# Algebraic constraints on the transition probability matrices produced from Lie-Markov models 

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## Some algebraic definitions

- Take $\mathcal{L} \subseteq \operatorname{Mat}_{n}(\mathbb{R})$ to be a linear subspace of matrices i.e. $A, B \in \mathcal{L} \Longrightarrow A+\lambda B \in \mathcal{L}$
- $\mathcal{L}$ is an 'algebra' if it is closed under a 'product' (binary operation):
(i.) Matrix algebra: $A B \in \mathcal{L}$
(ii.) Lie algebra: $[A, B]:=A B-B A \in \mathcal{L}$
(ii.) Jordan algebra: $\{A, B\}:=A B+B A \in \mathcal{L}$
(Were ' $A B$ ' is the usual matrix product we all know and love!)


## Continuous time Markov chains for DNA evolution



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- Generator matrix $Q \rightarrow P=e^{Q t}$, transition matrix - Exemplar DNA (A,G,C,T) models:

- Strand symmetric: $\operatorname{rate}(A \rightarrow G)=\operatorname{rate}(T \rightarrow C)$
- HKY: $\kappa$ is the 'transition/transversion' ratio (AG/CT)


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- Exemplar DNA (A,G,C,T) models:
'Strand symmetric'
(Casanellas, Sullivant, 2005)

$$
\begin{gathered}
\\
A \\
G \\
C \\
T
\end{gathered}\left[\begin{array}{llll}
A & G & C & T \\
* & \alpha & \beta & \gamma \\
\delta & * & \epsilon & \kappa \\
\kappa & \epsilon & * & \delta \\
\gamma & \beta & \alpha & *
\end{array}\right]
$$

## 'HKY'

(Hasegawa, Kishino, Yano, 1985)
$A$
$G$
$C$
$T$$\left[\begin{array}{cccc}A & G & C & T \\ * & \kappa \alpha_{G} & \alpha_{C} & \alpha_{T} \\ \kappa \alpha_{A} & * & \alpha_{C} & \alpha_{T} \\ \alpha_{A} & \alpha_{G} & * & \kappa \alpha_{T} \\ \alpha_{A} & \alpha_{G} & \kappa \alpha_{C} & *\end{array}\right]$

- Strand symmetric: $\operatorname{rate}(A \rightarrow G)=\operatorname{rate}(T \rightarrow C)$
- HKY: $\kappa$ is the 'transition/transversion' ratio ( $A G / C T$ )


## Multiplicative closure for CTMCs

$\rightarrow$ Transition matrices are multiplicative: $\left(P_{1}, P_{2}\right) \rightarrow P_{1} P_{2}$
But what about a particular model?

- If $P_{1}=e^{Q t_{1}}$ and $P_{2}=e^{Q t_{2}}$ then $P_{1} P_{2}=e^{Q\left(t_{1}+t_{2}\right)}$
i.e. same transition rates, longer time
$\rightarrow$ If the transition rates change:
Commuting case: $Q_{1} Q_{2}=Q_{2} Q_{1}$,

$$
P_{1} P_{2}=e^{Q_{1} t_{1}} e^{Q_{2} t_{2}}=e^{Q_{1} t_{1}+Q_{2} t_{2}}
$$

General case:

$$
\begin{aligned}
& \qquad \begin{aligned}
& P_{1} P_{2}=e^{Q_{1} t_{1}} e^{Q_{2} t_{2}}=e^{Q_{1} t_{1}+Q_{2} t_{2}+(\text { infinite series of corrections) }} \\
&=e^{Q_{1} t_{1}+Q_{2} t_{2}+\frac{1}{2} t_{1} t_{2}\left[Q_{1}, Q_{2}\right]+\ldots} \\
& \text { where }\left[Q_{1}, Q_{2}\right]=Q_{1} Q_{2}- Q_{2} Q_{1} \text { measures non-commutivity. }
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Some models are multiplicative closed, some are not

- Necessary and sufficient condition for closure (roughly): generators span a Lie algebra $\mathcal{L}: Q_{1}+\lambda Q_{2}$ and $\left[Q_{1}, Q_{2}\right] \in \mathcal{L}$
Strand-symm model is closed because the products $Q_{1} Q_{2} \in \mathcal{L}$ :


So some models form matrix algebras and we observe:


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\text { matrix algebra } \Longrightarrow \text { Lie algebra } \Longleftrightarrow \text { mult. closed }
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- HKY is not closed because it is non-linear:

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Q=\left(\begin{array}{cccc}
* & \kappa \alpha_{G} & \alpha_{C} & \alpha_{T} \\
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\alpha_{A} & \alpha_{G} & * & \kappa \alpha_{T} \\
\alpha_{A} & \alpha_{G} & \kappa \alpha_{C} & *
\end{array}\right) \Longrightarrow Q_{12} Q_{13}=Q_{43} Q_{42} \text {, etc. }
$$

## Structure of models that form matrix algebras

- A model where the generators span a matrix algebra is always closed:

$$
\begin{aligned}
e^{Q} & =\mathcal{I}+\left(Q+Q^{2} / 2+\ldots\right)=\mathcal{I}+\hat{Q} \\
\Longrightarrow e^{Q_{1}} e^{Q_{2}} & =\left(\mathcal{I}+\hat{Q}_{1}\right)\left(\mathcal{I}+\hat{Q}_{2}\right)=\mathcal{I}+\left(\hat{Q}_{1}+\hat{Q}_{2}+\hat{Q}_{1} \hat{Q}_{2}\right)
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i.e. closure under sums and products is sufficient (although the latter is not necessary...)

- Easy to infer the structure of the transition matrices:
i.e. "transition matrix $=\mathcal{I}+$ generator"
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## Multiplicatively closure is not required for " $\mathcal{M}=\mathcal{I}+\mathcal{L}$ "

- e.g., symmetric generators do not form a Lie algebra:


However,

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\left(Q^{2}\right)^{T}=Q^{2}, \quad\left(Q^{3}\right)^{T}=Q^{3} .
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- Generalizes to HKY and even the general time-reversible model:
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Not all multiplicatively closed models satisfy " $\mathcal{M}=\mathcal{I}+\mathcal{L}$ "

- Toy model $\mathcal{L}$ :

$$
Q=\left(\begin{array}{ccc}
* & \alpha+\beta & 2 \beta \\
0 & 0 & 0 \\
2 \alpha & \alpha+\beta & *
\end{array}\right)
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Intentionally designed so $\left[Q_{1}, Q_{2}\right] \in \mathcal{L}$ but $Q_{1} Q_{2} \notin \mathcal{L}$
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This Lie algebra is "algebraic" $\Longrightarrow \mathcal{M}$ has an algebraic description:


- In general these non-linear constraints are difficult to find and they are not always algebraic. (de Graff, Adrian, 2017)

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- This Lie algebra is "algebraic" $\Longrightarrow \mathcal{M}$ has an algebraic description:

$$
e^{Q} \sim P=\left(\begin{array}{lll}
* & a & z \\
0 & 1 & 0 \\
y & a & *
\end{array}\right), \quad \text { with } y+z-a(a-1)(a-2)=0
$$

- In general these non-linear constraints are difficult to find and they are not always algebraic. (de Graff, Adriaan, 2017)


## Conditions for " $\mathcal{M}=\mathcal{I}+\mathcal{L}$ "

- Require linearity plus closure under powers.
- Jordan algebra $\mathcal{J}$ : linearity and $\{A, B\}=A B+B A \in \mathcal{J}$.

Equivalent to closure under powers: $A^{2}=\frac{1}{2}(A A+A A)$ and $(A+B)^{2}=A^{2}+(A B+B A)+B^{2}$

- Symmetric case:
$\left(Q_{1} Q_{2}+Q_{2} Q_{1}\right)^{\top}=Q_{2}^{\top} Q_{1}^{\top}+Q_{1}^{\top} Q_{2}^{\top}=Q_{2} Q_{1}+Q_{1} Q_{2}=Q_{1} Q_{2}+Q_{2} Q_{1}$
- If we demand both the Lie and Jordan conditions, we obtain precisely a the matrix algebra case:

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A B=\frac{1}{2}[A, B]+\frac{1}{2}\{A, B\}
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## The end

- Efficient computations of matrix exponentials?
e.g. decompose relevant algebra into irreducible components
- Direct parametrisation of transition matrices?
i.e. bypass matrix exponentials altogether
- Insights into why certain results are provable for some models but not others? e.g. the equal-input model

Hasegawa M, Kishino H, Yano T (1985). "Dating of the human-ape splitting by a molecular clock of mitochondrial DNA". J. Mol. Evol
Casanellas M, Sullivant S (2005) Algebraic Statistics for Computational Biology, chap. The Strand Symmetric Model. Cambridge University Press, New York, pp 305-321
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