subset C$ we have that X is independent) is called a circuit of $\mathcal{M}$. We collect all circuits C of $\mathcal{M}$ into a set $\mathcal{C}$. This set has the following defining properties:

(C1) $\emptyset \notin \mathcal{C}$.

(C2) If $C_1, C_2 \in \mathcal{C}$ and $C_1 \subseteq C_2$, then $C_1 = C_2$.

(C3) If $C_1, C_2 \in \mathcal{C}$ such that C_1, C_2 are distinct and $\exists e \in C_1 \cap C_2$, then $\exists C_3 \in \mathcal{C}$ such that $C_3 \subseteq (C_1 \cup C_2) \backslash \{e\}$.

Definition 29. *Rank*
Let $\mathcal{M} = (E, \mathcal{I})$ be a matroid, and for $X \subseteq E$ let $\mathcal{M}|X = (X, \mathcal{I}')$ be the matroid with groundset X and $\mathcal{I}' = \{I \subseteq X \mid I \in \mathcal{I}\}$. We call the matroid $\mathcal{M}|X$ the restriction of M to X. The rank of X, written $r(X)$, is the cardinality of a basis of $\mathcal{M}|X$. Repeating this for all subsets $X \subseteq E$ defines the rank function $r : 2^E \to \mathbb{N}$, which has the following defining properties:

R1 If $X \subseteq E$ then $0 \leq r(X) \leq |X|$.

R2 If $X \subseteq Y \subseteq E$, then $r(X) \leq r(Y)$.

R3 If $X, Y \subseteq E$, then $r(X \cup Y) + r(X \cap Y) \leq r(X) + r(Y)$.

The rationale behind defining the above concepts is that if we know the set of bases, or the set of circuits, or the rank function of a matroid $\mathcal{M}$, then we can determine all the independent sets of $\mathcal{M}$ (i.e. we can determine $\mathcal{I}$), and hence recover all the information about $\mathcal{M}$.

The name might remind the reader of matrices, which isn't a coincidence, as for any $m \times n$ matrix there is a quick way of obtaining an associated matroid, called the *linear matroid*.

Definition 30. *Linear Matroid*
Let A be an $n \times m$ matrix with elements from the field k. Take $E = [m]$ as the groundset whose elements label the columns of the matrix M and let $I \subseteq E$ be an independent set if the collection of columns whose labels are in I, i.e. $\{c_i\}_{i \in I}$ where c_i is the i-th column of A, is linearly independent over the field k. Then collecting all such independent subsets into the set $\mathcal{I}$, we define the linear matroid $\mathcal{M}(A) = ([m], \mathcal{I})$ of the matrix A.

We leave it to the curious reader as an exercise to verify that this does indeed define a matroid. Now we give a quick example to help familiarise with the definition.

Example 31. *Let A be the following 3×4 matrix over $\mathbb{R}$,*

$$A = \begin{pmatrix} 4 & 0 & -1 & 5 \\ -7 & 2 & 8 & -2 \\ 1 & 3 & 1 & 0 \end{pmatrix}$$

We take $E = [4]$ and note that $\mathcal{I} = \{X \subseteq E \mid |X| \leq 3\}$ describes the set of sets of column indices which specify a collection of linearly independent columns of $\mathbb{R}$. Hence the linear matroid in this example is $\mathcal{M}(A) = ([4], \mathcal{I})$.

Whilst matrices gave rise to one of the earliest studied examples of matroids (along side with graphs), another type of matroid which we're interested in is called the *algebraic matroid*, whose definition we now give.

Definition 32. *Algebraic Matroid*
Let $V \subseteq k^n$ be an irreducible variety, $P = \mathbb{I}(V)$ be the vanishing ideal of V, and $E = [n]$ be the groundset. Let $S \subseteq E$ and let $k[S]$ denote the polynomial ring $k[x_{i_1}, \ldots, x_{i_d}]$ where each index $i_j \in S$. Then we define $S \in \mathcal{I}$ to be an independent set iff,

$$P \cap k[S] = \emptyset \tag{4}$$

*We then define the **algebraic matroid** of V (or equivalently P) to be $\mathcal{M}(V) = ([n], \mathcal{I})$.*

Remark 33. *A rewording of the above definition*
The ideal equation in the definition above, that is Equation 4 can be rephrased in terms of projections of the variety V. Let $S \subseteq [n]$ and let $\pi_S : k^n \to k^{|S|}$ be the projection map onto coordinates with indices in S. Moreover let $\overline{\pi_S(V)}$ denote the Zariski closure of the projection of V. Then the set of independent sets is given by,

$$\mathcal{I} = \{S \subseteq [n] \mid \overline{\pi_S(V)} = k^{|S|}\}$$

*The algebraic matroid $\mathcal{M}(V)$ is also referred to as the **coordinate projection matroid**.*

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Example 34. *Let $V_1 = \mathbb{V}(y - x^2)$ and $V_2 = \mathbb{V}(y + x^2)$ be two irreducible affine varieties in $\mathbb{A}^3_{\mathbb{R}}$, i.e. affine 3-space over the real numbers. It turns out that both algebraic matroids for V_1 and V_2, here we go through the calculation for V_1 and leave it as an exercise to the curious reader to analogously calculate the matroid for V_2. First, we take $E = [3]$ as the groundset of the matroid. Now, $\pi_{\{x\}}(V) = \pi_{\{z\}}(V) = \mathbb{R}$, which is already closed in the Zariski topology, hence $\{1\}, \{3\} \in \mathcal{I}$. The projection $\pi_{\{y\}}(V) = \{y \in \mathbb{R} \mid y \geq 0\}$ whose Zariski closure is $\mathbb{R}$, hence $\{2\} \in \mathcal{I}$. The projections onto the coordinate planes is given by,*

$$\pi_{\{1,2\}}(V) = \{(x, x^2) \mid x \in \mathbb{R}\},$$
$$\pi_{\{1,3\}}(V) = \mathbb{R}^2,$$
$$\pi_{\{2,3\}}(V) = \{(y, z) \mid y, z \in \mathbb{R} \text{ and } y \geq 0\},$$

Both $\pi_{\{1,2\}}(V)$ and $\pi_{\{1,3\}}(V)$ are already closed and the closure of $\pi_{\{2,3\}}(V)$ is $\mathbb{R}^2$, hence $\{1,3\},\{2,3\} \in \mathcal{I}$. Lastly $\pi_{\{1,2,3\}}(V) = V$ which is already closed and not equal to $\mathbb{R}^3$. We have now checked every subset $S \subseteq [3]$ and so we have fully determined all of the independent sets,

$$\mathcal{I} = \{\{1\},\{2\},\{3\},\{1,3\},\{2,3\}\}.$$

One of the key ideas in the *Hollering & Sullivant* paper is their Proposition 3.1, which states that given two irreducible algebraic models (here "models" should be interpreted as variety) M_1 and M_2, with $\dim(M_1) \geq \dim(M_2)$ and considering their algebraic matroids $\mathcal{M}(M_1) = ([n], \mathcal{I}_1)$ and $\mathcal{M}(M_2) = ([n], \mathcal{I}_2)$ respectively, if there exists an $S \in \mathcal{I}_1 \backslash \mathcal{I}_2$ then $\dim(M_1 \cap M_2) < \min(\dim(M_1), \dim(M_2))$. This proposition will allow us to verify that 2-mixture models are indeed generically identifiable in the sense of Definition 22 if we can show that their algebraic matroids are not equal.

But instead of naively attempting to calculate the algebraic matroids, we can make a further simplification which is to consider a related linear matroid. More precisely, we can invoke Proposition 6.7.10 of *Oxley*[8] which states that an algebraic matroid of an irreducible variety V defined over a field k of characteristic zero is equal to a linear matroid defined over the fraction field $k(T)$ where T is a finite set of transcendentals. In particular if the variety V is parameterised by $\psi(\theta_1, \ldots \theta_d) = (f_1(\theta_1, \ldots, \theta_d), \ldots, f_n(\theta_1, \ldots, \theta_d))$ then by defining the Jacobian matrix $J(\psi)$ as,

$$(J(\psi))_{ij} = \frac{\partial f_j}{\partial \theta_i}, \qquad \text{for } 1 \leq i \leq d \text{ and } 1 \leq j \leq n$$

the linear matroid of $J(\psi)$ over the fraction field $k(V)$ (we denote this matroid by $\mathcal{M}(J(\psi))$) is equal to the algebraic matroid of V. For more details on this we refer the reader to *Rosen* [10]. This is already a good simplification, as we can employ the powerful tools of linear algebra rather than toil with Groebner basis calculations in order to determine the independent sets of the matroid. Having said that, we still need to do symbolic calculations over the fraction field $k(V)$ which tend to be computationally complex for models with many parameters. It turns out that by choosing 'generic' values for the parameters of our model, that is a choice $\theta_0 \in \Theta$, and substituting them into $J(\psi)$ (we refer to this as specialisation), the linear matroid over the specialisation of $J(\psi)$, which we denote $\mathcal{M}(J(\psi(\theta_0)))$, is equal to the linear matroid over $J(\psi)$. We make this equality precise, as well as what we mean by 'generic' points in the following definition found in *Rosen*.

Definition 35. *NM-Locus*[[10] *Definition 2.2 and Proposition 2.5*]
*Let V be a variety parametrised by ψ of dimension d, the **Non-Matroidal Locus** denoted $\mathcal{NM}(\psi)$ is a subset of the parameter space Θ where the linear matroid of the specialisation of the Jacobian $J(\psi)$ is not equal to the algebraic matroid. That is for $\theta \in \mathcal{NM}(\psi)$ we have $\mathcal{M}(J(\psi(\theta))) \neq \mathcal{M}(V)$.*
Let $I_d(A)$ denote the ideal generated by the $d \times d$ minors of the matrix A, and let $A\{S\}$ denote the submatrix of A given by restricting A to the columns with indices in S. Then $\mathcal{NM}(\psi)$ is defined by the ideal:

$$I = \bigcap_{B \in \mathcal{B}} I_d(J(\psi)\{B\}) \tag{5}$$

this is a principal ideal generated by the lcm of all non-zero maximal minors.

The astute reader will notice that in Equation 5 which defines the non-matroidal locus, the intersection is indexed over the set of bases of $\mathcal{M}(J(\psi))$. This means that we can't use the non-matroidal

locus $\mathcal{NM}(\psi)$ to determine the matroid $\mathcal{M}(J(\psi))$ as to define $\mathcal{NM}(\psi)$ we would already have to had determined the bases of $\mathcal{M}(J(\psi))$, which is equivalent to determining $\mathcal{M}(J(\psi))$. Whilst the situation may seem bleak, it is a fact that the subset of the variety V corresponding to the non-matroidal locus has a lower dimension than the dimension of V. Therefore $\mathcal{NM}(\psi)$ is a set of measure zero and a randomly chosen point $\theta_0 \in \Theta$ in the parameter space lies outside of $\mathcal{NM}(\psi)$ with probability one.

We will see in the next section that the Jacobian matrix $J(\psi)$ of a 2-mixture model with the parametrisation map ψ has columns which are entirely filled with zeros. These "zero" columns don't add any information to the Matroid and only enlarge the groundset of the Matroid. Given that determining the independent sets of a Matroid can already be combinatorially demanding, we prove the following lemma which will allow us to simplify the calculations by removing these "zero" columns from consideration in the following precise sense:

Lemma 3. *Removing Zeros Lemma Let A be an $n \times m$ matrix which has the following form $A_1 = [A_1'\ 0]$ where A' is an $n \times (m-1)$ matrix, that is it contains a column of zeros as its last column. Then the linear matroids have the form $\mathcal{M}(A) = ([m], \mathcal{I})$ and $\mathcal{M}(A') = ([m-1], \mathcal{I})$, crucially the set of independent sets in both matroid is equal.*

Proof. Since we are considering linear matroids for the matrices A and A', by definition we know that the associated matroids have the form $\mathcal{M}(A) = ([m], \mathcal{I})$ and $\mathcal{M}(A') = ([m-1], \mathcal{I}')$. Therefore it suffices to show that $\mathcal{I} = \mathcal{I}'$, which we do by showing both inclusions separately.

First let $I \in \mathcal{I}$, then since $A = [A'\ 0]$ we have that $\forall x \in I$, $x < m$, which implies that I specifies a set of linearly independent columns of A', which by definition means that $I \in \mathcal{I}'$. Therefore $\mathcal{I} \subseteq \mathcal{I}'$.

Second let $I' \in \mathcal{I}'$, then since by construction the columns of A' are also the columns of A, the set I' specifies a set of linearly independent columns of A, which by definition means that $I' \in \mathcal{I}$. Therefore $\mathcal{I}' \subseteq \mathcal{I}$. $\qquad\square$

Remark 36. *Note that as a consequence of the above lemma, in its context, we can define an injective map $\phi : [m-1] \to [m]$ such that $I' \in \mathcal{I}'$ iff $\phi(I') \in \mathcal{I}$, by letting $\phi(j) = j$ and remembering that $\mathcal{I}' = \mathcal{I}$.*

Another situation which we will consider in the next section is given a matrix A and its linear matroid $\mathcal{M}(A)$, if we now consider a matrix σA which is obtained from A by permuting its columns in some way and its linear matroid $\mathcal{M}(\sigma A)$, then how can we relate the matroids $\mathcal{M}(A)$ and $\mathcal{M}(\sigma A)$. The answer to this comes in the form of the following lemma.

Lemma 4. *Swapping Lemma Let A be an $n \times m$ matrix and let A' be the matrix $n \times m$ obtained by swapping two columns of A. Then $\mathcal{M}(A) \cong \mathcal{M}(A')$.*

Proof. Let j_1 and j_2 be the indices of the columns of A which we swap to obtain A', and let $\phi : [m] \to [m]$ be the set isomorphism (permutation) given by,

$$\phi(j) = \begin{cases} j_1 & \text{if } j = j_2 \\ j_2 & \text{if } j = j_1 \\ j & \text{otherwise.} \end{cases}$$

note that ϕ is simply the permutation that we can write in cycle notation as $\phi = (j_1, j_2)$. It suffices to show now that ϕ preserves independent sets. Denote $\mathcal{M}(A) = ([m], \mathcal{I})$ and $\mathcal{M}(A') = ([m], \mathcal{I}')$.

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Let $I \in \mathcal{I}$, then we claim that the collection of columns $\{c_j\}_{j \in I}$ of A and the collection of columns $\{c'_j\}_{j \in \phi(I)}$ of A' is the same. This is immediate for $j_1, j_2 \notin I$ since by construction of A' we have that $c_j = c'_j$ for $j \notin \{j_1, j_2\}$, therefore let's assume without loss of generality that $j_1 \in I$. Then by definition $\phi(j_1) = j_2$ and by construction of A' we have that the column indexed by j_2 in A' is equal to the column indexed by j_1 in A, therefore $c_{j_1} = c'_{j_2}$. Likewise $\phi(j_2) = j_1$ and $c_{j_2} = c'_{j_1}$. Hence we have $\{c_j\}_{j \in I} = \{c'_j\}_{j \in \phi(I)}$ and since $\{c_j\}_{j \in I}$ is linearly independent (since $I \in \mathcal{I}$) we have that $\{c'_j\}_{j \in \phi(I)}$ is linearly independent, which implies that $\phi(I) \in \mathcal{I}'$. A completely analogous argument shows that if $I' \in \mathcal{I}'$ then $\phi^{-1}(I') \in \mathcal{I}$. Therefore, ϕ does indeed preserve independent sets, and hence it is the desired isomorphism of matroids which gives us the result $\mathcal{M}(A) \cong \mathcal{M}(A')$. □

Corollary 4.1. *Let A be an $n \times m$ matrix and let σA denote the $n \times m$ matrix obtained by permuting the columns of A in some way. Then $\mathcal{M}(A) \cong \mathcal{M}(\sigma A)$.*

Proof. Any permutation σ can be decomposed into a product of two cycles, therefore let $\sigma = \sigma_t \cdots \sigma_1$ be such a 2-cycles decomposition of σ into t 2-cycles. With this we can define a sequence of matrices, $A_0, A_1, \ldots A_t$ where $A_u = (\sigma_u \cdots \sigma_1)A$ and where $A_0 = A$ and $A_t = \sigma A$. Note that for each pair of consecutive matrices (A_{u-1}, A_u), the matrices differ by a 2-cycle, that is by a swapping of two columns. Hence for each of the t consecutive pairs (A_{u-1}, A_u), we can apply the Swapping Lemma to get a matroid isomorphism $\sigma_u : \mathcal{M}(A_{u-1}) \to \mathcal{M}(A_u)$. Composing all t matroid isomorphisms, we obtain the desired matroid isomorphism $\sigma = \sigma_t \cdots \sigma_1$ which gives the result $\mathcal{M}(A) \cong \mathcal{M}(\sigma A)$. □

Using the Removing Zeros Lemma 3 and Corollary 4.1 we prove the following theorem which will help in simplifying linear matroid calculations whenever we encounter a column of 0's.

Theorem 5. *Let A be an $n \times m$ matrix and $\{c_j\}_{j \in [m]}$ be the collection of the columns of A, such that c_j is the j-th column of A. Denote the linear matroid on A by $\mathcal{M}(A) = ([m], \mathcal{I})$. Additionally, assume that there exists an non-empty subset $\Lambda \subseteq [m]$ such that $\forall j \in \Lambda \; c_j = \underline{0}$ is the zero vector. Denote by A' the $n \times (m - |\Lambda|)$ matrix which is obtained from A by deleting the empty columns, that is deleting the columns c_j with index $j \in \Lambda$. Denote the linear matroid on A' by $\mathcal{M}(A') = ([m - |\Lambda|], \mathcal{I}')$. Then there exists an injective map $\phi : [m - |\Lambda|] \to [m]$ such that $I' \in \mathcal{I}'$ iff $\phi(I') \in \mathcal{I}$.*

Proof. First, we can permute all the empty columns to the right-most end of A such that only the columns with index $j > m - |\Lambda|$ are empty. Denote such a permuted matrix by σA. By Corollary 4.1 we have matroid isomorphism $\varphi_1 : [m] \to [m]$ such that $\mathcal{M}(A) \cong \mathcal{M}(\sigma A)$. Let $\mathcal{M}(\sigma A) = ([m], \sigma \mathcal{I})$, and let A_1 denote the matrix obtained from σA by removing the last column, that is by removing $(\sigma c)_m$. Since $(\sigma c)_m = \underline{0}$, then we can apply the Removing Zeros Lemma 3 to conclude that $\mathcal{M}(A_1) = ([m-1], \sigma \mathcal{I})$, i.e. the independent sets of the matroid $\mathcal{M}(A_1)$ and $\mathcal{M}(\sigma A)$ are equal. By iteratively removing the last column and applying Lemma 3 $|\Lambda - 1|$ more times, we see that $\mathcal{M}(A') = ([m - |\Lambda|], \sigma \mathcal{I})$. By Remark 36 we have an injective map $\varphi_2 : [m - |\Lambda|] \to [m]$ such that $I' \in \mathcal{I}'$ iff $\varphi_2(I') \in \sigma \mathcal{I}$. The required injective map is now given by $\phi = \varphi_1^{-1} \circ \varphi_2$. It is injective since it's a composition of the bijection φ_1 and the injection ϕ_2. It has the required property since by φ_2 we have

$$I' \in \mathcal{I}' \text{ iff } \varphi_2(I') \in \sigma \mathcal{I},$$

and by φ_1 we have

$$\sigma I \in \sigma \mathcal{I} \text{ iff } \varphi_1^{-1}(\sigma I) \in \mathcal{I},$$

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therefore combining the above iff statements we get,

$$I' \in \mathcal{I}' \text{ iff } \varphi_1^{-1}(\varphi_2(I')) \in \mathcal{I},$$

which is equivalent to $I' \in \mathcal{I}'$ iff $\phi(I') \in \mathcal{I}$. $\qquad\square$

The challenge with determining matroids boils down to the combinatorial complexity of these objects. For a linear matroid $\mathcal{M} = ([m], \mathcal{I})$ of rank r, we need to check $\binom{m}{r}$ subsets of $[m]$ to determine the set of bases $\mathcal{B}$, which determines the matroid $\mathcal{M}$. As m and r grow, $\binom{m}{r}$ can quickly become unmanageably large, to the point which even computational calculations become infeasible, or at the very least time-consuming. To give an example, in the next section we will be interested in determining a linear matroid with groundset $E = [31]$ and rank $r = 19$ over the fraction field of a polynomial ring in 19 variables, which here we denote F. This means that we will have to calculate the rank of $\binom{31}{19} = 141,120,525$ 19×19 matrices with entries over F. The large number of symbolic calculations proves to be a serious barrier to our efforts to determine this matroid. Instead of trying to calculate the full matroid, *Hollering&Sullivant* implement an algorithm which tries to guess a subset $S \subseteq [m]$ which is an independent set of one matroid but not the other, and we will discuss this algorithm in more detail in the next section.

Many computer algebra software languages have a way to implement matroid calculations. Whilst *Hollering & Sullivant* use the Wolfram Mathematica language, in this paper we will use SageMath and include all of the code used as well as its outputs in the appendix A.

4 Model & Current Work

Remark 37. *Goal of this paper*
Hollering & Sullivant have outlined an algorithm which uses Matroid Theory to determine the identifiability of 2-mixture group-based models. In this paper we aim to understand the methods they have used and particularly to understand the structure of the matroids corresponding to the 2-mixture models. Direct computation of these matroids seems infeasible due to the enormous combinatorial complexity of these objects, therefore a more fruitful direction may be to describe in as much detail as possible the matroids of these 2-mixture models and to try and reproduce a Sage version of the Algorithms used in Hollering & Sullivant.

4.1 Model

To explain and showcase Algorithm 3.3 in detail, we need to specify a pair of phylogenetic 2-mixture CFN models on 6 leaves. Therefore, let T_1, S_1, S_2 be the phylogenetic trees on 6 leaves as shown below, and consider the pair of 2-mixture CFN models M_1, M_2 which have tree parameters $\mathbf{T} = \{T_1, T_1\}$ and $\mathbf{S} = \{S_1, S_2\}$.

Remark 38. *repeat tree parameters?* *In the Definition 20 of mixture models we don't place any restriction on the what trees we allow in our mixtures, therefore we can take 2-mixtures in which the two trees have the same tree parameter. Having said that, it will be useful to distinguish in the 2-mixture model whether we are talking about the parameters of the first copy of T_1 or the second copy of T_1. We will do that by using the letter α to denote the parameters coming from the first copy, and by using the letter β to denote the parameters coming from the second copy.*

For the trees T_1, S_1 and S_2 we have that the set of non-trivial splits is:

$$\Sigma^*(T_1) = \{12|3456, 34|1256, 56|1234\}$$
$$\Sigma^*(S_1) = \{12|3456, 123|456, 45|1236\}$$
$$\Sigma^*(S_2) = \{23|1456, 123|456, 56|1234\}$$

Now we wish to find the parametrisation maps $\psi_{\mathbf{T}}$ and $\psi_{\mathbf{S}}$, which can be described in terms of the (simpler) parametrisation maps ψ_{T_1}, ψ_{S_1} and ψ_{S_2}. Moreover, since CFN is a group-based model, we can write the parametrisation maps in terms of the Fourier coordinates, which should nicely simplify the equations.

Note that the trees T_1, S_1, S_2 are all unrooted trees, that is we don't have a distinguished inner vertex which we can call the root in these trees. However, in order to calculate the probabilities of observing a collection of states at the leaves, we need to specify a root. To remedy this, we simply choose an inner vertex of our unrooted tree and declare it to be the root, in this way we have turned an unrooted tree and made it a rooted tree. As remarked before, for group-based models the choice of root is arbitrary and so we make some arbitrary choice of inner vertex to be the root. For the unrooted tree T we will denote and refer to the corresponding rooted tree as T as well, this should hopefully not cause confusion and be clear from the context if we mean the rooted or unrooted tree.

Figure 5 shows the (arbitrary) choices of root we have made which allows us to write down the probability coordinates. Note that in the figure below we haven't explicitly labelled the roots of the tree, rather we have distinguished the root vertices in those trees by placing them at the top of the tree, as per convention.

The probability of observing the states $g_1 g_2 g_3 g_4 g_5 g_6$ at the leaves of the phylogenetic model on T_1, that is of observing the general probability coordinate, $p_{g^{(1)} \ldots g^{(6)}}$ is given by:

$$\sum_{(g^{(r)}, g^{(12)}, g^{(34)}, g^{(56)}) \in (\mathbb{Z}_2)^4} \pi_{g^{(r)}} \prod_{A \in \Sigma(T_1)} a^A_{s(A)-t(A)}$$

$$= \frac{1}{2}(a^{(12)}_0 a^{(34)}_0 a^{(56)}_0 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}} + a^{(12)}_0 a^{(34)}_0 a^{(56)}_1 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}}$$

$$+a^{(12)}_0 a^{(34)}_1 a^{(56)}_0 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}} + a^{(12)}_0 a^{(34)}_1 a^{(56)}_1 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}}$$

$$+a^{(12)}_1 a^{(34)}_0 a^{(56)}_0 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}} + a^{(12)}_1 a^{(34)}_0 a^{(56)}_1 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}}$$

$$+a^{(12)}_1 a^{(34)}_1 a^{(56)}_0 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}} + a^{(12)}_1 a^{(34)}_1 a^{(56)}_1 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}})$$

$$+\frac{1}{2}(a^{(12)}_0 a^{(34)}_0 a^{(56)}_0 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}} + a^{(12)}_0 a^{(34)}_0 a^{(56)}_1 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}}$$

$$+a^{(12)}_0 a^{(34)}_1 a^{(56)}_0 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}} + a^{(12)}_0 a^{(34)}_1 a^{(56)}_1 a^{(1)}_{1-g^{(1)}} a^{(2)}_{1-g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}}$$

$$+a^{(12)}_1 a^{(34)}_0 a^{(56)}_0 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}} + a^{(12)}_1 a^{(34)}_0 a^{(56)}_1 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{1-g^{(3)}} a^{(4)}_{1-g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}}$$

$$+a^{(12)}_1 a^{(34)}_1 a^{(56)}_0 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{1-g^{(5)}} a^{(6)}_{1-g^{(6)}} + a^{(12)}_1 a^{(34)}_1 a^{(56)}_1 a^{(1)}_{g^{(1)}} a^{(2)}_{g^{(2)}} a^{(3)}_{g^{(3)}} a^{(4)}_{g^{(4)}} a^{(5)}_{g^{(5)}} a^{(6)}_{g^{(6)}}).$$

The unwieldy parametrisation above, for the tree T_1, can be expressed much more succinctly in terms

of the Fourier coordinates, which is given by,

$$q_{g^{(1)}\ldots g^{(6)}} = \begin{cases} \alpha_{g^{(1)}}^{(1)}\alpha_{g^{(2)}}^{(2)}\alpha_{g^{(3)}}^{(3)}\alpha_{g^{(4)}}^{(4)}\alpha_{g^{(5)}}^{(5)}\alpha_{g^{(6)}}^{(6)}\alpha_{g^{(1)}+g^{(2)}}^{(12)}\alpha_{g^{(3)}+g^{(4)}}^{(34)}\alpha_{g^{(5)}+g^{(6)}}^{(56)}, & \text{if } \sum_{i=1}^{6} g^{(i)} = 0 \\ 0, & \text{otherwise} \end{cases} \qquad (6)$$

Similarly, we can write the parametrisation map for the tree S_1 in terms of the original continuous parameters. For the general probability coordinate $p_{g^{(1)}\ldots g^{(6)}}$ we have:

$$\sum_{(g^{(r)},g^{(12)},g^{(123)},g^{(45)})\in(\mathbb{Z}_2)^4} \pi_{g^{(r)}} \prod_{A\in\Sigma(S_1)} c_{s(A)-t(A)}^{A}$$

$$=\frac{1}{2}(c_0^{(12)}c_0^{(123)}c_0^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)} + c_0^{(12)}c_0^{(123)}c_1^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)}$$

$$+c_0^{(12)}c_1^{(123)}c_0^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)} + c_0^{(12)}c_1^{(123)}c_1^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)}$$

$$+c_1^{(12)}c_0^{(123)}c_0^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)} + c_1^{(12)}c_0^{(123)}c_1^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)}$$

$$+c_1^{(12)}c_1^{(123)}c_0^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)} + c_1^{(12)}c_1^{(123)}c_1^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)})$$

$$+\frac{1}{2}(c_0^{(12)}c_0^{(123)}c_0^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)} + c_0^{(12)}c_0^{(123)}c_1^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)}$$

$$+c_0^{(12)}c_1^{(123)}c_0^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)} + c_0^{(12)}c_1^{(123)}c_1^{(45)}c_{1-g^{(1)}}^{(1)}c_{1-g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)}$$

$$+c_1^{(12)}c_0^{(123)}c_0^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)} + c_1^{(12)}c_0^{(123)}c_1^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{1-g^{(3)}}^{(3)}c_{1-g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)}$$

$$+c_1^{(12)}c_1^{(123)}c_0^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{1-g^{(5)}}^{(5)}c_{1-g^{(6)}}^{(6)} + c_1^{(12)}c_1^{(123)}c_1^{(45)}c_{g^{(1)}}^{(1)}c_{g^{(2)}}^{(2)}c_{g^{(3)}}^{(3)}c_{g^{(4)}}^{(4)}c_{g^{(5)}}^{(5)}c_{g^{(6)}}^{(6)}).$$

and in the Fourier parameters this becomes,

$$q_{g^{(1)}\ldots g^{(6)}} = \begin{cases} \gamma_{g^{(1)}}^{(1)}\gamma_{g^{(2)}}^{(2)}\gamma_{g^{(3)}}^{(3)}\gamma_{g^{(4)}}^{(4)}\gamma_{g^{(5)}}^{(5)}\gamma_{g^{(6)}}^{(6)}\gamma_{g^{(1)}+g^{(2)}}^{(12)}\gamma_{g^{(1)}+g^{(2)}+g^{(3)}}^{(123)}\gamma_{g^{(4)}+g^{(5)}}^{(45)}, & \text{if } \sum_{i=1}^{6} g^{(i)} = 0 \\ 0, & \text{otherwise} \end{cases} \qquad (7)$$

Lastly, the parametrisation of the model on the tree S_2 in the original continuous parameters is given by,

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$$\sum_{(g^{(r)},g^{(23)},g^{(123)},g^{(56)})\in(\mathbb{Z}_2)^4} \pi_{g^{(r)}} \prod_{A\in\Sigma(S_1)} d^A_{s(A)-t(A)}$$

$$=\frac{1}{2}(d_0^{(23)} d_0^{(123)} d_0^{(56)} d_1^{(1)} d_{g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)} + d_0^{(23)} d_0^{(123)} d_1^{(56)} d_{g^{(1)}}^{(1)} d_{g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)}$$

$$+d_0^{(23)} d_1^{(123)} d_0^{(56)} d_{g^{(1)}}^{(1)} d_{g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)} + d_0^{(23)} d_1^{(123)} d_1^{(56)} d_{g^{(1)}}^{(1)} d_{g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)}$$

$$+d_1^{(23)} d_0^{(123)} d_0^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)} + d_1^{(23)} d_0^{(123)} d_1^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)}$$

$$+d_1^{(23)} d_1^{(123)} d_0^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)} + d_1^{(23)} d_1^{(123)} d_1^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)})$$

$$+\frac{1}{2}(d_0^{(23)} d_0^{(123)} d_0^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)} + d_0^{(23)} d_0^{(123)} d_1^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)}$$

$$+d_0^{(23)} d_1^{(123)} d_0^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)} + d_0^{(23)} d_1^{(123)} d_1^{(56)} d_{1-g^{(1)}}^{(1)} d_{1-g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)}$$

$$+d_1^{(23)} d_0^{(123)} d_0^{(56)} d_{g^{(1)}}^{(1)} d_{g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)} + d_1^{(23)} d_0^{(123)} d_1^{(56)} d_{g^{(1)}}^{(1)} d_{g^{(2)}}^{(2)} d_{1-g^{(3)}}^{(3)} d_{1-g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)}$$

$$+d_1^{(23)} d_1^{(123)} d_0^{(56)} d_{g^{(1)}}^{(1)} d_{g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{1-g^{(5)}}^{(5)} d_{1-g^{(6)}}^{(6)} + d_1^{(23)} d_1^{(123)} d_1^{(56)} d_{g^{(1)}}^{(1)} d_{g^{(2)}}^{(2)} d_{g^{(3)}}^{(3)} d_{g^{(4)}}^{(4)} d_{g^{(5)}}^{(5)} d_{g^{(6)}}^{(6)}).$$

and in the Fourier parameters this becomes,

$$q_{g^{(1)}\ldots g^{(6)}} = \begin{cases} \delta_{g^{(1)}}^{(1)} \delta_{g^{(2)}}^{(2)} \delta_{g^{(3)}}^{(3)} \delta_{g^{(4)}}^{(4)} \delta_{g^{(5)}}^{(5)} \delta_{g^{(6)}}^{(6)} \delta_{g^{(1)}+g^{(2)}}^{(23)} \delta_{g^{(1)}+g^{(2)}+g^{(3)}}^{(123)} \delta_{g^{(4)}+g^{(5)}}^{(56)}, & \text{if } \sum_{i=1}^6 g^{(i)} = 0 \\ 0, & \text{otherwise} \end{cases} \tag{8}$$

Note that Equation 6 defines the parametrisation map ψ_{T_1}, Equation 7 defines the parametrisation map ψ_{S_1}, and Equation 8 defines the parametrisation map ψ_{S_2}. Now, we can think of the parametrisation maps of the 2-mixture models as,

$$\psi_{\mathbf{T}}(\theta_1, \theta_2, \lambda) = \lambda\psi_{T_1}(\theta_1) + (1-\lambda)\psi_{T_1}(\theta_2) \tag{9}$$

$$\psi_{\mathbf{S}}(\theta'_1, \theta'_2, \lambda') = \lambda'\psi_{S_1}(\theta'_1) + (1-\lambda')\psi_{S_2}(\theta'_2) \tag{10}$$

We denote the variety parametrised by $\psi_{\mathbf{T}}$ by $V_{\mathbf{T}}$ and we denote the variety parametrised by $\psi_{\mathbf{S}}$ by $V_{\mathbf{S}}$.

4.2 Computing the Transposed-Jacobian for Matroid Calculation

As remarked earlier, the result from *Oxley* guarantees that the algebraic matroids $\mathcal{M}(V_{\mathbf{T}})$ and $\mathcal{M}(V_{\mathbf{S}})$ will be equal to the linear matroids $\mathcal{M}(J(\psi_{\mathbf{T}}))$ and $\mathcal{M}(J(\psi_{\mathbf{S}}))$ respectively. Therefore we turn our attention to computing both $J(\psi_{\mathbf{T}})$ and $J(\psi_{\mathbf{S}})$.

The computations are done in Sage and the code used in this and other computation can be found in the appendix. Here we record a succinct way to describe an arbitrary entry of the Jacobian matrices. First we give some clarification. The Fourier transform for the CFN model transforms the continuous parameters of our phylogenetic model in such a way that given arbitrary edge parameters $a^A = (a_0^A, a_1^A)^T$, (here T just denotes the transpose!) they're related to the transformed parameters $\alpha^A = (\alpha_0^A, \alpha_1^A)^T$ by the following equation,

$$\begin{pmatrix} \alpha_0^A \\ \alpha_1^A \end{pmatrix} = \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix} \begin{pmatrix} a_0^A \\ a_1^A \end{pmatrix}$$

hence $\alpha_0^A = a_0^A + a_1^A$ and $\alpha_1^A = a_0^A - a_1^A$. Remembering that the parameters a_0^A and a_1^A come from transition matrices, we know that by definition the rows of these matrices must sum to one, which immediately implies that we can rewrite $a_1^A = 1 - a_0^A$. Substituting this expression for a_1^A into the equations for the transformed parameters we see that $\alpha_0^A = 1$ and $\alpha_1^A = 1 - 2a_0^A$. Importantly $\alpha_0^A = 1$, hence whenever in the Fourier parametrisation a parameter with subscript 0 occurs we can substitute 1 in the monomial expression. From this we see that the only non-trivial parameters left in the Fourier parametrisation are the parameters of the form α_1^A, and hence when calculating the Jacobians we only need to differentiate with respect to those parameters of the individual tree models. Since we are are considering 2-mixture models of phylogenetic models on 6-leaf binary trees, the total number of parameters in the parametrisation will be $9 + 9 + 1 = 19$, where each of the two trees in the 2-mixture contributes 9 parameters and we have an additional mixing parameter. The columns of the Jacobian matrix will be indexed by binary numbers of length 6, i.e. $j = g^{(1)}g^{(2)}g^{(3)}g^{(4)}g^{(5)}g^{(6)}$, which represent the combined-state observed at the leaves of the model. Meanwhile the rows of the Jacobian matrix will be indexed by the 19 parameters appearing in the 2-mixture model. Let $\Theta_\zeta(T)$ represent the set of non-trivial transformed parameters for the phylogenetic model on tree T written using the dummy variable ζ. For example, for the model on tree T_1 we have,

$$\Theta_\alpha(T_1) = \{\alpha_1^{(1)}, \alpha_1^{(2)}, \alpha_1^{(3)}, \alpha_1^{(4)}, \alpha_1^{(5)}, \alpha_1^{(6)}, \alpha_1^{(12)}, \alpha_1^{(34)}, \alpha_1^{(56)}\}.$$

With that out of the way, for $J(\psi_{\mathbf{T}})$ we can write,

$$J(\psi_{\mathbf{T}})_{ij} = \begin{cases} \frac{\partial}{\partial i}(\lambda\alpha_{g^{(1)}}^{(1)}\alpha_{g^{(2)}}^{(2)}\alpha_{g^{(3)}}^{(3)}\alpha_{g^{(4)}}^{(4)}\alpha_{g^{(5)}}^{(5)}\alpha_{g^{(6)}}^{(6)}\alpha_{g^{(1)}+g^{(2)}}^{(12)}\alpha_{g^{(3)}+g^{(4)}}^{(34)}\alpha_{g^{(5)}+g^{(6)}}^{(56)}) & \text{if } \sum_{k=1}^{6} g^{(k)} = 0 \text{ and } i \in \Theta_\alpha(T_1), \\[2ex] \frac{\partial}{\partial i}((1-\lambda)\beta_{g^{(1)}}^{(1)}\beta_{g^{(2)}}^{(2)}\beta_{g^{(3)}}^{(3)}\beta_{g^{(4)}}^{(4)}\beta_{g^{(5)}}^{(5)}\beta_{g^{(6)}}^{(6)}\beta_{g^{(1)}+g^{(2)}}^{(12)}\beta_{g^{(3)}+g^{(4)}}^{(34)}\beta_{g^{(5)}+g^{(6)}}^{(56)}) & \text{if } \sum_{k=1}^{6} g^{(k)} = 0 \text{ and } i \in \Theta_\beta(T_1), \\[2ex] \begin{aligned} & \alpha_{g^{(1)}}^{(1)}\alpha_{g^{(2)}}^{(2)}\alpha_{g^{(3)}}^{(3)}\alpha_{g^{(4)}}^{(4)}\alpha_{g^{(5)}}^{(5)}\alpha_{g^{(6)}}^{(6)}\alpha_{g^{(1)}+g^{(2)}}^{(12)}\alpha_{g^{(3)}+g^{(4)}}^{(34)}\alpha_{g^{(5)}+g^{(6)}}^{(56)} \\ & -\beta_{g^{(1)}}^{(1)}\beta_{g^{(2)}}^{(2)}\beta_{g^{(3)}}^{(3)}\beta_{g^{(4)}}^{(4)}\beta_{g^{(5)}}^{(5)}\beta_{g^{(6)}}^{(6)}\beta_{g^{(1)}+g^{(2)}}^{(12)}\beta_{g^{(3)}+g^{(4)}}^{(34)}\beta_{g^{(5)}+g^{(6)}}^{(56)} \end{aligned} & \text{if } \sum_{k=1}^{6} g^{(k)} = 0 \text{ and } i = \lambda, \\[2ex] 0 & \text{otherwise.} \end{cases}$$

and for the other 2-mixture model parametrisation,

$$J(\psi_{\mathbf{S}})_{ij} = \begin{cases} \frac{\partial}{\partial i}(\lambda'\gamma_{g^{(1)}}^{(1)}\gamma_{g^{(2)}}^{(2)}\gamma_{g^{(3)}}^{(3)}\gamma_{g^{(4)}}^{(4)}\gamma_{g^{(5)}}^{(5)}\gamma_{g^{(6)}}^{(6)}\gamma_{g^{(1)}+g^{(2)}}^{(12)}\gamma_{g^{(1)}+g^{(2)}+g^{(3)}}^{(123)}\gamma_{g^{(4)}+g^{(5)}}^{(45)}) & \text{if } \sum_{k=1}^{6} g^{(k)} = 0 \text{ and } i \in \Theta_\gamma(S_1), \\[2ex] \frac{\partial}{\partial i}((1-\lambda')\delta_{g^{(1)}}^{(1)}\delta_{g^{(2)}}^{(2)}\delta_{g^{(3)}}^{(3)}\delta_{g^{(4)}}^{(4)}\delta_{g^{(5)}}^{(5)}\delta_{g^{(6)}}^{(6)}\delta_{g^{(2)}+g^{(3)}}^{(23)}\delta_{g^{(1)}+g^{(2)}+g^{(3)}}^{(123)}\delta_{g^{(5)}+g^{(6)}}^{(56)}) & \text{if } \sum_{k=1}^{6} g^{(k)} = 0 \text{ and } i \in \Theta_\delta(S_2), \\[2ex] \begin{aligned} & \gamma_{g^{(1)}}^{(1)}\gamma_{g^{(2)}}^{(2)}\gamma_{g^{(3)}}^{(3)}\gamma_{g^{(4)}}^{(4)}\gamma_{g^{(5)}}^{(5)}\gamma_{g^{(6)}}^{(6)}\gamma_{g^{(1)}+g^{(2)}}^{(12)}\gamma_{g^{(1)}+g^{(2)}+g^{(3)}}^{(123)}\gamma_{g^{(4)}+g^{(5)}}^{(45)} \\ & -\delta_{g^{(1)}}^{(1)}\delta_{g^{(2)}}^{(2)}\delta_{g^{(3)}}^{(3)}\delta_{g^{(4)}}^{(4)}\delta_{g^{(5)}}^{(5)}\delta_{g^{(6)}}^{(6)}\delta_{g^{(2)}+g^{(3)}}^{(23)}\delta_{g^{(1)}+g^{(2)}+g^{(3)}}^{(123)}\delta_{g^{(5)}+g^{(6)}}^{(56)} \end{aligned} & \text{if } \sum_{k=1}^{6} g^{(k)} = 0 \text{ and } i = \lambda', \\[2ex] 0 & \text{otherwise.} \end{cases}$$

Remark 39. *Notation in SageMath When defining variables in SageMath, it is generally encouraged to subscript rather than superscript variables which are used in computations. To my knowledge, there isn't an easy way to define variables with superscripts like we may wish given our notation for the transformed parameters of the 2-mixture models. Therefore, we will adopt the following convention: the parameter α_1^A will be written α_A, and similarly for any other dummy Greek letter we may wish to*

use when writing our parameters. For example, $\beta_1^{(12)}$ will be denoted in the SageMath code as β_{12} (note that we have dropped the brackets around the split!). Note that any parameters $\alpha_0^A = 1$ as remarked before, hence this change in notation should not be unambiguous as the only non-trivial parameters are of the form α_1^A. The reader might wonder why we don't apply this notational change more widely to the notation used in this report, the answer being that we still want to reason about both α_0^A and α_1^A parameters which the new notation for SageMath doesn't allow us to do.

The resulting Jacobian matrices have size 19×64, corresponding to the 19 parameters of the 2-mixture models and 64 probability coordinates. Note, however, that the majority of the columns of these Jacobians will be empty, therefore we can use Theorem 5 to conclude that the sub-matrices of these Jacobians defined by removing all the empty columns will give us closely related matroids. We will refer to these sub-matrices as the *clean Jacobians*, and we will denote them by $J^c(\psi_{\mathbf{T}})$ for the Jacobian $J(\psi_{\mathbf{T}})$, and similarly $J^c(\psi_{\mathbf{S}})$ for the Jacobian $J(\psi_{\mathbf{S}})$.

4.3 Proof of Theorem 4.6

Theorem 4.6 of *Hollering & Sullivant* establishes generic identifiability for 2-mixture CFN models on at least six leaves, and it is the result we wish to clearly explain in this paper. The proof of this theorem relies on Theorem 23 and it's Corollary 25 found in *Matsen et al.*[11]. To this pair of results *Hollering&Sturmfels* give the name Six-To-Infinity Theorem. The first thing we'd like to do in examining the proof of Theorem 4.6 is to have a closer look at the results found in *Matsen et al.* we mentioned above.

But before we get into those results, we need to introduce the combinatorial concept of disentanglement of phylogenetic trees. We proceed to give definitions.

Definition 40. *Restrictions.*
*Let T be a phylogenetic tree with label set X, and suppose that $X' \subseteq X$ is non-empty. The **restriction** of T to X', denoted $T|_{X'}$ is the phylogenetic tree on label set X' for which,*

$$\Sigma(T_{X'}) = \{A \cap X' | B \cap X' \ : \ A|B \in \Sigma(T) \text{ and both } A \cap X', B \cap X' \neq \emptyset\}.$$

Definition 41. *Disentanglement.*
Let $B(X)$ denote the collection of binary phylogenetic trees labelled by the elements of X. For our considerations we may take $X = [n]$ for some $n \in \mathbb{N}$ which represents the number of leaves of the tree. Let $B(X, k)$ denote the collection of subsets of $B(X)$ of size at most k. For a binary tree $T \in B(X)$ and $Y \subseteq X$, let $T|_Y$ denote the induced binary phylogenetic tree obtained from T by restricting the leaf set to Y. For $\mathcal{P} = \{T_1, \ldots, T_j\} \in B(X, k)$ define $\mathcal{P}|_Y = (T_1|_Y, \ldots, T_j|_Y) \in B(Y, k)$.
*A collection M of subsets of X **disentangles** $B(X, k)$ if for any pair $\mathcal{P}, \mathcal{P}' \in B(X, k)$ we have,*

$$\mathcal{P} = \mathcal{P}' \text{ iff } \mathcal{P}|_Y = \mathcal{P}'|_Y \text{ for all } Y \in M.$$

*Moreover, a collection M of subsets of X **effectively disentagle** $B(X, k)$ if there exists a polynomial-time algorithm that reconstructs $\mathcal{P}$ from the set $\{\mathcal{P}|_Y \mid Y \in M\}$.*

Theorem 6 (Theorem 23 [11]). *$B(X, 2)$ can be effectively disentangled by the subsets of X of size at most six.*

To prove Theorem 6, *Matsen et al.* employ the following lemma,

Lemma 7 (Lemma 24 [11]). *Let T be a binary phylogenetic tree on seven leaves, and call the set of leaf labels Y. Suppose that $S = \{a, b, c\} \subseteq Y$ and let $x, y \in Y \backslash S$ be two distinct elements. Then the quartet tree $T|_{S \cup \{x\}}$ is determined by the collection of quartet trees $T|_q$ as q ranges over the following quartets:*

(i) $\{a, b, x, y\}$, $\{a, c, x, y\}$, $\{b, c, x, y\}$, *and,*

(ii) $\{a, b, c, y\}$.

Whilst *Matsen et al.* provide a proof of this lemma, here we will go over their proof in greater detail. But first we will need another lemma from *Semple & Steel*[4] which we state without proof.

Lemma 8 (Lemma 6.3.4 [4]). *Let T be a phylogenetic tree with with label set X, and let $A|B$ be a split of X (i.e. a bipartition). Then $A|B$ is a split of T iff for all $a, a' \in A$ and $b, b' \in B$,*

$$\{a, a'\}|\{b, b'\} \in \Sigma(T|_{\{a, a', b, b'\}}).$$

Proof. (of Lemma 7.) The proof is split into three cases, conditioned on the particular split of the quartet tree $T|_{\{a,b,c,y\}}$ we consider, of which there are three possible choices. Each of these cases is then broken down into three cases, conditioned on the particular split of another quartet tree, this give us in total nine cases we have to consider. We will present in detail the argument for the three cases in which $T|_{\{a,b,c,y\}} = ab|cy$, and since the other six cases are argued analogously, for the sake of brevity we will leave it as an exercise for the curious reader.

Therefore, without loss of generality let $T|_{\{a,b,c,y\}} = ab|cy$. We then consider the three cases conditioned on the non-trivial split of the quartet tree $T_{\{a,b,x,y\}}$.

First, assume that $T|_{\{a,b,x,y\}} = ab|xy$. Then by Lemma 8 $\exists A_1|B_1, A_2|B_2 \in \Sigma(T)$ such that $a, b \in A_1$ and $c, y \in B_1$ (since we have $T|_{\{a,b,c,y\}} = ab|cy$) and such that $a, b \in A_2$ and $x, y \in B_2$ (since we have $T_{\{a,b,x,y\}} = ab|xy$). Since $A_1|B_1, A_2|B_2 \in \Sigma(T)$ are splits on T, they must be compatible, and hence we know that one of the intersections

$$A_1 \cap A_2, \qquad\qquad A_1 \cap B_2, \qquad\qquad B_1 \cap A_2, \qquad\qquad B_1 \cap B_2,$$

must be empty. Now by examining the element memberships above we see that,

$$a \in A_1 \cap A_2 \neq \emptyset \text{ and } y \in B_1 \cap B_2 \neq \emptyset.$$

This leaves us with two possible choices, either $A_1 \cap B_2 = \emptyset$ or $B_1 \cap A_2 = \emptyset$. If $A_1 \cap B_2 = \emptyset$, then by definition $A_i = Y \backslash B_i$ for $i = 1, 2$ which in this case implies that $A_1 \subseteq A_2$ and equivalently $B_2 \subseteq B_1$. Recalling the element memberships, we see that $a, b \in A_1$ and $c, y, x \in B_1$, and by Lemma 8 we have that $T|_{\{a,b,c,x\}} = ab|cx$.

Second, assume that $T|_{\{a,b,x,y\}} = ax|by$. Then by Lemma 8 $\exists A_1|B_1, A_2|B_2 \in \Sigma(T)$ such that $a, b \in A_1$ and $c, y \in B_1$ and such that $a, x \in A_2$ and $b, y \in B_2$. Since $A_1|B_1, A_2|B_2 \in \Sigma(T)$ are splits on T, they must be compatible, and we know that one of the intersections

$$A_1 \cap A_2, \qquad\qquad A_1 \cap B_2, \qquad\qquad B_1 \cap A_2, \qquad\qquad B_1 \cap B_2,$$

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must be empty. Now by examining the element memberships above we see that,

$$a \in A_1 \cap A_2 \neq \emptyset \text{ and } y \in B_1 \cap B_2 \neq \emptyset \text{ and } b \in A_1 \cap B_2 \neq \emptyset.$$

This leaves us with the only possibility, $B_1 \cap A_2 = \emptyset$. This implies that $A_2 \subseteq A_1$ and equivalently $B_1 \subseteq B_2$. Recalling the element memberships, we see that $a, x \in A_2$ and $b, c, y \in B_2$, and by Lemma 8 we have that $T|_{\{a,b,c,x\}} = ax|bc$.

Third, assume that $T|_{\{a,b,x,y\}} = ay|bx$. Then by Lemma 8 $\exists A_1|B_1, A_2|B_2 \in \Sigma(T)$ such that $a, b \in A_1$ and $c, y \in B_1$ and such that $a, y \in A_2$ and $b, x \in B_2$. Since $A_1|B_1, A_2|B_2 \in \Sigma(T)$ are splits on T, they must be compatible, and hence we know that one of the intersections

$$A_1 \cap A_2, \qquad\qquad A_1 \cap B_2, \qquad\qquad B_1 \cap A_2, \qquad\qquad B_1 \cap B_2,$$

must be empty. Now by examining the element memberships above we see that,

$$a \in A_1 \cap A_2 \neq \emptyset \text{ and } y \in B_1 \cap A_2 \neq \emptyset \text{ and } b \in A_1 \cap B_2 \neq \emptyset.$$

This leaves us with the only possibility, $B_1 \cap B_2 = \emptyset$. This implies that $B_2 \subseteq A_1$ and equivalently $B_1 \subseteq A_2$. Recalling the element memberships, we see that $a, c, y \in A_2$ and $b, x \in B_2$, and by Lemma 8 we have that $T|_{\{a,b,c,x\}} = bx|ac$.

The other six cases, first three for $T_|\{a, b, c, y\} = ac|by$ and conditioned on $T_|\{a, c, x, y\}$ and the second three for $T_|\{a, b, c, y\} = ay|bc$ and conditioned on $T_|\{b, c, x, y\}$, follow completely analogously. $\qquad\square$

For the proof of Theorem 6 we refer the reader to *Matsen et al.*[11]. It is from this theorem that the *Six-To-Infinity* follows as a corollary, which is itself a restatement of Corollary 25 in *Matsen et al.*

**Theorem 9. *Six-To-Infinity:* [*Theorem 4.5 in Hollering&Sullivant [1]*] *Suppose that the tree parameters T_1, T_2 are identifiable for a 2-tree mixture model for trees with six leaves. Then the tree parameters are identifiable for trees with n leaves for all $n \geq 6$.*

We wish to check that each possible pair of 2-mixture models is identifiable. There are 105 total possible unrooted 6-leaf phylogenetic trees. There are a total of $\frac{105(105-1)}{2} + 105 = 5565$ multisets of the possible unrooted 6-leaf trees of cardinality two. Therefore there are $\frac{5565(5565-1)}{2} = 15481830$ possible pairs of multisets of cardinality two that we have to check. Note that each mulitsets corresponds to the tree parameters of a 2-mixture model. Now, we can greatly reduce the number of cases we need to check down to 22773 by considering the tree-parameters up to the action of a permutation $\sigma \in \mathfrak{S}_6$ on the set of leaves [6]. To explain further why this simplification works, we will need the following lemma:

Lemma 10. *Let $\sigma \in \mathfrak{S}_6$ be a permutation of the leaf-label set [6]. Define the action of σ on a 6-leaf phylogenetic tree T by switching all the leaf-labels i of T with $\sigma(i)$, i.e. if $\mathcal{L} \subseteq \mathcal{V}$ is the set of leaves of T, and $l : \mathcal{L} \to [6]$ is the labelling-function which labels the leaves of T by elements of [6], then σT is a 6-leaf phylogenetic tree with labelling-function $l_\sigma : \mathcal{L} \to [6]$ such that $l_\sigma(v) = \sigma \circ l(v)$. Then the Fourier coordinates $\underline{q}$ of the model on T and the Fourier coordinates $\sigma \underline{q}$ of the model on σT are related as follows. For the non-zero elements of $\sigma \underline{q}$:*

$$\sigma q_{g(1)\ldots g(6)} = \prod_{A \in \Sigma(\sigma T)} \alpha_{\sum_{i \in A} g^{(i)}}^{(A)} = \prod_{\sigma^{-1} A \in \Sigma(T)} \alpha_{\sum_{i \in \sigma^{-1}A} g^{(i)}}^{(\sigma^{-1}A)} = q_{g(\sigma^{-1}(1))\ldots g(\sigma^{-1}(6))} \tag{11}$$

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where we define $\sigma A = \{\sigma(i) \mid i \in A\}$, and for the zero elements of $\sigma \underline{q}$ we have,

$$\sigma q_{g^{(1)} \ldots g^{(6)}} = 0 = q_{g^{(\sigma^{-1}(1))} \ldots g^{(\sigma^{-1}(6))}}$$

Proof. Let T be a six-leaf phylogenetic tree, $\sigma \in \mathfrak{S}_6$, and σT denote the phylogenetic tree with the permuted leaf labellings. Note that given a split $A \in \Sigma(T)$ of the tree T, $\sigma A \in \Sigma(\sigma T)$ is a split of the tree σT. Similarly for any split $A \in \Sigma(\sigma T)$ of the tree σT we have that $\sigma^{-1} A \in \Sigma(T)$. Since σ is a bijection, this sets up a bijective map between the sets of splits $\Sigma(T)$ and $\Sigma(\sigma T)$, hence we may rewrite,

$$A \in \Sigma(\sigma T) \ \text{as} \ \sigma^{-1} A \in \Sigma(T).$$

Considering a general element of $\sigma \underline{q}$ indexed by $g^{(1)} \cdots g^{(6)}$, by applying the above result we obtain Equation 11. Since the permutation σ only permutes the binary number $g^{(1)} \cdots g^{(6)}$ and doesn't flip any 1's to 0's or vice versa, it follows that $g^{(1)} \cdots g^{(6)}$ and $g^{(\sigma^{-1}(1))} \cdots g^{(\sigma^{-1}(6))}$ have the same number of 1's, and thus if both have an odd number of ones then it follows that $\sigma q_{g^{(1)} \ldots g^{(6)}} = 0 = q_{g^{(\sigma^{-1}(1))} \ldots g^{(\sigma^{-1}(6))}}$. This covers both cases and hence establishes the result. $\qquad \square$

Note that the above lemma tells us that the Fourier coordinates have the same "shape" up to re-indexing and up to re-parametrising. Furthermore, note that this lemma holds for general number of leaves n, and we leave it to the curious reader to establish the more general result if they wish. For us, the $n = 6$ case suffices and we will continue onwards. With the help of the above lemma we can prove the following Theorem which will let us only check tree-parameters up to the action of $\mathfrak{S}_6$ on the set of all 2-mixture model tree parameters:

Theorem 11. *Let $\mathbf{T} = \{T_1, T_2\}$ and $\mathbf{S} = \{S_1, S_2\}$ be the tree parameters of the pair of 2-mixture models $M_\mathbf{T}$ and $M_\mathbf{S}$, and let $\sigma \in \mathfrak{S}_6$. Let $\sigma \mathbf{T} = \{\sigma T_1, \sigma T_2\}$ and $\sigma \mathbf{S} = \{\sigma S_1, \sigma S_2\}$ be the tree parameters of the pair of 2-mixture models $M_{\sigma \mathbf{T}}$ and $M_{\sigma \mathbf{S}}$. Then there exists a bijective map $\phi : [64] \to [64]$ induced by the permutation σ which is both a matroid bijection for $\phi : \mathcal{M}(J(\psi_\mathbf{T})) \to \mathcal{M}(J(\psi_{\sigma \mathbf{T}}))$ and for $\phi : \mathcal{M}(J(\psi_\mathbf{S})) \to \mathcal{M}(J(\psi_{\sigma \mathbf{S}}))$.*

Proof. By applying Lemma 10 to the phylogenetic models on the trees T_1 and T_2 we can conclude that the Fourier coordinates of the 2-mixture model with the tree parameters $\sigma \mathbf{T} = \{\sigma T_1, \sigma T_2\}$ are a permutation of the Fourier coordinates of the 2-mixture model with the tree parameters $\mathbf{T} = \{T_1, T_2\}$ (with potentially different parameter labels). Similarly, we can apply Lemma 10 to conclude that the Fourier coordinates of the 2-mixture model with tree parameters $\sigma \mathbf{S}$ are a permutation of the Fourier coordinates of the 2-mixture model with tree parameters $\mathbf{S}$. More specifically, let $D_{64} = \{n \mid n \in \mathbb{Z}, 0 \leq n < 64,\ n \text{ written in decimal}\}$ be the set of non-negative integers from 0 to 63 inclusive which are written in decimal, and let $B_{64} = \{n \mid n \in \mathbb{Z}, 0 \leq n < 64,\ n \text{ written in binary with length six}\}$ be the set of non-negative integers from 0 to 63 inclusive which are written in binary strings of length six, i.e. the number 11 would be written 001011. Let's define the map $\omega : D_{64} \to B_{64}$ to be the map which rewrites a number n written in decimal as a number in binary of length six, e.g. $\omega(11) = 001011$. It's immediate that ω is a bijection, and hence we can talk of the inverse map $\omega^{-1} : B_{64} \to D_{64}$. When the Fourier coordinates of the 2-mixture models are indexed by elements of B_{64}, it follows that $\sigma : B_{64} \to B_{64}$ is the permutation which relates the Fourier coordinates of the 2-mixture on $\mathbf{T}$ with the Fourier coordinates of the 2-mixture on $\sigma \mathbf{T}$, more precisely we have that:

$$q_{g^{(\sigma(1))} \ldots g^{(\sigma(6))}} = \sigma q_{g^{(1)} \ldots g^{(6)}}$$

If we wish to index the Fourier coordinates by elements of D_{64}, then instead the permutation is given by $\phi = \omega^{-1} \circ \sigma \circ \omega$. Crucially the same permutation ϕ relates the Fourier coordinates of the 2-mixture models with tree parameters $\mathbf{T}$ and $\sigma\mathbf{T}$, as well as the 2-mixture models with tree parameters $\mathbf{S}$ and $\sigma\mathbf{S}$.

Now, from the definition of $J(\psi_{\mathbf{T}})$ and $J(\psi_{\mathbf{S}})$ we see that permuting the Fourier coordinates by σ obtained from the parametrisation maps $\psi_{\mathbf{T}}$ and $\psi_{\mathbf{S}}$, results in a permutation by ϕ of the columns of the matrices $J(\psi_{\mathbf{T}})$ and $J(\psi_{\mathbf{S}})$. Note here that the columns of the transposed-Jacobian matrices are indexed by integers from 0 to 63, whilst for the matroid isomorphism we want to index the columns of the matrices by integers from 1 to 64. Therefore to be strictly correct we define the map $s : \mathbb{Z} \to \mathbb{Z}$ such that $s(n) = n + 1$, and using s and ϕ we define the bijective map $\phi' = s \circ \phi \circ s^{-1}$, which is the same permutation of columns but with the indices shifted by one. By Corollary 4.1 we can conclude that $\phi' : [64] \to [64]$ gives in fact a matroid isomorphism such that $\mathcal{M}(J(\psi_{\mathbf{T}})) \cong \mathcal{M}(J(\psi_{\sigma\mathbf{T}}))$ and such that $\mathcal{M}(J(\psi_{\mathbf{S}})) \cong \mathcal{M}(J(\psi_{\sigma\mathbf{S}}))$. □

From Theorem 11 we obtain the following corollary which will let us establish generic identifiability results for all 2-mixture models whose parameters are related by some permutation $\sigma \in \mathfrak{S}_6$ just by proving generic identifiability for one of those 2-mixture models.

Corollary 11.1. *Let* $\mathbf{T} = \{T_1, T_2\}$ *and* $\mathbf{S} = \{S_1, S_2\}$ *be the tree parameters of the pair of 2-mixture models* $M_{\mathbf{T}}$ *and* $M_{\mathbf{S}}$, *and let* $\sigma \in \mathfrak{S}_6$. *Then if there exists* $I \in \mathcal{I}_{J(\psi_{\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\mathbf{S}})}$, *then* $\phi(I) \in \mathcal{I}_{J(\psi_{\sigma\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\sigma\mathbf{S}})}$.

Proof. By Theorem 11 we have the bijective map ϕ such that $\mathcal{M}(J(\psi_{\mathbf{T}})) \cong \mathcal{M}(J(\psi_{\sigma\mathbf{T}}))$ and $\mathcal{M}(J(\psi_{\mathbf{S}})) \cong \mathcal{M}(J(\psi_{\sigma\mathbf{S}}))$. Therefore, if we additionally have and independent set $I \subseteq E$ such that $I \in \mathcal{I}_{J(\psi_{\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\mathbf{S}})}$, then by definition of matroid isomorphism we know that both $\phi(I) \in \mathcal{I}_{J(\psi_{\sigma\mathbf{T}})}$ and $\phi(I) \notin \mathcal{I}_{J(\psi_{\sigma\mathbf{S}})}$, from which we obtain the desired result $\phi(I) \in \mathcal{I}_{J(\psi_{\sigma\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\sigma\mathbf{S}})}$. □

Let $\mathbf{T} = \{T_1, T_2\}$ and $\mathbf{S} = \{S_1, S_2\}$ be the tree parameters for a pair of 2-mixture models on six leaves, and let $\sigma \in \mathfrak{S}_6$. Furthermore, let's assume that we have subset $S \subseteq [64]$ of column indices of the Jacobians $J(\psi_{\mathbf{T}})$ and $J(\psi_{\mathbf{S}})$ such that $S \in \mathcal{I}_{J(\psi_{\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\mathbf{S}})}$. Then as a consequence we also have a subset $\phi(S) \subseteq [64]$ such that $\phi(S) \in \mathcal{I}_{J(\psi_{\sigma\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\sigma\mathbf{S}})}$. Since permutations are bijections, we can also consider starting with a pair 2-mixture models on six leaves with tree parameters $\sigma\mathbf{T} = \{\sigma T_1, \sigma T_2\}$ and $\sigma\mathbf{S} = \{\sigma S_1, \sigma S_2\}$, together with a set $S \in \mathcal{I}_{J(\psi_{\sigma\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\sigma\mathbf{S}})}$, and applying Corollary 11.1 with the permutation σ^{-1} to obtain the subset $\phi^{-1}(S) \in \mathcal{I}_{J(\psi_{\mathbf{T}})} \backslash \mathcal{I}_{J(\psi_{\mathbf{S}})}$. Thus proving generic identifiability for one pair of 2-mixture models with tree parameters $\mathbf{T}$ and $\mathbf{S}$ is equivalent to proving generic identifiability for the pair of 2-mixture models with tree parameters $\sigma\mathbf{T}$ and $\sigma\mathbf{S}$. Hence instead of checking each of the 15481830 possible pairs of 2-multisets, we only have to take representatives of the orbits of 2-multisets induced by the action of the group $\mathfrak{S}_6$. This fact let's us greatly reduce the number of cases to consider, down to 22773, and with this simplification step out of the way it's now time to discuss Algorithm 3.3 which will allow us to establish generic identifiability for those 22773 cases.

4.4 Algorithm 3.3

Here we explain in detail the key concepts behind the *Hollering & Sturmfels* algorithm. One of those key concepts is captured in the following proposition.

Proposition 42. *[Proposition 3.1 [1]]*
Let M_1 and M_2 be two irreducible algebraic models which sit inside the probability simplex Δ_r. Without loss of generality assume $\dim(M_1) \geq \dim(M_2)$. Let $\mathcal{M}(M_1) = ([r], \mathcal{I}_1)$ and $\mathcal{M}(M_2) = ([r], \mathcal{I}_2)$ be the algebraic matroids of the models M_1 and M_2 respectively. If there exists a subset $I \subseteq \{x_1, \ldots, x_r\}$ of the coordinates of the probability simplex such that,

$$I \in \mathcal{I}_1 \backslash \mathcal{I}_2, \tag{12}$$

then $\dim(M_1 \cap M_2) < \min(\dim(M_1), \dim(M_2))$.

The main consequence of the above proposition is that we can show generic identifiability of a pair of 2-mixture models by showing that their matroids are not equal. This is the theoretical heart of the algorithm, and everything else now focuses on optimising the computations that we have to carry out to distinguish the algebraic matroids. First, recall that by Proposition 6.7.10 of *Oxley*[8] we have the following equality,

$$\mathcal{M}(V_{\mathbf{T}}) = \mathcal{M}(J(\psi_{\mathbf{T}})), \tag{13}$$

between the algebraic matroid of $V_{\mathbf{T}}$ and the linear matroid on $J(\psi_{\mathbf{T}})$. Note that in *Hollering & Sullivant* the authors sometimes refer to $\mathcal{M}(J(\psi_{\mathbf{T}}))$ as the *symbolic matroid*, and we may do so here too. Computing the algebraic matroid $\mathcal{M}(V_{\mathbf{T}})$ requires the computationally expensive calculation of the Groebner basis for $V_{\mathbf{T}}$, and hence computing the algebraic matroid to determine the dimension of the intersection $M_1 \cap M_2$ isn't that much better computationally (if at all!) to computing $M_1 \cap M_2$ using the Groebner basis. On the other hand, the linear matroid $\mathcal{M}(J(\psi_{\mathbf{T}}))$ avoids Groebner basis calculations, however we have to work over the fraction field $k(\Theta)$ which again tends to be computationally expensive, but not as much as the Groebner basis computations.

Second, recalling Definition 35 **if** we choose a parameter $\theta_0 \in \Theta$ from the parameters space such that $\theta_0 \notin \mathcal{NM}(\psi_{\mathbf{T}})$ then we have the following equality,

$$\mathcal{M}(J(\psi_{\mathbf{T}})) = \mathcal{M}(J(\psi_{\mathbf{T}}(\theta_0))), \tag{14}$$

between the symbolic matroid and the linear matroid on $J(\psi_{\mathbf{T}}(\theta_0))$, the Jacobian evaluated at θ_0. The reader will recall that $\dim(V_{\mathcal{NM}}) < \dim(V_{\mathbf{T}})$, where $V_{\mathcal{NM}}$ is the variety corresponding to the non-matroidal locus $\mathcal{NM}(\psi) \subseteq \Theta$ which is a subset of the parameter space. Therefore by picking a random parameter value θ_0, then the probability that $\theta_0 \in \mathcal{NM}(\psi_{\mathbf{T}})$ is zero. Having said that, even though that for a random $\theta_0 \in \Theta$, $\mathbb{P}(\theta_0 \in \mathcal{NM}(\psi_{\mathbf{T}})) = 0$ it is not *impossible* that a randomly picked parameter θ_0 is in the non-matroidal locus, hence whilst picking random parameter values and verifying independent sets for the computationally inexpensive $J(\psi_{\mathbf{T}}(\theta_0))$ almost surely will correspond to the independent sets of $J(\psi_{\mathbf{T}})$, this is not guaranteed with a level of rigour we desire. So the idea of the algorithm is to find candidate a independent set S by working with the fixed matrices $\psi_{\mathbf{T}}(\theta_0)$ and $\psi_{\mathbf{S}}(\theta_0)$ for some randomly chosen $\theta_0 \in \Theta$, and then verify that S is indeed an independent set for the symbolic matroids of $J(\psi_{\mathbf{T}})$ and $J(\psi_{\mathbf{S}})$ (and hence for the algebraic matroids) by doing a single but computationally expensive calculation over the fraction field $k(\Theta)$. We now present the algorithm in *Hollering & Sullivant*:

Algorithm 43. *[Algorithm 3.3 [1]]*
`Input:  Two maps` ψ_T `and` ψ_S`, parametrising the models` M_1 `and` M_2 `in` k^n `with` $\dim(M_1) \geq$

$\dim(M_2)$, *and a number of trials* t.
Output: An independent set I *which satisfies Equation 12 in Proposition 42.*

For $i = 1, 2, \ldots, t$:

- *Randomly select* $S \subseteq [n]$ *such that* $|S| \le \dim(M_2)$.

- *If* $S \in \mathcal{I}_{J(\psi_\mathbf{T}(\theta_0))} \backslash \mathcal{I}_{J(\psi_\mathbf{S}(\theta_0))}$:

    - *If* $S \in \mathcal{I}_{J(\psi_\mathbf{T})} \backslash \mathcal{I}_{J(\psi_\mathbf{S})}$:

        then $I = S$; *return* I

Otherwise; return "No Certificate Found."

We present our implementation of this algorithm in the Appendix A. For our model example, we were able to verify using the Mathematica code from *Hollering & Sullivant* that the set

$$S = \{24, 40, 59, 34, 7, 54, 58, 64, 35, 30, 55, 18, 11, 19\},$$

satisfies $S \in \mathcal{I}_{J(\psi_\mathbf{T}(\theta_0))} \backslash \mathcal{I}_{J(\psi_\mathbf{S}(\theta_0))}$, where $\mathrm{rank}(J(\psi_\mathbf{T}(\theta_0))) = 14 \ne 13 = \mathrm{rank}(J(\psi_\mathbf{S}(\theta_0)))$. Moreover, we were able to verify that for this set S we have $S \in \mathcal{I}_{J(\psi_\mathbf{T})} \backslash \mathcal{I}_{J(\psi_\mathbf{S})})$, again using the Mathematica code from *Hollering & Sullivant*. It seems that symbolic calculations are faster in Mathematica than compared to SageMath, and if we had more time we would have liked to either see if our SageMath code could be optimised for symbolic computations or alternatively whether we could have written our own implementation of Algorithm 3.3 in Mathematica.

5   Conclusion

We have thoroughly discussed the ideas behind and implementation of the matroid distinguishing algorithm used in *Hollering & Sullivant* [1] which establishes generic identifiability results for 2-mixture phylogenetic CFN models on six leaves, and combined with the results of *Matsen et al.* [11] this result is extended to generic identifiability for 2-mixture phylogenetic CFN models on *at least* six leaves. It's important to mention that *Hollering & Sullivant* establish identifiability results for other group based model mixtures, for example have shown generic identifiability for 2-mixtures phylogenetic K3P models on at least four leaves. Given more time we would have liked to discuss those results as well, and to explain the modifications to the arguments for the CFN models needed to establish results for the K3P models.

Hollering & Sullivant have demonstrated the benefits and applicability of matroid theory as a tool to study phylogenetic models. For future research directions we would suggest to see how Theorem 4.6 can be adapted to prove identifiability results for r-mixture with $r > 2$. This would involve computing the maximal sized subsets needed to disentangle $B(X, r)$, as well as potentially a revision of Algorithm 3.3 to improve efficiency as the number of cases to consider (even with simplifications due to the action of $\mathfrak{S}_n$) are likely to explode for these larger mixtures. Matroid theory is finding new applications in the field of phylogenetic algebraic geometry, and we are eagerly looking forward to see where it leads.

A SageMath Code

```
def all_bin(n):

    """
    Takes a positive integer n and outputs a list of strings of binary numbers of
    length n
    Inputs:
    n | positive integer, number of leaves
    Outputs:
    bin_list | list of strings of all binary numbers of length n
    """

    bin_list = [f'{i:0{n}b}' for i in range(1 << n)]

    return bin_list
```

```
def empty_index(n):

    """
    Takes the number of leaves and outputs the list of numbers whose base 2 representation
    has an odd number of 1's.  These are the indices of the coordinates of the parametrisation
    map which will vanish in the Fourier parametrisation of the model.
    Inputs:
    n | positive integer, number of leaves
    Outputs:
    empty_cols | list of integers which contains the indices of coordinates equal to
    0 in the Fourier parametrisation of the models.
    """

    empty_cols = []

    for i, state in enumerate(all_bin(n)):  # loops over all binary numbers of length
                                            # n and determines which have odd number
                                            # of 1's.
        tot = 0

        for leaf in state:  # sums all the digits of a binary number.

            tot += int(leaf)

            if tot%2 == 1:  # checks whether the number of 1's is odd or even

                empty_cols.append(i)
```

```
        return empty_cols


def inner_state(bin_num, splits):

    """
    For a particular binary number bin_num which represents the combined-state observed
    at the leaves of an n-leaf tree, it calculates what subscripts will appear on
    the transformed parameters of the inner edges in the Fourier parametrisation of
    the model.
    Inputs:
    bin_num | a string of length n which represents a binary number.
    splits | a list of non-trivial tree which the phylogenetic model is based on.
    Outputs:
    inner_state | a string of length n-3 which represents a binary number.
    """

    n = len(bin_num)

    inner_state = ''

    for split in splits:  # loops over the tree splits, using them to determine states
                          # at the inner nodes.
        tot = 0

        for leaf in split:  # determines the state at the inner node which is the terminal
                            # node of the split.

            tot += int(bin_num[leaf-1])

            inner_state = inner_state + f'{tot % 2}'

    return inner_state


def fourier_map(splits, n, label):

    """
    Given the splits of the tree T and number of leaves, calculates the fourier parametrisation
    of the CFN model on T. Note that label serves the role of a dummy variable which
    acts as the placeholder for the subscripts and superscripts which actually contain
    information.
    Inputs:
    splits | a list of non-trivial tree which the phylogenetic model is based on.
    n | natural number, number of leaves.
    label | a string which is used as a dummy variable in the parametrisation.
```

```
Outputs:
fourier_coords | a list which contains the Fourier coordinates of the phylogenetic
model.
param_list | a list of variables which represent the transformed paramters of the
model.
"""

param_list = []

for i in range(1,n+1):  # creates transformed parameters corresponding to trivial
                        # splits.

    param_list.append(var(label+f'{i}'))

for split in splits:  # creates transformed parameters corresponding to non-trivial
                      # splits.

    comb = ''

    for leaf in split:

    comb = comb+f'{leaf}'

    param_list.append(var(label+f'comb'))

fourier_coords = []

for state in all_bin(n):  # loops over all possible binary combined-states and
                          # determines the corresponding Fourier coordinates.

    check = 0

    for leaf in state:

        check += int(leaf)

    if check%2 == 0:  # We obtain non-zero coordinates iff the states (digits of
                      # binary number) sum to zero.

        coord = 1

        for i, leaf in enumerate(state):  # Loops over states at the leaves and
                                          # appends Fourier parameters if appropriate.

            if leaf == '1':
```

```
                    coord = coordparam_list[i]

            in_state = inner_state(state, splits)

            for i, digit in enumerate(in_state):  # Loops over states of the inner
                                                  # nodes and append Fourier parameters
                                                  # if appropriate.

                if digit == '1':

                    coord = coordparam_list[n+i]

            fourier_coords.append(coord)

        else:

            fourier_coords.append(0)

    return fourier_coords, param_list

    ___


def twomix_fourier_map(map1, map2, params1, params2, mix):

    """
    Given two parametrisations in Fourier coordinates, defines the 2-mixture model parametrisation
    in terms of the Fourier coordinates.
    Inputs:
    map1 | a list of Fourier coordinates of the first model in the 2-mixture.
    map2 | a list of Fourier coordinates of the second model in the 2-mixture.
    params1 | a list of transformed parameters used in the parametrisation of the first
    model.
    params1 | a list of transformed parameters used in the parametrisation of the second
    model.
    mix | a string which will serve as the symbol we use for the mixing parameter of the
    2 -mixture model.
    Outputs:
    twomix_map | a list of Fourier coordinates of the 2-mixture model.
    all_params | a list of transformed parameters used in the parametrisation of the 2-mixture
    model.
    """

    mix_sym = var(mix)

    all_params = params1 + params2
    all_params.append(mix_sym)
```

```
    twomix_map = []

    for i in range(len(map1)):  # for each pair of Fourier coordinates, one from each
                                # model, this will create the corresponding coordinate
                                of the 2-mixture model, as the weighted sum.
                                # of the 2-mixture model, as the weighted sum.

        twomix_map.append(mix_sym*map1[i] + (1 - mix_sym)*map2[i])

    return twomix_map, all_params


def matrix_remove_cols(M, cols_to_del):

    """
    Removes the columns with indices specifies in cols_to_del from matrix M, and returns
    thus obtained submatrix.
    Inputs:
    M | matrix.
    cols_to_del | list, of column indices of M to delete.
    Outputs:
    sub_M | matrix, which is a submatrix of M.
    """

    ncols = M.ncols()

    # determines which columns of M to keep.
    cols_to_keep = list(set([i for i in range(ncols)]) - set(cols_to_del))

    sub_M = M.matrix_from_columns(cols_to_keep)

    return sub_M


import random as ran

def special_matrix(M, params, seed):

    """
    Takes a matrix M whose entries are polynomials in terms of the variables in params
    (i.e.  the matrix has ground field C(params), the fraaction field over C with variables
    in params), and evaluates those entries based on random parameter values to create
    a new matrix whose entries are the evaluated polynomials (and now this is a matrix
    over the ground field C).
    Inputs:
    M | Matrix, the jacobian of the parametrisation of the 2-mixture model.
```

```
    params| list, of parameters used in the parametrisation.  seed | positive integer,
    used to allow for reproducibility when using the random library.
    Outputs:
    M_spec | Matrix, whose entries are now evaluated polynomials for random parameter
    values.
    """

    ran.seed(int(seed)) # set seed for reproducibilty.

    M_spec = copy(M)

    in_dict = dict() # dictionary which will record the random values our parameters take.

    for k in range(len(params)-1):  # initialises random values for the transformed parameters,
                                     # which can take any value from -1 to 1.

        in_dict[params[k]] = 2*ran.random()-1

    in_dict[params[len(params)-1]] = ran.random() # initialises random value for the mixing
                                                  # parameter, which can take any value
                                                  # from 0 to 1.

    for i in range(M.nrows()):  # loops over each entry of M and evaluates polynomials
                                # based on values in in_dict.

        for j in range(M.ncols()):

            poly = M[i,j]

            poly = poly.subs(in_dict) # evaluates the polynomial entry.

            M_spec[i,j] = poly

    M_spec = Matrix(CC, M_spec) # defines the new specialised matrix over C.

    return M_spec

___

import random as ran

def certificate_finder(mat1, mat2, ntrials, params1, params2, seed1, seed2, s=19):

    """
    Randomly picks a subset S of column indices of cardinality s (the default is s = 19)
    and first checks if S is an independent set for one of the linear matroids but not
    the other, and if so subsequently checks whether S is an independent set for one of
```

the symbolic matroids but not the other. Either returns a subset which differentiates
between the symbolic matroids, or if no such subset is found returns False.
Inputs:
mat1 | matrix, Jacobian of the parametrisation of the first 2-mixture model.
mat2 | matrix, Jacobian of the parametrisation of the second 2-mixture model.
ntrials | positive integer, number of tries we wish to give the program to find a
suitable independent set ranS.
params1 | list, of parameters used to parametrise the first 2-mixture model.
params2 | list, of parameters used to parametrise the second 2-mixture model.
seed1 | positive integer, seed for the first Jacobian when calling special_matrix().
seed2 | positive integer, seed for the second Jacobian when calling special_matrix().
s | positive integer, the cardinality of S that we want to specify (default s = 19).
Outputs:
S | list, of column indices which are an independent set for one matroid but not the
other.
"""

```
groundset = [i for i in range(31)] sub = Subsets(groundset, s)

mat1_spec = special_matrix(mat1, params1, seed1) # defines the fixed specialised Jacobians.
mat2_spec = special_matrix(mat2, params2, seed2)

for i in range(ntrials):

    # picks a random subset of the groundset of cardinality 19.
    ranS = ran.choices(range(sub.cardinality()), k=1)
    S = list(sub[ranS[0]])

    # checks if S is a certificate for specialised Jacobians.
    if mat1_spec.matrix_from_columns(S).rank() != mat2_spec.matrix_from_columns(S).rank():

        # checks if S is a certificate for the symbolic Jacobians.
        if mat1.matrix_from_columns(S).rank() != mat2.matrix_from_columns(S).rank():

            return S

return False
```

B Clean Jacobians of the 2-mixture models

We would like to explicitly present the (clean) Jacobian matrices for the parametrisations $\psi_{\mathbf{T}}$ and $\psi_{\mathbf{S}}$, but in order to do this we will have to break them apart into 10 $19 \times w$ matrices, where $2 \leq w \leq 4$ which we denote by $A_1, \ldots A_{10}$ for the blocks of $J^c(\psi_{\mathbf{T}})$ and $B_1, \ldots B_{10}$ for the blocks of $J^c(\psi_{\mathbf{S}})$. We first present the blocks for $J^c(\psi_{\mathbf{T}})$:

$$
A_1 = \begin{pmatrix}
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & \alpha_6\alpha_{34}\alpha_{56}\lambda \\
0 & \alpha_6\alpha_{34}\alpha_{56}\lambda & \alpha_5\alpha_{34}\alpha_{56}\lambda & 0 \\
\alpha_6\lambda & 0 & \alpha_4\alpha_{34}\alpha_{56}\lambda & 0 \\
\alpha_5\lambda & \alpha_4\alpha_{34}\alpha_{56}\lambda & 0 & \alpha_3\alpha_{34}\alpha_{56}\lambda \\
0 & 0 & 0 & 0 \\
0 & \alpha_4\alpha_6\alpha_{56}\lambda & \alpha_4\alpha_5\alpha_{56}\lambda & \alpha_3\alpha_6\alpha_{56}\lambda \\
0 & \alpha_4\alpha_6\alpha_{34}\lambda & \alpha_4\alpha_5\alpha_{34}\lambda & \alpha_3\alpha_6\alpha_{34}\lambda \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & -\beta_6\beta_{34}\beta_{56}\lambda + \beta_6\beta_{34}\beta_{56} \\
0 & -\beta_6\beta_{34}\beta_{56}\lambda + \beta_6\beta_{34}\beta_{56} & -\beta_5\beta_{34}\beta_{56}\lambda + \beta_5\beta_{34}\beta_{56} & 0 \\
-\beta_6\lambda + \beta_6 & 0 & -\beta_4\beta_{34}\beta_{56}\lambda + \beta_4\beta_{34}\beta_{56} & 0 \\
-\beta_5\lambda + \beta_5 & -\beta_4\beta_{34}\beta_{56}\lambda + \beta_4\beta_{34}\beta_{56} & 0 & -\beta_3\beta_{34}\beta_{56}\lambda + \beta_3\beta_{34}\beta_{56} \\
0 & 0 & 0 & 0 \\
0 & -\beta_4\beta_6\beta_{56}\lambda + \beta_4\beta_6\beta_{56} & -\beta_4\beta_5\beta_{56}\lambda + \beta_4\beta_5\beta_{56} & -\beta_3\beta_6\beta_{56}\lambda + \beta_3\beta_6\beta_{56} \\
0 & -\beta_4\beta_6\beta_{34}\lambda + \beta_4\beta_6\beta_{34} & -\beta_4\beta_5\beta_{34}\lambda + \beta_4\beta_5\beta_{34} & -\beta_3\beta_6\beta_{34}\lambda + \beta_3\beta_6\beta_{34} \\
\alpha_5\alpha_6 - \beta_5\beta_6 & \alpha_4\alpha_6\alpha_{34}\alpha_{56} - \beta_4\beta_6\beta_{34}\beta_{56} & \alpha_4\alpha_5\alpha_{34}\alpha_{56} - \beta_4\beta_5\beta_{34}\beta_{56} & \alpha_3\alpha_6\alpha_{34}\alpha_{56} - \beta_3\beta_6\beta_{34}\beta_{56}
\end{pmatrix}
$$

$$
A_2 = \begin{pmatrix}
0 & 0 & 0 & 0 \\
0 & 0 & 0 & \alpha_6\alpha_{12}\alpha_{56}\lambda \\
\alpha_5\alpha_{34}\alpha_{56}\lambda & \alpha_4\lambda & \alpha_4\alpha_5\alpha_6\lambda & 0 \\
0 & \alpha_3\lambda & \alpha_3\alpha_5\alpha_6\lambda & 0 \\
\alpha_3\alpha_{34}\alpha_{56}\lambda & 0 & \alpha_3\alpha_4\alpha_6\lambda & 0 \\
0 & 0 & \alpha_3\alpha_4\alpha_5\lambda & \alpha_2\alpha_{12}\alpha_{56}\lambda \\
0 & 0 & 0 & \alpha_2\alpha_6\alpha_{56}\lambda \\
\alpha_3\alpha_5\alpha_{56}\lambda & 0 & 0 & 0 \\
\alpha_3\alpha_5\alpha_{34}\lambda & 0 & 0 & \alpha_2\alpha_6\alpha_{12}\lambda \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & -\beta_6\beta_{12}\beta_{56}\lambda + \beta_6\beta_{12}\beta_{56} \\
-\beta_5\beta_{34}\beta_{56}\lambda + \beta_5\beta_{34}\beta_{56} & -\beta_4\lambda + \beta_4 & -\beta_4\beta_5\beta_6\lambda + \beta_4\beta_5\beta_6 & 0 \\
0 & -\beta_3\lambda + \beta_3 & -\beta_3\beta_5\beta_6\lambda + \beta_3\beta_5\beta_6 & 0 \\
-\beta_3\beta_{34}\beta_{56}\lambda + \beta_3\beta_{34}\beta_{56} & 0 & -\beta_3\beta_4\beta_6\lambda + \beta_3\beta_4\beta_6 & 0 \\
0 & 0 & -\beta_3\beta_4\beta_5\lambda + \beta_3\beta_4\beta_5 & -\beta_2\beta_{12}\beta_{56}\lambda + \beta_2\beta_{12}\beta_{56} \\
0 & 0 & 0 & -\beta_2\beta_6\beta_{56}\lambda + \beta_2\beta_6\beta_{56} \\
-\beta_3\beta_5\beta_{56}\lambda + \beta_3\beta_5\beta_{56} & 0 & 0 & 0 \\
-\beta_3\beta_5\beta_{34}\lambda + \beta_3\beta_5\beta_{34} & 0 & 0 & -\beta_2\beta_6\beta_{12}\lambda + \beta_2\beta_6\beta_{12} \\
\alpha_3\alpha_5\alpha_{34}\alpha_{56} - \beta_3\beta_5\beta_{34}\beta_{56} & \alpha_3\alpha_4 - \beta_3\beta_4 & \alpha_3\alpha_4\alpha_5\alpha_6 - \beta_3\beta_4\beta_5\beta_6 & \alpha_2\alpha_6\alpha_{12}\alpha_{56} - \beta_2\beta_6\beta_{12}\beta_{56}
\end{pmatrix}
$$

$$A_3 = \begin{pmatrix}
0 & 0 & 0 \\
\alpha_5\alpha_{12}\alpha_{56}\lambda & \alpha_4\alpha_{12}\alpha_{34}\lambda & \alpha_4\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda \\
0 & 0 & 0 \\
0 & \alpha_2\alpha_{12}\alpha_{34}\lambda & \alpha_2\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda \\
\alpha_2\alpha_{12}\alpha_{56}\lambda & 0 & \alpha_2\alpha_4\alpha_6\alpha_{12}\alpha_{34}\lambda \\
0 & 0 & \alpha_2\alpha_4\alpha_5\alpha_{12}\alpha_{34}\lambda \\
\alpha_2\alpha_5\alpha_{56}\lambda & \alpha_2\alpha_4\alpha_{34}\lambda & \alpha_2\alpha_4\alpha_5\alpha_6\alpha_{34}\lambda \\
0 & \alpha_2\alpha_4\alpha_{12}\lambda & \alpha_2\alpha_4\alpha_5\alpha_6\alpha_{12}\lambda \\
\alpha_2\alpha_5\alpha_{12}\lambda & 0 & 0 \\
0 & 0 & 0 \\
-\beta_5\beta_{12}\beta_{56}\lambda+\beta_5\beta_{12}\beta_{56} & -\beta_4\beta_{12}\beta_{34}\lambda+\beta_4\beta_{12}\beta_{34} & -\beta_4\beta_5\beta_6\beta_{12}\beta_{34}\lambda+\beta_4\beta_5\beta_6\beta_{12}\beta_{34} \\
0 & 0 & 0 \\
0 & -\beta_2\beta_{12}\beta_{34}\lambda+\beta_2\beta_{12}\beta_{34} & -\beta_2\beta_5\beta_6\beta_{12}\beta_{34}\lambda+\beta_2\beta_5\beta_6\beta_{12}\beta_{34} \\
-\beta_2\beta_{12}\beta_{56}\lambda+\beta_2\beta_{12}\beta_{56} & 0 & -\beta_2\beta_4\beta_6\beta_{12}\beta_{34}\lambda+\beta_2\beta_4\beta_6\beta_{12}\beta_{34} \\
0 & 0 & -\beta_2\beta_4\beta_5\beta_{12}\beta_{34}\lambda+\beta_2\beta_4\beta_5\beta_{12}\beta_{34} \\
-\beta_2\beta_5\beta_{56}\lambda+\beta_2\beta_5\beta_{56} & -\beta_2\beta_4\beta_{34}\lambda+\beta_2\beta_4\beta_{34} & -\beta_2\beta_4\beta_5\beta_6\beta_{34}\lambda+\beta_2\beta_4\beta_5\beta_6\beta_{34} \\
0 & -\beta_2\beta_4\beta_{12}\lambda+\beta_2\beta_4\beta_{12} & -\beta_2\beta_4\beta_5\beta_6\beta_{12}\lambda+\beta_2\beta_4\beta_5\beta_6\beta_{12} \\
-\beta_2\beta_5\beta_{12}\lambda+\beta_2\beta_5\beta_{12} & 0 & 0 \\
\alpha_2\alpha_5\alpha_{12}\alpha_{56}-\beta_2\beta_5\beta_{12}\beta_{56} & \alpha_2\alpha_4\alpha_{12}\alpha_{34}-\beta_2\beta_4\beta_{12}\beta_{34} & \alpha_2\alpha_4\alpha_5\alpha_6\alpha_{12}\alpha_{34}-\beta_2\beta_4\beta_5\beta_6\beta_{12}\beta_{34}
\end{pmatrix}$$

$$A_4 = \begin{pmatrix}
0 & 0 & 0 \\
\alpha_3\alpha_{12}\alpha_{34}\lambda & \alpha_3\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda & \alpha_3\alpha_4\alpha_6\alpha_{12}\alpha_{56}\lambda \\
\alpha_2\alpha_{12}\alpha_{34}\lambda & \alpha_2\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda & \alpha_2\alpha_4\alpha_6\alpha_{12}\alpha_{56}\lambda \\
0 & 0 & \alpha_2\alpha_3\alpha_6\alpha_{12}\alpha_{56}\lambda \\
0 & \alpha_2\alpha_3\alpha_6\alpha_{12}\alpha_{34}\lambda & 0 \\
0 & \alpha_2\alpha_3\alpha_5\alpha_{12}\alpha_{34}\lambda & \alpha_2\alpha_3\alpha_4\alpha_{12}\alpha_{56}\lambda \\
\alpha_2\alpha_3\alpha_{34}\lambda & \alpha_2\alpha_3\alpha_5\alpha_6\alpha_{34}\lambda & \alpha_2\alpha_3\alpha_4\alpha_6\alpha_{56}\lambda \\
\alpha_2\alpha_3\alpha_{12}\lambda & \alpha_2\alpha_3\alpha_5\alpha_6\alpha_{12}\lambda & 0 \\
0 & 0 & \alpha_2\alpha_3\alpha_4\alpha_6\alpha_{12}\lambda \\
0 & 0 & 0 \\
-\beta_3\beta_{12}\beta_{34}\lambda+\beta_3\beta_{12}\beta_{34} & -\beta_3\beta_5\beta_6\beta_{12}\beta_{34}\lambda+\beta_3\beta_5\beta_6\beta_{12}\beta_{34} & -\beta_3\beta_4\beta_6\beta_{12}\beta_{56}\lambda+\beta_3\beta_4\beta_6\beta_{12}\beta_{56} \\
-\beta_2\beta_{12}\beta_{34}\lambda+\beta_2\beta_{12}\beta_{34} & -\beta_2\beta_5\beta_6\beta_{12}\beta_{34}\lambda+\beta_2\beta_5\beta_6\beta_{12}\beta_{34} & -\beta_2\beta_4\beta_6\beta_{12}\beta_{56}\lambda+\beta_2\beta_4\beta_6\beta_{12}\beta_{56} \\
0 & 0 & -\beta_2\beta_3\beta_6\beta_{12}\beta_{56}\lambda+\beta_2\beta_3\beta_6\beta_{12}\beta_{56} \\
0 & -\beta_2\beta_3\beta_6\beta_{12}\beta_{34}\lambda+\beta_2\beta_3\beta_6\beta_{12}\beta_{34} & 0 \\
0 & -\beta_2\beta_3\beta_5\beta_{12}\beta_{34}\lambda+\beta_2\beta_3\beta_5\beta_{12}\beta_{34} & -\beta_2\beta_3\beta_4\beta_{12}\beta_{56}\lambda+\beta_2\beta_3\beta_4\beta_{12}\beta_{56} \\
-\beta_2\beta_3\beta_{34}\lambda+\beta_2\beta_3\beta_{34} & -\beta_2\beta_3\beta_5\beta_6\beta_{34}\lambda+\beta_2\beta_3\beta_5\beta_6\beta_{34} & -\beta_2\beta_3\beta_4\beta_6\beta_{56}\lambda+\beta_2\beta_3\beta_4\beta_6\beta_{56} \\
-\beta_2\beta_3\beta_{12}\lambda+\beta_2\beta_3\beta_{12} & -\beta_2\beta_3\beta_5\beta_6\beta_{12}\lambda+\beta_2\beta_3\beta_5\beta_6\beta_{12} & 0 \\
0 & 0 & -\beta_2\beta_3\beta_4\beta_6\beta_{12}\lambda+\beta_2\beta_3\beta_4\beta_6\beta_{12} \\
\alpha_2\alpha_3\alpha_{12}\alpha_{34}-\beta_2\beta_3\beta_{12}\beta_{34} & \alpha_2\alpha_3\alpha_5\alpha_6\alpha_{12}\alpha_{34}-\beta_2\beta_3\beta_5\beta_6\beta_{12}\beta_{34} & \alpha_2\alpha_3\alpha_4\alpha_6\alpha_{12}\alpha_{56}-\beta_2\beta_3\beta_4\beta_6\beta_{12}\beta_{56}
\end{pmatrix}$$

$$A_5 = \begin{pmatrix}
0 & \alpha_6\alpha_{12}\alpha_{56}\lambda & \alpha_5\alpha_{12}\alpha_{56}\lambda \\
\alpha_3\alpha_4\alpha_5\alpha_{12}\alpha_{56}\lambda & 0 & 0 \\
\alpha_2\alpha_4\alpha_5\alpha_{12}\alpha_{56}\lambda & 0 & 0 \\
\alpha_2\alpha_3\alpha_5\alpha_{12}\alpha_{56}\lambda & 0 & 0 \\
\alpha_2\alpha_3\alpha_4\alpha_{12}\alpha_{56}\lambda & 0 & \alpha_1\alpha_{12}\alpha_{56}\lambda \\
0 & \alpha_1\alpha_{12}\alpha_{56}\lambda & 0 \\
\alpha_2\alpha_3\alpha_4\alpha_5\alpha_{56}\lambda & \alpha_1\alpha_6\alpha_{56}\lambda & \alpha_1\alpha_5\alpha_{56}\lambda \\
0 & 0 & 0 \\
\alpha_2\alpha_3\alpha_4\alpha_5\alpha_{12}\lambda & \alpha_1\alpha_6\alpha_{12}\lambda & \alpha_1\alpha_5\alpha_{12}\lambda \\
0 & -\beta_6\beta_{12}\beta_{56}\lambda+\beta_6\beta_{12}\beta_{56} & -\beta_5\beta_{12}\beta_{56}\lambda+\beta_5\beta_{12}\beta_{56} \\
-\beta_3\beta_4\beta_5\beta_{12}\beta_{56}\lambda+\beta_3\beta_4\beta_5\beta_{12}\beta_{56} & 0 & 0 \\
-\beta_2\beta_4\beta_5\beta_{12}\beta_{56}\lambda+\beta_2\beta_4\beta_5\beta_{12}\beta_{56} & 0 & 0 \\
-\beta_2\beta_3\beta_5\beta_{12}\beta_{56}\lambda+\beta_2\beta_3\beta_5\beta_{12}\beta_{56} & 0 & 0 \\
-\beta_2\beta_3\beta_4\beta_{12}\beta_{56}\lambda+\beta_2\beta_3\beta_4\beta_{12}\beta_{56} & 0 & -\beta_1\beta_{12}\beta_{56}\lambda+\beta_1\beta_{12}\beta_{56} \\
0 & -\beta_1\beta_{12}\beta_{56}\lambda+\beta_1\beta_{12}\beta_{56} & 0 \\
-\beta_2\beta_3\beta_4\beta_5\beta_{56}\lambda+\beta_2\beta_3\beta_4\beta_5\beta_{56} & -\beta_1\beta_6\beta_{56}\lambda+\beta_1\beta_6\beta_{56} & -\beta_1\beta_5\beta_{56}\lambda+\beta_1\beta_5\beta_{56} \\
0 & 0 & 0 \\
-\beta_2\beta_3\beta_4\beta_5\beta_{12}\lambda+\beta_2\beta_3\beta_4\beta_5\beta_{12} & -\beta_1\beta_6\beta_{12}\lambda+\beta_1\beta_6\beta_{12} & -\beta_1\beta_5\beta_{12}\lambda+\beta_1\beta_5\beta_{12} \\
\alpha_2\alpha_3\alpha_4\alpha_5\alpha_{12}\alpha_{56}-\beta_2\beta_3\beta_4\beta_5\beta_{12}\beta_{56} & \alpha_1\alpha_6\alpha_{12}\alpha_{56}-\beta_1\beta_6\beta_{12}\beta_{56} & \alpha_1\alpha_5\alpha_{12}\alpha_{56}-\beta_1\beta_5\beta_{12}\beta_{56}
\end{pmatrix}$$

$$A_6 = \begin{pmatrix}
\alpha_4\alpha_{12}\alpha_{34}\lambda & \alpha_4\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda & \alpha_3\alpha_{12}\alpha_{34}\lambda \\
0 & 0 & 0 \\
0 & 0 & \alpha_1\alpha_{12}\alpha_{34}\lambda \\
\alpha_1\alpha_{12}\alpha_{34}\lambda & \alpha_1\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda & 0 \\
0 & \alpha_1\alpha_4\alpha_6\alpha_{12}\alpha_{34}\lambda & 0 \\
0 & \alpha_1\alpha_4\alpha_5\alpha_{12}\alpha_{34}\lambda & 0 \\
\alpha_1\alpha_4\alpha_{34}\lambda & \alpha_1\alpha_4\alpha_5\alpha_6\alpha_{34}\lambda & \alpha_1\alpha_3\alpha_{34}\lambda \\
\alpha_1\alpha_4\alpha_{12}\lambda & \alpha_1\alpha_4\alpha_5\alpha_6\alpha_{12}\lambda & \alpha_1\alpha_3\alpha_{12}\lambda \\
0 & 0 & 0 \\
-\beta_4\beta_{12}\beta_{34}\lambda+\beta_4\beta_{12}\beta_{34} & -\beta_4\beta_5\beta_6\beta_{12}\beta_{34}\lambda+\beta_4\beta_5\beta_6\beta_{12}\beta_{34} & -\beta_3\beta_{12}\beta_{34}\lambda+\beta_3\beta_{12}\beta_{34} \\
0 & 0 & 0 \\
0 & 0 & -\beta_1\beta_{12}\beta_{34}\lambda+\beta_1\beta_{12}\beta_{34} \\
-\beta_1\beta_{12}\beta_{34}\lambda+\beta_1\beta_{12}\beta_{34} & -\beta_1\beta_5\beta_6\beta_{12}\beta_{34}\lambda+\beta_1\beta_5\beta_6\beta_{12}\beta_{34} & 0 \\
0 & -\beta_1\beta_4\beta_6\beta_{12}\beta_{34}\lambda+\beta_1\beta_4\beta_6\beta_{12}\beta_{34} & 0 \\
0 & -\beta_1\beta_4\beta_5\beta_{12}\beta_{34}\lambda+\beta_1\beta_4\beta_5\beta_{12}\beta_{34} & 0 \\
-\beta_1\beta_4\beta_{34}\lambda+\beta_1\beta_4\beta_{34} & -\beta_1\beta_4\beta_5\beta_6\beta_{34}\lambda+\beta_1\beta_4\beta_5\beta_6\beta_{34} & -\beta_1\beta_3\beta_{34}\lambda+\beta_1\beta_3\beta_{34} \\
-\beta_1\beta_4\beta_{12}\lambda+\beta_1\beta_4\beta_{12} & -\beta_1\beta_4\beta_5\beta_6\beta_{12}\lambda+\beta_1\beta_4\beta_5\beta_6\beta_{12} & -\beta_1\beta_3\beta_{12}\lambda+\beta_1\beta_3\beta_{12} \\
0 & 0 & 0 \\
\alpha_1\alpha_4\alpha_{12}\alpha_{34}-\beta_1\beta_4\beta_{12}\beta_{34} & \alpha_1\alpha_4\alpha_5\alpha_6\alpha_{12}\alpha_{34}-\beta_1\beta_4\beta_5\beta_6\beta_{12}\beta_{34} & \alpha_1\alpha_3\alpha_{12}\alpha_{34}-\beta_1\beta_3\beta_{12}\beta_{34}
\end{pmatrix}$$

$$A_7 = \begin{pmatrix}
\alpha_3\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda & \alpha_3\alpha_4\alpha_6\alpha_{12}\alpha_{56}\lambda & \alpha_3\alpha_4\alpha_5\alpha_{12}\alpha_{56}\lambda \\
0 & 0 & 0 \\
\alpha_1\alpha_5\alpha_6\alpha_{12}\alpha_{34}\lambda & \alpha_1\alpha_4\alpha_6\alpha_{12}\alpha_{56}\lambda & \alpha_1\alpha_4\alpha_5\alpha_{12}\alpha_{56}\lambda \\
0 & \alpha_1\alpha_3\alpha_6\alpha_{12}\alpha_{56}\lambda & \alpha_1\alpha_3\alpha_5\alpha_{12}\alpha_{56}\lambda \\
\alpha_1\alpha_3\alpha_6\alpha_{12}\alpha_{34}\lambda & 0 & \alpha_1\alpha_3\alpha_4\alpha_{12}\alpha_{56}\lambda \\
\alpha_1\alpha_3\alpha_5\alpha_{12}\alpha_{34}\lambda & \alpha_1\alpha_3\alpha_4\alpha_{12}\alpha_{56}\lambda & 0 \\
\alpha_1\alpha_3\alpha_5\alpha_6\alpha_{34}\lambda & \alpha_1\alpha_3\alpha_4\alpha_6\alpha_{56}\lambda & \alpha_1\alpha_3\alpha_4\alpha_5\alpha_{56}\lambda \\
\alpha_1\alpha_3\alpha_5\alpha_6\alpha_{12}\lambda & 0 & 0 \\
0 & \alpha_1\alpha_3\alpha_4\alpha_6\alpha_{12}\lambda & \alpha_1\alpha_3\alpha_4\alpha_5\alpha_{12}\lambda \\
-\beta_3\beta_5\beta_6\beta_{12}\beta_{34}\lambda + \beta_3\beta_5\beta_6\beta_{12}\beta_{34} & -\beta_3\beta_4\beta_6\beta_{12}\beta_{56}\lambda + \beta_3\beta_4\beta_6\beta_{12}\beta_{56} & -\beta_3\beta_4\beta_5\beta_{12}\beta_{56}\lambda + \beta_3\beta_4\beta_5\beta_{12}\beta_{56} \\
0 & 0 & 0 \\
-\beta_1\beta_5\beta_6\beta_{12}\beta_{34}\lambda + \beta_1\beta_5\beta_6\beta_{12}\beta_{34} & -\beta_1\beta_4\beta_6\beta_{12}\beta_{56}\lambda + \beta_1\beta_4\beta_6\beta_{12}\beta_{56} & -\beta_1\beta_4\beta_5\beta_{12}\beta_{56}\lambda + \beta_1\beta_4\beta_5\beta_{12}\beta_{56} \\
0 & -\beta_1\beta_3\beta_6\beta_{12}\beta_{56}\lambda + \beta_1\beta_3\beta_6\beta_{12}\beta_{56} & -\beta_1\beta_3\beta_5\beta_{12}\beta_{56}\lambda + \beta_1\beta_3\beta_5\beta_{12}\beta_{56} \\
-\beta_1\beta_3\beta_6\beta_{12}\beta_{34}\lambda + \beta_1\beta_3\beta_6\beta_{12}\beta_{34} & 0 & -\beta_1\beta_3\beta_4\beta_{12}\beta_{56}\lambda + \beta_1\beta_3\beta_4\beta_{12}\beta_{56} \\
-\beta_1\beta_3\beta_5\beta_{12}\beta_{34}\lambda + \beta_1\beta_3\beta_5\beta_{12}\beta_{34} & -\beta_1\beta_3\beta_4\beta_{12}\beta_{56}\lambda + \beta_1\beta_3\beta_4\beta_{12}\beta_{56} & 0 \\
-\beta_1\beta_3\beta_5\beta_6\beta_{34}\lambda + \beta_1\beta_3\beta_5\beta_6\beta_{34} & -\beta_1\beta_3\beta_4\beta_6\beta_{56}\lambda + \beta_1\beta_3\beta_4\beta_6\beta_{56} & -\beta_1\beta_3\beta_4\beta_5\beta_{56}\lambda + \beta_1\beta_3\beta_4\beta_5\beta_{56} \\
-\beta_1\beta_3\beta_5\beta_6\beta_{12}\lambda + \beta_1\beta_3\beta_5\beta_6\beta_{12} & 0 & 0 \\
0 & -\beta_1\beta_3\beta_4\beta_6\beta_{12}\lambda + \beta_1\beta_3\beta_4\beta_6\beta_{12} & -\beta_1\beta_3\beta_4\beta_5\beta_{12}\lambda + \beta_1\beta_3\beta_4\beta_5\beta_{12} \\
\alpha_1\alpha_3\alpha_5\alpha_6\alpha_{12}\alpha_{34} - \beta_1\beta_3\beta_5\beta_6\beta_{12}\beta_{34} & \alpha_1\alpha_3\alpha_4\alpha_6\alpha_{12}\alpha_{56} - \beta_1\beta_3\beta_4\beta_6\beta_{12}\beta_{56} & \alpha_1\alpha_3\alpha_4\alpha_5\alpha_{12}\alpha_{56} - \beta_1\beta_3\beta_4\beta_5\beta_{12}\beta_{56}
\end{pmatrix}$$

$$A_8 = \begin{pmatrix}
\alpha_2\lambda & \alpha_2\alpha_5\alpha_6\lambda & \alpha_2\alpha_4\alpha_6\alpha_{34}\alpha_{56}\lambda \\
\alpha_1\lambda & \alpha_1\alpha_5\alpha_6\lambda & \alpha_1\alpha_4\alpha_6\alpha_{34}\alpha_{56}\lambda \\
0 & 0 & 0 \\
0 & 0 & \alpha_1\alpha_2\alpha_6\alpha_{34}\alpha_{56}\lambda \\
0 & \alpha_1\alpha_2\alpha_6\lambda & 0 \\
0 & \alpha_1\alpha_2\alpha_5\lambda & \alpha_1\alpha_2\alpha_4\alpha_{34}\alpha_{56}\lambda \\
0 & 0 & 0 \\
0 & 0 & \alpha_1\alpha_2\alpha_4\alpha_6\alpha_{56}\lambda \\
0 & 0 & \alpha_1\alpha_2\alpha_4\alpha_6\alpha_{34}\lambda \\
-\beta_2\lambda + \beta_2 & -\beta_2\beta_5\beta_6\lambda + \beta_2\beta_5\beta_6 & -\beta_2\beta_4\beta_6\beta_{34}\beta_{56}\lambda + \beta_2\beta_4\beta_6\beta_{34}\beta_{56} \\
-\beta_1\lambda + \beta_1 & -\beta_1\beta_5\beta_6\lambda + \beta_1\beta_5\beta_6 & -\beta_1\beta_4\beta_6\beta_{34}\beta_{56}\lambda + \beta_1\beta_4\beta_6\beta_{34}\beta_{56} \\
0 & 0 & 0 \\
0 & 0 & -\beta_1\beta_2\beta_6\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_6\beta_{34}\beta_{56} \\
0 & -\beta_1\beta_2\beta_6\lambda + \beta_1\beta_2\beta_6 & 0 \\
0 & -\beta_1\beta_2\beta_5\lambda + \beta_1\beta_2\beta_5 & -\beta_1\beta_2\beta_4\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_4\beta_{34}\beta_{56} \\
0 & 0 & 0 \\
0 & 0 & -\beta_1\beta_2\beta_4\beta_6\beta_{56}\lambda + \beta_1\beta_2\beta_4\beta_6\beta_{56} \\
0 & 0 & -\beta_1\beta_2\beta_4\beta_6\beta_{34}\lambda + \beta_1\beta_2\beta_4\beta_6\beta_{34} \\
\alpha_1\alpha_2 - \beta_1\beta_2 & \alpha_1\alpha_2\alpha_5\alpha_6 - \beta_1\beta_2\beta_5\beta_6 & \alpha_1\alpha_2\alpha_4\alpha_6\alpha_{34}\alpha_{56} - \beta_1\beta_2\beta_4\beta_6\beta_{34}\beta_{56}
\end{pmatrix}$$

$$A_9 = \begin{pmatrix}
\alpha_2\alpha_4\alpha_5\alpha_{34}\alpha_{56}\lambda & \alpha_2\alpha_3\alpha_6\alpha_{34}\alpha_{56}\lambda & \alpha_2\alpha_3\alpha_5\alpha_{34}\alpha_{56}\lambda \\
\alpha_1\alpha_4\alpha_5\alpha_{34}\alpha_{56}\lambda & \alpha_1\alpha_3\alpha_6\alpha_{34}\alpha_{56}\lambda & \alpha_1\alpha_3\alpha_5\alpha_{34}\alpha_{56}\lambda \\
0 & \alpha_1\alpha_2\alpha_6\alpha_{34}\alpha_{56}\lambda & \alpha_1\alpha_2\alpha_5\alpha_{34}\alpha_{56}\lambda \\
\alpha_1\alpha_2\alpha_5\alpha_{34}\alpha_{56}\lambda & 0 & 0 \\
\alpha_1\alpha_2\alpha_4\alpha_{34}\alpha_{56}\lambda & 0 & \alpha_1\alpha_2\alpha_3\alpha_{34}\alpha_{56}\lambda \\
0 & \alpha_1\alpha_2\alpha_3\alpha_{34}\alpha_{56}\lambda & 0 \\
0 & 0 & 0 \\
\alpha_1\alpha_2\alpha_4\alpha_5\alpha_{56}\lambda & \alpha_1\alpha_2\alpha_3\alpha_6\alpha_{56}\lambda & \alpha_1\alpha_2\alpha_3\alpha_5\alpha_{56}\lambda \\
\alpha_1\alpha_2\alpha_4\alpha_5\alpha_{34}\lambda & \alpha_1\alpha_2\alpha_3\alpha_6\alpha_{34}\lambda & \alpha_1\alpha_2\alpha_3\alpha_5\alpha_{34}\lambda \\
-\beta_2\beta_4\beta_5\beta_{34}\beta_{56}\lambda + \beta_2\beta_4\beta_5\beta_{34}\beta_{56} & -\beta_2\beta_3\beta_6\beta_{34}\beta_{56}\lambda + \beta_2\beta_3\beta_6\beta_{34}\beta_{56} & -\beta_2\beta_3\beta_5\beta_{34}\beta_{56}\lambda + \beta_2\beta_3\beta_5\beta_{34}\beta_{56} \\
-\beta_1\beta_4\beta_5\beta_{34}\beta_{56}\lambda + \beta_1\beta_4\beta_5\beta_{34}\beta_{56} & -\beta_1\beta_3\beta_6\beta_{34}\beta_{56}\lambda + \beta_1\beta_3\beta_6\beta_{34}\beta_{56} & -\beta_1\beta_3\beta_5\beta_{34}\beta_{56}\lambda + \beta_1\beta_3\beta_5\beta_{34}\beta_{56} \\
0 & -\beta_1\beta_2\beta_6\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_6\beta_{34}\beta_{56} & -\beta_1\beta_2\beta_5\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_5\beta_{34}\beta_{56} \\
-\beta_1\beta_2\beta_5\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_5\beta_{34}\beta_{56} & 0 & 0 \\
-\beta_1\beta_2\beta_4\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_4\beta_{34}\beta_{56} & 0 & -\beta_1\beta_2\beta_3\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_3\beta_{34}\beta_{56} \\
0 & -\beta_1\beta_2\beta_3\beta_{34}\beta_{56}\lambda + \beta_1\beta_2\beta_3\beta_{34}\beta_{56} & 0 \\
0 & 0 & 0 \\
-\beta_1\beta_2\beta_4\beta_5\beta_{56}\lambda + \beta_1\beta_2\beta_4\beta_5\beta_{56} & -\beta_1\beta_2\beta_3\beta_6\beta_{56}\lambda + \beta_1\beta_2\beta_3\beta_6\beta_{56} & -\beta_1\beta_2\beta_3\beta_5\beta_{56}\lambda + \beta_1\beta_2\beta_3\beta_5\beta_{56} \\
-\beta_1\beta_2\beta_4\beta_5\beta_{34}\lambda + \beta_1\beta_2\beta_4\beta_5\beta_{34} & -\beta_1\beta_2\beta_3\beta_6\beta_{34}\lambda + \beta_1\beta_2\beta_3\beta_6\beta_{34} & -\beta_1\beta_2\beta_3\beta_5\beta_{34}\lambda + \beta_1\beta_2\beta_3\beta_5\beta_{34} \\
\alpha_1\alpha_2\alpha_4\alpha_5\alpha_{34}\alpha_{56} - \beta_1\beta_2\beta_4\beta_5\beta_{34}\beta_{56} & \alpha_1\alpha_2\alpha_3\alpha_6\alpha_{34}\alpha_{56} - \beta_1\beta_2\beta_3\beta_6\beta_{34}\beta_{56} & \alpha_1\alpha_2\alpha_3\alpha_5\alpha_{34}\alpha_{56} - \beta_1\beta_2\beta_3\beta_5\beta_{34}\beta_{56}
\end{pmatrix}$$

$$A_{10} = \begin{pmatrix}
\alpha_2\alpha_3\alpha_4\lambda & \alpha_2\alpha_3\alpha_4\alpha_5\alpha_6\lambda \\
\alpha_1\alpha_3\alpha_4\lambda & \alpha_1\alpha_3\alpha_4\alpha_5\alpha_6\lambda \\
\alpha_1\alpha_2\alpha_4\lambda & \alpha_1\alpha_2\alpha_4\alpha_5\alpha_6\lambda \\
\alpha_1\alpha_2\alpha_3\lambda & \alpha_1\alpha_2\alpha_3\alpha_5\alpha_6\lambda \\
0 & \alpha_1\alpha_2\alpha_3\alpha_4\alpha_6\lambda \\
0 & \alpha_1\alpha_2\alpha_3\alpha_4\alpha_5\lambda \\
0 & 0 \\
0 & 0 \\
0 & 0 \\
-\beta_2\beta_3\beta_4\lambda + \beta_2\beta_3\beta_4 & -\beta_2\beta_3\beta_4\beta_5\beta_6\lambda + \beta_2\beta_3\beta_4\beta_5\beta_6 \\
-\beta_1\beta_3\beta_4\lambda + \beta_1\beta_3\beta_4 & -\beta_1\beta_3\beta_4\beta_5\beta_6\lambda + \beta_1\beta_3\beta_4\beta_5\beta_6 \\
-\beta_1\beta_2\beta_4\lambda + \beta_1\beta_2\beta_4 & -\beta_1\beta_2\beta_4\beta_5\beta_6\lambda + \beta_1\beta_2\beta_4\beta_5\beta_6 \\
-\beta_1\beta_2\beta_3\lambda + \beta_1\beta_2\beta_3 & -\beta_1\beta_2\beta_3\beta_5\beta_6\lambda + \beta_1\beta_2\beta_3\beta_5\beta_6 \\
0 & -\beta_1\beta_2\beta_3\beta_4\beta_6\lambda + \beta_1\beta_2\beta_3\beta_4\beta_6 \\
0 & -\beta_1\beta_2\beta_3\beta_4\beta_5\lambda + \beta_1\beta_2\beta_3\beta_4\beta_5 \\
0 & 0 \\
0 & 0 \\
0 & 0 \\
\alpha_1\alpha_2\alpha_3\alpha_4 - \beta_1\beta_2\beta_3\beta_4 & \alpha_1\alpha_2\alpha_3\alpha_4\alpha_5\alpha_6 - \beta_1\beta_2\beta_3\beta_4\beta_5\beta_6
\end{pmatrix}$$

Then the clean Jacobian of the parametrisation $\psi_{\mathbf{T}}$ is given by $J^c(\psi_{\mathbf{T}}) = [A_1 \cdots A_{10}]$ to give a 19×31 matrix. Similarly, we present the blocks for $J^c(\psi_{\mathbf{T}})$:

$$
B_1 = \begin{pmatrix}
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & \gamma_6\gamma_{123}\lambda' \\
0 & \gamma_6\gamma_{45}\lambda' & \gamma_5\lambda' & 0 \\
\gamma_6\gamma_{45}\lambda' & 0 & \gamma_4\lambda' & 0 \\
\gamma_5\gamma_{45}\lambda' & \gamma_4\gamma_{45}\lambda' & 0 & \gamma_3\gamma_{123}\lambda' \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & \gamma_3\gamma_6\lambda' \\
\gamma_5\gamma_6\lambda' & \gamma_4\gamma_6\lambda' & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & -\delta_6\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_6\delta_{23}\delta_{123}\delta_{56} \\
0 & -\delta_6\delta_{56}\lambda' + \delta_6\delta_{56} & -\delta_5\delta_{56}\lambda' + \delta_5\delta_{56} & 0 \\
-\delta_6\lambda' + \delta_6 & 0 & -\delta_4\delta_{56}\lambda' + \delta_4\delta_{56} & 0 \\
-\delta_5\lambda' + \delta_5 & -\delta_4\delta_{56}\lambda' + \delta_4\delta_{56} & 0 & -\delta_3\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_3\delta_{23}\delta_{123}\delta_{56} \\
0 & 0 & 0 & -\delta_3\delta_6\delta_{123}\delta_{56}\lambda' + \delta_3\delta_6\delta_{123}\delta_{56} \\
0 & 0 & 0 & -\delta_3\delta_6\delta_{23}\delta_{56}\lambda' + \delta_3\delta_6\delta_{23}\delta_{56} \\
0 & -\delta_4\delta_6\lambda' + \delta_4\delta_6 & -\delta_4\delta_5\lambda' + \delta_4\delta_5 & -\delta_3\delta_6\delta_{23}\delta_{123}\lambda' + \delta_3\delta_6\delta_{23}\delta_{123} \\
\gamma_5\gamma_6\gamma_{45} - \delta_5\delta_6 & \gamma_4\gamma_6\gamma_{45} - \delta_4\delta_6\delta_{56} & -\delta_4\delta_5\delta_{56} + \gamma_4\gamma_5 & -\delta_3\delta_6\delta_{23}\delta_{123}\delta_{56} + \gamma_3\gamma_6\gamma_{123}
\end{pmatrix}
$$

$$
B_2 = \begin{pmatrix}
0 & 0 & 0 \\
0 & 0 & 0 \\
\gamma_5\gamma_{123}\gamma_{45}\lambda' & \gamma_4\gamma_{123}\gamma_{45}\lambda' & \gamma_4\gamma_5\gamma_6\gamma_{123}\lambda' \\
0 & \gamma_3\gamma_{123}\gamma_{45}\lambda' & \gamma_3\gamma_5\gamma_6\gamma_{123}\lambda' \\
\gamma_3\gamma_{123}\gamma_{45}\lambda' & 0 & \gamma_3\gamma_4\gamma_6\gamma_{123}\lambda' \\
0 & 0 & \gamma_3\gamma_4\gamma_5\gamma_{123}\lambda' \\
0 & 0 & 0 \\
\gamma_3\gamma_5\gamma_{45}\lambda' & \gamma_3\gamma_4\gamma_{45}\lambda' & \gamma_3\gamma_4\gamma_5\gamma_6\lambda' \\
\gamma_3\gamma_5\gamma_{123}\lambda' & \gamma_3\gamma_4\gamma_{123}\lambda' & 0 \\
0 & 0 & 0 \\
0 & 0 & 0 \\
-\delta_5\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_5\delta_{23}\delta_{123}\delta_{56} & -\delta_4\delta_{23}\delta_{123}\lambda' + \delta_4\delta_{23}\delta_{123} & -\delta_4\delta_5\delta_6\delta_{23}\delta_{123}\lambda' + \delta_4\delta_5\delta_6\delta_{23}\delta_{123} \\
0 & -\delta_3\delta_{23}\delta_{123}\lambda' + \delta_3\delta_{23}\delta_{123} & -\delta_3\delta_5\delta_6\delta_{23}\delta_{123}\lambda' + \delta_3\delta_5\delta_6\delta_{23}\delta_{123} \\
-\delta_3\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_3\delta_{23}\delta_{123}\delta_{56} & 0 & -\delta_3\delta_4\delta_6\delta_{23}\delta_{123}\lambda' + \delta_3\delta_4\delta_6\delta_{23}\delta_{123} \\
0 & 0 & -\delta_3\delta_4\delta_5\delta_{23}\delta_{123}\lambda' + \delta_3\delta_4\delta_5\delta_{23}\delta_{123} \\
-\delta_3\delta_5\delta_{123}\delta_{56}\lambda' + \delta_3\delta_5\delta_{123}\delta_{56} & -\delta_3\delta_4\delta_{123}\lambda' + \delta_3\delta_4\delta_{123} & -\delta_3\delta_4\delta_5\delta_6\delta_{123}\lambda' + \delta_3\delta_4\delta_5\delta_6\delta_{123} \\
-\delta_3\delta_5\delta_{23}\delta_{56}\lambda' + \delta_3\delta_5\delta_{23}\delta_{56} & -\delta_3\delta_4\delta_{23}\lambda' + \delta_3\delta_4\delta_{23} & -\delta_3\delta_4\delta_5\delta_6\delta_{23}\lambda' + \delta_3\delta_4\delta_5\delta_6\delta_{23} \\
-\delta_3\delta_5\delta_{23}\delta_{123}\lambda' + \delta_3\delta_5\delta_{23}\delta_{123} & 0 & 0 \\
-\delta_3\delta_5\delta_{23}\delta_{123}\delta_{56} + \gamma_3\gamma_5\gamma_{123}\gamma_{45} & \gamma_3\gamma_4\gamma_{123}\gamma_{45} - \delta_3\delta_4\delta_{23}\delta_{123} & -\delta_3\delta_4\delta_5\delta_6\delta_{23}\delta_{123} + \gamma_3\gamma_4\gamma_5\gamma_6\gamma_{123}
\end{pmatrix}
$$

$$
B_3 = \begin{pmatrix}
0 & 0 & 0 \\
\gamma_6\gamma_{12}\gamma_{123}\lambda' & \gamma_5\gamma_{12}\gamma_{123}\gamma_{45}\lambda' & \gamma_4\gamma_{12}\gamma_{123}\gamma_{45}\lambda' \\
0 & 0 & 0 \\
0 & 0 & \gamma_2\gamma_{12}\gamma_{123}\gamma_{45}\lambda' \\
0 & \gamma_2\gamma_{12}\gamma_{123}\gamma_{45}\lambda' & 0 \\
\gamma_2\gamma_{12}\gamma_{123}\lambda' & 0 & 0 \\
\gamma_2\gamma_6\gamma_{123}\lambda' & \gamma_2\gamma_5\gamma_{123}\gamma_{45}\lambda' & \gamma_2\gamma_4\gamma_{123}\gamma_{45}\lambda' \\
\gamma_2\gamma_6\gamma_{12}\lambda' & \gamma_2\gamma_5\gamma_{12}\gamma_{45}\lambda' & \gamma_2\gamma_4\gamma_{12}\gamma_{45}\lambda' \\
0 & \gamma_2\gamma_5\gamma_{12}\gamma_{123}\lambda' & \gamma_2\gamma_4\gamma_{12}\gamma_{123}\lambda' \\
0 & 0 & 0 \\
-\delta_6\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_6\delta_{23}\delta_{123}\delta_{56} & -\delta_5\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_5\delta_{23}\delta_{123}\delta_{56} & -\delta_4\delta_{23}\delta_{123}\lambda' + \delta_4\delta_{23}\delta_{123} \\
0 & 0 & 0 \\
0 & 0 & -\delta_2\delta_{23}\delta_{123}\lambda' + \delta_2\delta_{23}\delta_{123} \\
0 & -\delta_2\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_2\delta_{23}\delta_{123}\delta_{56} & 0 \\
-\delta_2\delta_{23}\delta_{123}\delta_{56}\lambda' + \delta_2\delta_{23}\delta_{123}\delta_{56} & 0 & 0 \\
-\delta_2\delta_6\delta_{123}\delta_{56}\lambda' + \delta_2\delta_6\delta_{123}\delta_{56} & -\delta_2\delta_5\delta_{123}\delta_{56}\lambda' + \delta_2\delta_5\delta_{123}\delta_{56} & -\delta_2\delta_4\delta_{123}\lambda' + \delta_2\delta_4\delta_{123} \\
-\delta_2\delta_6\delta_{23}\delta_{56}\lambda' + \delta_2\delta_6\delta_{23}\delta_{56} & -\delta_2\delta_5\delta_{23}\delta_{56}\lambda' + \delta_2\delta_5\delta_{23}\delta_{56} & -\delta_2\delta_4\delta_{23}\lambda' + \delta_2\delta_4\delta_{23} \\
-\delta_2\delta_6\delta_{23}\delta_{123}\lambda' + \delta_2\delta_6\delta_{23}\delta_{123} & -\delta_2\delta_5\delta_{23}\delta_{123}\lambda' + \delta_2\delta_5\delta_{23}\delta_{123} & 0 \\
-\delta_2\delta_6\delta_{23}\delta_{123}\delta_{56} + \gamma_2\gamma_6\gamma_{12}\gamma_{123} & \gamma_2\gamma_5\gamma_{12}\gamma_{123}\gamma_{45} - \delta_2\delta_5\delta_{23}\delta_{123}\delta_{56} & \gamma_2\gamma_4\gamma_{12}\gamma_{123}\gamma_{45} - \delta_2\delta_4\delta_{23}\delta_{123}
\end{pmatrix}
$$

$$
B_4 = \begin{pmatrix}
0 & 0 & 0 \\
\gamma_4\gamma_5\gamma_6\gamma_{12}\gamma_{123}\lambda' & \gamma_3\gamma_{12}\lambda' & \gamma_3\gamma_5\gamma_6\gamma_{12}\gamma_{45}\lambda' \\
0 & \gamma_2\gamma_{12}\lambda' & \gamma_2\gamma_5\gamma_6\gamma_{12}\gamma_{45}\lambda' \\
\gamma_2\gamma_5\gamma_6\gamma_{12}\gamma_{123}\lambda' & 0 & 0 \\
\gamma_2\gamma_4\gamma_6\gamma_{12}\gamma_{123}\lambda' & 0 & \gamma_2\gamma_3\gamma_6\gamma_{12}\gamma_{45}\lambda' \\
\gamma_2\gamma_4\gamma_5\gamma_{12}\gamma_{123}\lambda' & 0 & \gamma_2\gamma_3\gamma_5\gamma_{12}\gamma_{45}\lambda' \\
\gamma_2\gamma_4\gamma_5\gamma_6\gamma_{123}\lambda' & \gamma_2\gamma_3\lambda' & \gamma_2\gamma_3\gamma_5\gamma_6\gamma_{45}\lambda' \\
\gamma_2\gamma_4\gamma_5\gamma_6\gamma_{12}\lambda' & 0 & 0 \\
0 & 0 & \gamma_2\gamma_3\gamma_5\gamma_6\gamma_{12}\lambda' \\
0 & 0 & 0 \\
-\delta_4\delta_5\delta_6\delta_{23}\delta_{123}\lambda' + \delta_4\delta_5\delta_6\delta_{23}\delta_{123} & -\delta_3\lambda' + \delta_3 & -\delta_3\delta_5\delta_6\lambda' + \delta_3\delta_5\delta_6 \\
0 & -\delta_2\lambda' + \delta_2 & -\delta_2\delta_5\delta_6\lambda' + \delta_2\delta_5\delta_6 \\
-\delta_2\delta_5\delta_6\delta_{23}\delta_{123}\lambda' + \delta_2\delta_5\delta_6\delta_{23}\delta_{123} & 0 & 0 \\
-\delta_2\delta_4\delta_6\delta_{23}\delta_{123}\lambda' + \delta_2\delta_4\delta_6\delta_{23}\delta_{123} & 0 & -\delta_2\delta_3\delta_6\lambda' + \delta_2\delta_3\delta_6 \\
-\delta_2\delta_4\delta_5\delta_{23}\delta_{123}\lambda' + \delta_2\delta_4\delta_5\delta_{23}\delta_{123} & 0 & -\delta_2\delta_3\delta_5\lambda' + \delta_2\delta_3\delta_5 \\
-\delta_2\delta_4\delta_5\delta_6\delta_{123}\lambda' + \delta_2\delta_4\delta_5\delta_6\delta_{123} & 0 & 0 \\
-\delta_2\delta_4\delta_5\delta_6\delta_{23}\lambda' + \delta_2\delta_4\delta_5\delta_6\delta_{23} & 0 & 0 \\
0 & 0 & 0 \\
\gamma_2\gamma_4\gamma_5\gamma_6\gamma_{12}\gamma_{123} - \delta_2\delta_4\delta_5\delta_6\delta_{23}\delta_{123} & \gamma_2\gamma_3\gamma_{12} - \delta_2\delta_3 & \gamma_2\gamma_3\gamma_5\gamma_6\gamma_{12}\gamma_{45} - \delta_2\delta_3\delta_5\delta_6
\end{pmatrix}
$$

$$B_5 = \begin{pmatrix}
0 & 0 & \gamma_6\gamma_{12}\gamma_{123}\lambda' \\
\gamma_3\gamma_4\gamma_6\gamma_{12}\gamma_{45}\lambda' & \gamma_3\gamma_4\gamma_5\gamma_{12}\lambda' & 0 \\
\gamma_2\gamma_4\gamma_6\gamma_{12}\gamma_{45}\lambda' & \gamma_2\gamma_4\gamma_5\gamma_{12}\lambda' & 0 \\
\gamma_2\gamma_3\gamma_6\gamma_{12}\gamma_{45}\lambda' & \gamma_2\gamma_3\gamma_5\gamma_{12}\lambda' & 0 \\
0 & \gamma_2\gamma_3\gamma_4\gamma_{12}\lambda' & 0 \\
\gamma_2\gamma_3\gamma_4\gamma_{12}\gamma_{45}\lambda' & 0 & \gamma_1\gamma_{12}\gamma_{123}\lambda' \\
\gamma_2\gamma_3\gamma_4\gamma_6\gamma_{45}\lambda' & \gamma_2\gamma_3\gamma_4\gamma_5\lambda' & \gamma_1\gamma_6\gamma_{123}\lambda' \\
0 & 0 & \gamma_1\gamma_6\gamma_{12}\lambda' \\
\gamma_2\gamma_3\gamma_4\gamma_6\gamma_{12}\lambda' & 0 & 0 \\
0 & 0 & -\delta_6\delta_{123}\delta_{56}\lambda' + \delta_6\delta_{123}\delta_{56} \\
-\delta_3\delta_4\delta_6\delta_{56}\lambda' + \delta_3\delta_4\delta_6\delta_{56} & -\delta_3\delta_4\delta_5\delta_{56}\lambda' + \delta_3\delta_4\delta_5\delta_{56} & 0 \\
-\delta_2\delta_4\delta_6\delta_{56}\lambda' + \delta_2\delta_4\delta_6\delta_{56} & -\delta_2\delta_4\delta_5\delta_{56}\lambda' + \delta_2\delta_4\delta_5\delta_{56} & 0 \\
-\delta_2\delta_3\delta_6\delta_{56}\lambda' + \delta_2\delta_3\delta_6\delta_{56} & -\delta_2\delta_3\delta_5\delta_{56}\lambda' + \delta_2\delta_3\delta_5\delta_{56} & 0 \\
0 & -\delta_2\delta_3\delta_4\delta_{56}\lambda' + \delta_2\delta_3\delta_4\delta_{56} & 0 \\
-\delta_2\delta_3\delta_4\delta_{56}\lambda' + \delta_2\delta_3\delta_4\delta_{56} & 0 & -\delta_1\delta_{123}\delta_{56}\lambda' + \delta_1\delta_{123}\delta_{56} \\
0 & 0 & 0 \\
0 & 0 & -\delta_1\delta_6\delta_{56}\lambda' + \delta_1\delta_6\delta_{56} \\
-\delta_2\delta_3\delta_4\delta_6\lambda' + \delta_2\delta_3\delta_4\delta_6 & -\delta_2\delta_3\delta_4\delta_5\lambda' + \delta_2\delta_3\delta_4\delta_5 & -\delta_1\delta_6\delta_{123}\lambda' + \delta_1\delta_6\delta_{123} \\
\gamma_2\gamma_3\gamma_4\gamma_6\gamma_{12}\gamma_{45} - \delta_2\delta_3\delta_4\delta_6\delta_{56} & \gamma_2\gamma_3\gamma_4\gamma_5\gamma_{12} - \delta_2\delta_3\delta_4\delta_5\delta_{56} & \gamma_1\gamma_6\gamma_{12}\gamma_{123} - \delta_1\delta_6\delta_{123}\delta_{56}
\end{pmatrix}$$

$$B_6 = \begin{pmatrix}
\gamma_5\gamma_{12}\gamma_{123}\gamma_{45}\lambda' & \gamma_4\gamma_{12}\gamma_{123}\gamma_{45}\lambda' & \gamma_4\gamma_5\gamma_6\gamma_{12}\gamma_{123}\lambda' \\
0 & 0 & 0 \\
0 & 0 & 0 \\
0 & \gamma_1\gamma_{12}\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_5\gamma_6\gamma_{12}\gamma_{123}\lambda' \\
\gamma_1\gamma_{12}\gamma_{123}\gamma_{45}\lambda' & 0 & \gamma_1\gamma_4\gamma_6\gamma_{12}\gamma_{123}\lambda' \\
0 & 0 & \gamma_1\gamma_4\gamma_5\gamma_{12}\gamma_{123}\lambda' \\
\gamma_1\gamma_5\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_4\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_4\gamma_5\gamma_6\gamma_{123}\lambda' \\
\gamma_1\gamma_5\gamma_{12}\gamma_{45}\lambda' & \gamma_1\gamma_4\gamma_{12}\gamma_{45}\lambda' & \gamma_1\gamma_4\gamma_5\gamma_6\gamma_{12}\lambda' \\
\gamma_1\gamma_5\gamma_{12}\gamma_{123}\lambda' & \gamma_1\gamma_4\gamma_{12}\gamma_{123}\lambda' & 0 \\
-\delta_5\delta_{123}\delta_{56}\lambda' + \delta_5\delta_{123}\delta_{56} & -\delta_4\delta_{123}\lambda' + \delta_4\delta_{123} & -\delta_4\delta_5\delta_6\delta_{123}\lambda' + \delta_4\delta_5\delta_6\delta_{123} \\
0 & 0 & 0 \\
0 & 0 & 0 \\
0 & -\delta_1\delta_{123}\lambda' + \delta_1\delta_{123} & -\delta_1\delta_5\delta_6\delta_{123}\lambda' + \delta_1\delta_5\delta_6\delta_{123} \\
-\delta_1\delta_{123}\delta_{56}\lambda' + \delta_1\delta_{123}\delta_{56} & 0 & -\delta_1\delta_4\delta_6\delta_{123}\lambda' + \delta_1\delta_4\delta_6\delta_{123} \\
0 & 0 & -\delta_1\delta_4\delta_5\delta_{123}\lambda' + \delta_1\delta_4\delta_5\delta_{123} \\
0 & 0 & 0 \\
-\delta_1\delta_5\delta_{56}\lambda' + \delta_1\delta_5\delta_{56} & -\delta_1\delta_4\lambda' + \delta_1\delta_4 & -\delta_1\delta_4\delta_5\delta_6\lambda' + \delta_1\delta_4\delta_5\delta_6 \\
-\delta_1\delta_5\delta_{123}\lambda' + \delta_1\delta_5\delta_{123} & 0 & 0 \\
\gamma_1\gamma_5\gamma_{12}\gamma_{123}\gamma_{45} - \delta_1\delta_5\delta_{123}\delta_{56} & \gamma_1\gamma_4\gamma_{12}\gamma_{123}\gamma_{45} - \delta_1\delta_4\delta_{123} & \gamma_1\gamma_4\gamma_5\gamma_6\gamma_{12}\gamma_{123} - \delta_1\delta_4\delta_5\delta_6\delta_{123}
\end{pmatrix}$$

$$B_7 = \begin{pmatrix}
\gamma_3\gamma_{12}\lambda' & \gamma_3\gamma_5\gamma_6\gamma_{12}\gamma_{45}\lambda' & \gamma_3\gamma_4\gamma_6\gamma_{12}\gamma_{45}\lambda' \\
0 & 0 & 0 \\
\gamma_1\gamma_{12}\lambda' & \gamma_1\gamma_5\gamma_6\gamma_{12}\gamma_{45}\lambda' & \gamma_1\gamma_4\gamma_6\gamma_{12}\gamma_{45}\lambda' \\
0 & 0 & \gamma_1\gamma_3\gamma_6\gamma_{12}\gamma_{45}\lambda' \\
0 & \gamma_1\gamma_3\gamma_6\gamma_{12}\gamma_{45}\lambda' & 0 \\
0 & \gamma_1\gamma_3\gamma_5\gamma_{12}\gamma_{45}\lambda' & \gamma_1\gamma_3\gamma_4\gamma_{12}\gamma_{45}\lambda' \\
\gamma_1\gamma_3\lambda' & \gamma_1\gamma_3\gamma_5\gamma_6\gamma_{45}\lambda' & \gamma_1\gamma_3\gamma_4\gamma_6\gamma_{45}\lambda' \\
0 & 0 & 0 \\
0 & \gamma_1\gamma_3\gamma_5\gamma_6\gamma_{12}\lambda' & \gamma_1\gamma_3\gamma_4\gamma_6\gamma_{12}\lambda' \\
-\delta_3\delta_{23}\lambda' + \delta_3\delta_{23} & -\delta_3\delta_5\delta_6\delta_{23}\lambda' + \delta_3\delta_5\delta_6\delta_{23} & -\delta_3\delta_4\delta_6\delta_{23}\delta_{56}\lambda' + \delta_3\delta_4\delta_6\delta_{23}\delta_{56} \\
0 & 0 & 0 \\
-\delta_1\delta_{23}\lambda' + \delta_1\delta_{23} & -\delta_1\delta_5\delta_6\delta_{23}\lambda' + \delta_1\delta_5\delta_6\delta_{23} & -\delta_1\delta_4\delta_6\delta_{23}\delta_{56}\lambda' + \delta_1\delta_4\delta_6\delta_{23}\delta_{56} \\
0 & 0 & -\delta_1\delta_3\delta_6\delta_{23}\delta_{56}\lambda' + \delta_1\delta_3\delta_6\delta_{23}\delta_{56} \\
0 & -\delta_1\delta_3\delta_6\delta_{23}\lambda' + \delta_1\delta_3\delta_6\delta_{23} & 0 \\
0 & -\delta_1\delta_3\delta_5\delta_{23}\lambda' + \delta_1\delta_3\delta_5\delta_{23} & -\delta_1\delta_3\delta_4\delta_{23}\delta_{56}\lambda' + \delta_1\delta_3\delta_4\delta_{23}\delta_{56} \\
-\delta_1\delta_3\lambda' + \delta_1\delta_3 & -\delta_1\delta_3\delta_5\delta_6\lambda' + \delta_1\delta_3\delta_5\delta_6 & -\delta_1\delta_3\delta_4\delta_6\delta_{56}\lambda' + \delta_1\delta_3\delta_4\delta_6\delta_{56} \\
0 & 0 & 0 \\
0 & 0 & -\delta_1\delta_3\delta_4\delta_6\delta_{23}\lambda' + \delta_1\delta_3\delta_4\delta_6\delta_{23} \\
\gamma_1\gamma_3\gamma_{12} - \delta_1\delta_3\delta_{23} & \gamma_1\gamma_3\gamma_5\gamma_6\gamma_{12}\gamma_{45} - \delta_1\delta_3\delta_5\delta_6\delta_{23} & \gamma_1\gamma_3\gamma_4\gamma_6\gamma_{12}\gamma_{45} - \delta_1\delta_3\delta_4\delta_6\delta_{23}\delta_{56}
\end{pmatrix}$$

$$B_8 = \begin{pmatrix}
\gamma_3\gamma_4\gamma_5\gamma_{12}\lambda' & \gamma_2\lambda' & \gamma_2\gamma_5\gamma_6\gamma_{45}\lambda' \\
0 & \gamma_1\lambda' & \gamma_1\gamma_5\gamma_6\gamma_{45}\lambda' \\
\gamma_1\gamma_4\gamma_5\gamma_{12}\lambda' & 0 & 0 \\
\gamma_1\gamma_3\gamma_5\gamma_{12}\lambda' & 0 & 0 \\
\gamma_1\gamma_3\gamma_4\gamma_{12}\lambda' & 0 & \gamma_1\gamma_2\gamma_6\gamma_{45}\lambda' \\
0 & 0 & \gamma_1\gamma_2\gamma_5\gamma_{45}\lambda' \\
\gamma_1\gamma_3\gamma_4\gamma_5\lambda' & 0 & 0 \\
0 & 0 & 0 \\
0 & 0 & \gamma_1\gamma_2\gamma_5\gamma_6\lambda' \\
-\delta_3\delta_4\delta_5\delta_{23}\delta_{56}\lambda' + \delta_3\delta_4\delta_5\delta_{23}\delta_{56} & -\delta_2\delta_{23}\lambda' + \delta_2\delta_{23} & -\delta_2\delta_5\delta_6\delta_{23}\lambda' + \delta_2\delta_5\delta_6\delta_{23} \\
0 & -\delta_1\delta_{23}\lambda' + \delta_1\delta_{23} & -\delta_1\delta_5\delta_6\delta_{23}\lambda' + \delta_1\delta_5\delta_6\delta_{23} \\
-\delta_1\delta_4\delta_5\delta_{23}\delta_{56}\lambda' + \delta_1\delta_4\delta_5\delta_{23}\delta_{56} & 0 & 0 \\
-\delta_1\delta_3\delta_5\delta_{23}\delta_{56}\lambda' + \delta_1\delta_3\delta_5\delta_{23}\delta_{56} & 0 & 0 \\
-\delta_1\delta_3\delta_4\delta_{23}\delta_{56}\lambda' + \delta_1\delta_3\delta_4\delta_{23}\delta_{56} & 0 & -\delta_1\delta_2\delta_6\delta_{23}\lambda' + \delta_1\delta_2\delta_6\delta_{23} \\
0 & 0 & -\delta_1\delta_2\delta_5\delta_{23}\lambda' + \delta_1\delta_2\delta_5\delta_{23} \\
-\delta_1\delta_3\delta_4\delta_5\delta_{56}\lambda' + \delta_1\delta_3\delta_4\delta_5\delta_{56} & -\delta_1\delta_2\lambda' + \delta_1\delta_2 & -\delta_1\delta_2\delta_5\delta_6\lambda' + \delta_1\delta_2\delta_5\delta_6 \\
0 & 0 & 0 \\
-\delta_1\delta_3\delta_4\delta_5\delta_{23}\lambda' + \delta_1\delta_3\delta_4\delta_5\delta_{23} & 0 & 0 \\
-\delta_1\delta_3\delta_4\delta_5\delta_{23}\delta_{56} + \gamma_1\gamma_3\gamma_4\gamma_5\gamma_{12} & -\delta_1\delta_2\delta_{23} + \gamma_1\gamma_2 & \gamma_1\gamma_2\gamma_5\gamma_6\gamma_{45} - \delta_1\delta_2\delta_5\delta_6\delta_{23}
\end{pmatrix}$$

$$B_9 = \begin{pmatrix}
\gamma_2\gamma_4\gamma_6\gamma_{45}\lambda' & \gamma_2\gamma_4\gamma_5\lambda' & \gamma_2\gamma_3\gamma_6\gamma_{123}\lambda' \\
\gamma_1\gamma_4\gamma_6\gamma_{45}\lambda' & \gamma_1\gamma_4\gamma_5\lambda' & \gamma_1\gamma_3\gamma_6\gamma_{123}\lambda' \\
0 & 0 & \gamma_1\gamma_2\gamma_6\gamma_{123}\lambda' \\
\gamma_1\gamma_2\gamma_6\gamma_{45}\lambda' & \gamma_1\gamma_2\gamma_5\lambda' & 0 \\
0 & \gamma_1\gamma_2\gamma_4\lambda' & 0 \\
\gamma_1\gamma_2\gamma_4\gamma_{45}\lambda' & 0 & \gamma_1\gamma_2\gamma_3\gamma_{123}\lambda' \\
0 & 0 & 0 \\
0 & 0 & \gamma_1\gamma_2\gamma_3\gamma_6\lambda' \\
\gamma_1\gamma_2\gamma_4\gamma_6\lambda' & 0 & 0 \\
-\delta_2\delta_4\delta_6\delta_{23}\delta_{56}\lambda' + \delta_2\delta_4\delta_6\delta_{23}\delta_{56} & -\delta_2\delta_4\delta_5\delta_{23}\delta_{56}\lambda' + \delta_2\delta_4\delta_5\delta_{23}\delta_{56} & -\delta_2\delta_3\delta_6\delta_{123}\delta_{56}\lambda' + \delta_2\delta_3\delta_6\delta_{123}\delta_{56} \\
-\delta_1\delta_4\delta_6\delta_{23}\delta_{56}\lambda' + \delta_1\delta_4\delta_6\delta_{23}\delta_{56} & -\delta_1\delta_4\delta_5\delta_{23}\delta_{56}\lambda' + \delta_1\delta_4\delta_5\delta_{23}\delta_{56} & -\delta_1\delta_3\delta_6\delta_{123}\delta_{56}\lambda' + \delta_1\delta_3\delta_6\delta_{123}\delta_{56} \\
0 & 0 & -\delta_1\delta_2\delta_6\delta_{123}\delta_{56}\lambda' + \delta_1\delta_2\delta_6\delta_{123}\delta_{56} \\
-\delta_1\delta_2\delta_6\delta_{23}\delta_{56}\lambda' + \delta_1\delta_2\delta_6\delta_{23}\delta_{56} & -\delta_1\delta_2\delta_5\delta_{23}\delta_{56}\lambda' + \delta_1\delta_2\delta_5\delta_{23}\delta_{56} & 0 \\
0 & -\delta_1\delta_2\delta_4\delta_{23}\delta_{56}\lambda' + \delta_1\delta_2\delta_4\delta_{23}\delta_{56} & 0 \\
-\delta_1\delta_2\delta_4\delta_{23}\delta_{56}\lambda' + \delta_1\delta_2\delta_4\delta_{23}\delta_{56} & 0 & -\delta_1\delta_2\delta_3\delta_{123}\delta_{56}\lambda' + \delta_1\delta_2\delta_3\delta_{123}\delta_{56} \\
-\delta_1\delta_2\delta_4\delta_6\delta_{56}\lambda' + \delta_1\delta_2\delta_4\delta_6\delta_{56} & -\delta_1\delta_2\delta_4\delta_5\delta_{56}\lambda' + \delta_1\delta_2\delta_4\delta_5\delta_{56} & 0 \\
0 & 0 & -\delta_1\delta_2\delta_3\delta_6\delta_{56}\lambda' + \delta_1\delta_2\delta_3\delta_6\delta_{56} \\
-\delta_1\delta_2\delta_4\delta_6\delta_{23}\lambda' + \delta_1\delta_2\delta_4\delta_6\delta_{23} & -\delta_1\delta_2\delta_4\delta_5\delta_{23}\lambda' + \delta_1\delta_2\delta_4\delta_5\delta_{23} & -\delta_1\delta_2\delta_3\delta_6\delta_{123}\lambda' + \delta_1\delta_2\delta_3\delta_6\delta_{123} \\
-\delta_1\delta_2\delta_4\delta_6\delta_{23}\delta_{56} + \gamma_1\gamma_2\gamma_4\gamma_6\gamma_{45} & -\delta_1\delta_2\delta_4\delta_5\delta_{23}\delta_{56} + \gamma_1\gamma_2\gamma_4\gamma_5 & -\delta_1\delta_2\delta_3\delta_6\delta_{123}\delta_{56} + \gamma_1\gamma_2\gamma_3\gamma_6\gamma_{123}
\end{pmatrix}$$

$$B_{10} = \begin{pmatrix}
\gamma_2\gamma_3\gamma_5\gamma_{123}\gamma_{45}\lambda' & \gamma_2\gamma_3\gamma_4\gamma_{123}\gamma_{45}\lambda' & \gamma_2\gamma_3\gamma_4\gamma_5\gamma_6\gamma_{123}\lambda' \\
\gamma_1\gamma_3\gamma_5\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_3\gamma_4\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_3\gamma_4\gamma_5\gamma_6\gamma_{123}\lambda' \\
\gamma_1\gamma_2\gamma_5\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_2\gamma_4\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_2\gamma_4\gamma_5\gamma_6\gamma_{123}\lambda' \\
0 & \gamma_1\gamma_2\gamma_3\gamma_{123}\gamma_{45}\lambda' & \gamma_1\gamma_2\gamma_3\gamma_5\gamma_6\gamma_{123}\lambda' \\
\gamma_1\gamma_2\gamma_3\gamma_{123}\gamma_{45}\lambda' & 0 & \gamma_1\gamma_2\gamma_3\gamma_4\gamma_6\gamma_{123}\lambda' \\
0 & 0 & \gamma_1\gamma_2\gamma_3\gamma_4\gamma_5\gamma_{123}\lambda' \\
0 & 0 & 0 \\
\gamma_1\gamma_2\gamma_3\gamma_5\gamma_{45}\lambda' & \gamma_1\gamma_2\gamma_3\gamma_4\gamma_{45}\lambda' & \gamma_1\gamma_2\gamma_3\gamma_4\gamma_5\gamma_6\lambda' \\
\gamma_1\gamma_2\gamma_3\gamma_5\gamma_{123}\lambda' & \gamma_1\gamma_2\gamma_3\gamma_4\gamma_{123}\lambda' & 0 \\
-\delta_2\delta_3\delta_5\delta_{123}\delta_{56}\lambda' + \delta_2\delta_3\delta_5\delta_{123}\delta_{56} & -\delta_2\delta_3\delta_4\delta_{123}\lambda' + \delta_2\delta_3\delta_4\delta_{123} & -\delta_2\delta_3\delta_4\delta_5\delta_6\delta_{123}\lambda' + \delta_2\delta_3\delta_4\delta_5\delta_6\delta_{123} \\
-\delta_1\delta_3\delta_5\delta_{123}\delta_{56}\lambda' + \delta_1\delta_3\delta_5\delta_{123}\delta_{56} & -\delta_1\delta_3\delta_4\delta_{123}\lambda' + \delta_1\delta_3\delta_4\delta_{123} & -\delta_1\delta_3\delta_4\delta_5\delta_6\delta_{123}\lambda' + \delta_1\delta_3\delta_4\delta_5\delta_6\delta_{123} \\
-\delta_1\delta_2\delta_5\delta_{123}\delta_{56}\lambda' + \delta_1\delta_2\delta_5\delta_{123}\delta_{56} & -\delta_1\delta_2\delta_4\delta_{123}\lambda' + \delta_1\delta_2\delta_4\delta_{123} & -\delta_1\delta_2\delta_4\delta_5\delta_6\delta_{123}\lambda' + \delta_1\delta_2\delta_4\delta_5\delta_6\delta_{123} \\
0 & -\delta_1\delta_2\delta_3\delta_{123}\lambda' + \delta_1\delta_2\delta_3\delta_{123} & -\delta_1\delta_2\delta_3\delta_5\delta_6\delta_{123}\lambda' + \delta_1\delta_2\delta_3\delta_5\delta_6\delta_{123} \\
-\delta_1\delta_2\delta_3\delta_{123}\delta_{56}\lambda' + \delta_1\delta_2\delta_3\delta_{123}\delta_{56} & 0 & -\delta_1\delta_2\delta_3\delta_4\delta_6\delta_{123}\lambda' + \delta_1\delta_2\delta_3\delta_4\delta_6\delta_{123} \\
0 & 0 & -\delta_1\delta_2\delta_3\delta_4\delta_5\delta_{123}\lambda' + \delta_1\delta_2\delta_3\delta_4\delta_5\delta_{123} \\
0 & 0 & 0 \\
-\delta_1\delta_2\delta_3\delta_5\delta_{56}\lambda' + \delta_1\delta_2\delta_3\delta_5\delta_{56} & -\delta_1\delta_2\delta_3\delta_4\lambda' + \delta_1\delta_2\delta_3\delta_4 & -\delta_1\delta_2\delta_3\delta_4\delta_5\delta_6\lambda' + \delta_1\delta_2\delta_3\delta_4\delta_5\delta_6 \\
-\delta_1\delta_2\delta_3\delta_5\delta_{123}\lambda' + \delta_1\delta_2\delta_3\delta_5\delta_{123} & 0 & 0 \\
\gamma_1\gamma_2\gamma_3\gamma_5\gamma_{123}\gamma_{45} - \delta_1\delta_2\delta_3\delta_5\delta_{123}\delta_{56} & \gamma_1\gamma_2\gamma_3\gamma_4\gamma_{123}\gamma_{45} - \delta_1\delta_2\delta_3\delta_4\delta_{123} & \gamma_1\gamma_2\gamma_3\gamma_4\gamma_5\gamma_6\gamma_{123} - \delta_1\delta_2\delta_3\delta_4\delta_5\delta_6\delta_{123}
\end{pmatrix}$$

Then the clean Jacobian of the parametrisation $\psi_{\mathbf{S}}$ is given by $J^c(\psi_{\mathbf{S}}) = [B_1 \cdots B_{10}]$ to give a 19×31 matrix.

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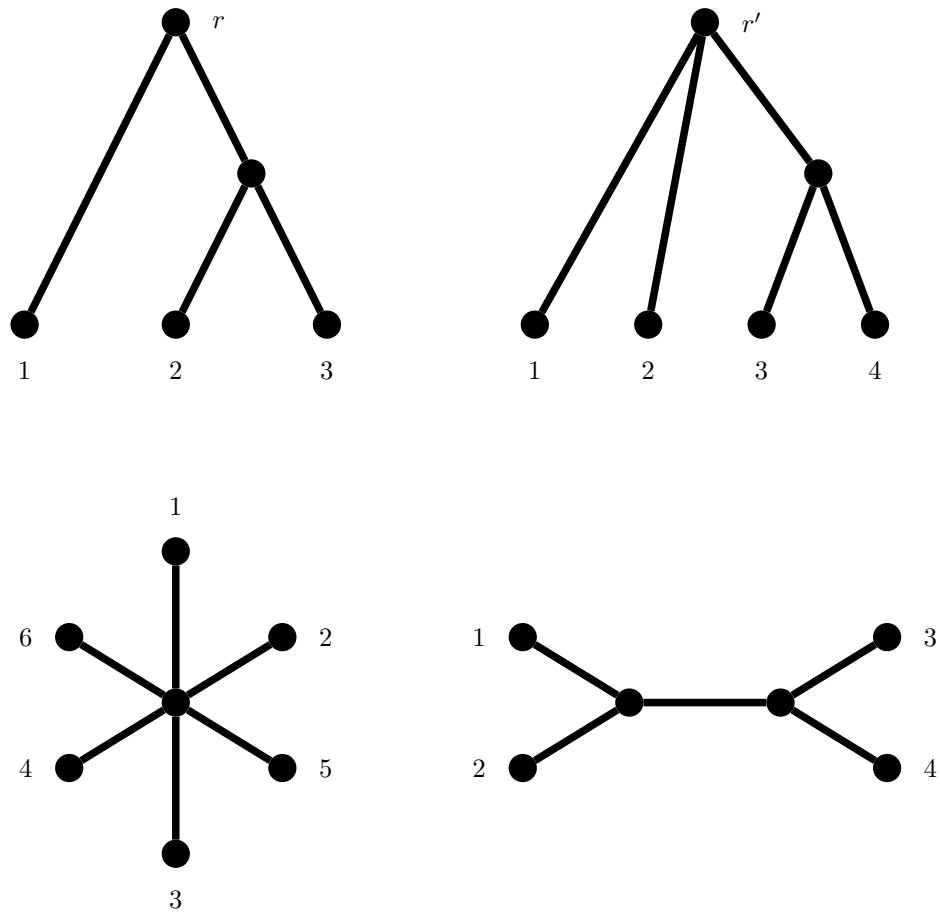
Figure 1: Four phylogenetic trees. The top two trees are rooted, the two right-most trees are binary. Note that the top-right tree can be obtained from the bottom-right tree by distinguishing one of the inner nodes as the root.
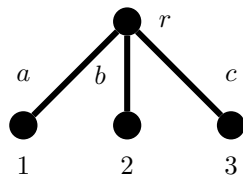

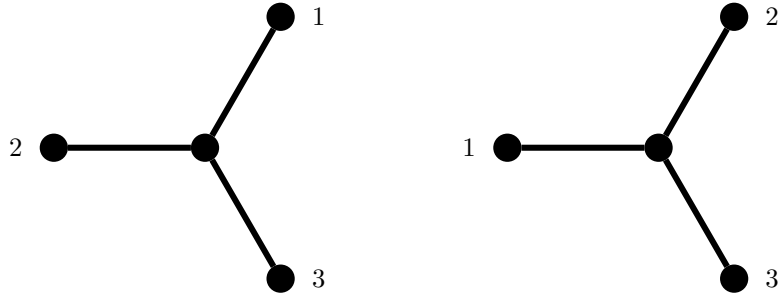Figure 2: Phylogenetic model on the tree phylogenetic tree $T = K_{1,3}$.

Figure 3: Two phylogenetic trees with the same set of splits.

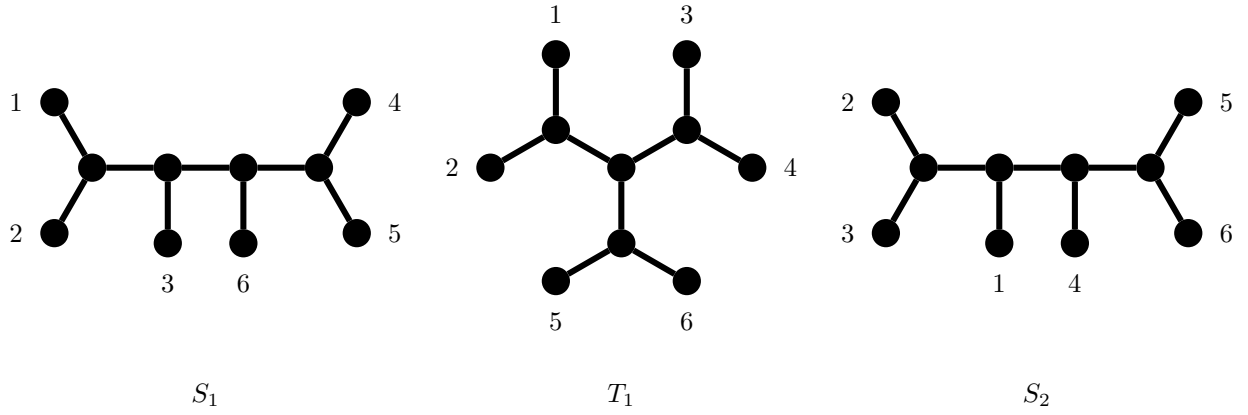S_1 T_1 S_2

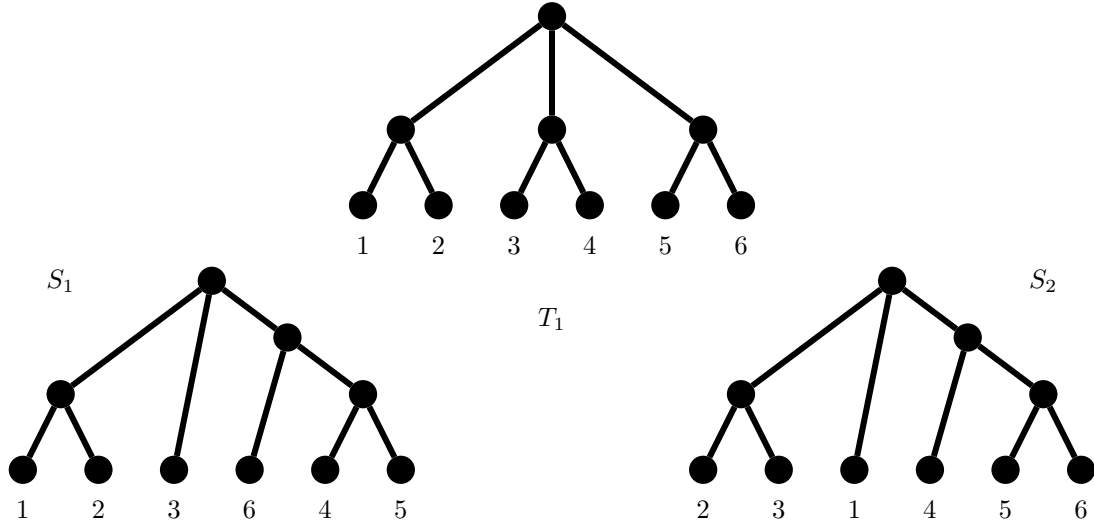Figure 4: The unrooted trees used in our example 2-mixture models, with labels underneath each tree.

Figure 5: Rooted analogues of the trees in Figure 4.