

# Troubleshooting



Joëlle Barido-Sottani, Denise Kühnert, Jūlija Pečerska,  
David Rasmussen

# Possible scenarios

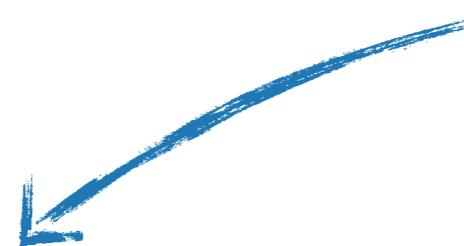
Beast analysis

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Initialisation failed

Start likelihood: -Infinity after 1000  
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Fatal exception: Could not find a  
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another seed.  
 $P(\text{posterior}) = -\text{Infinity}$  (was -Infinity)



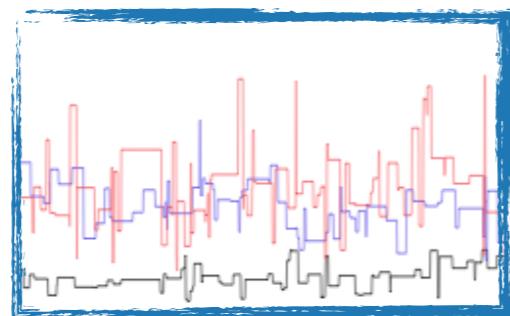
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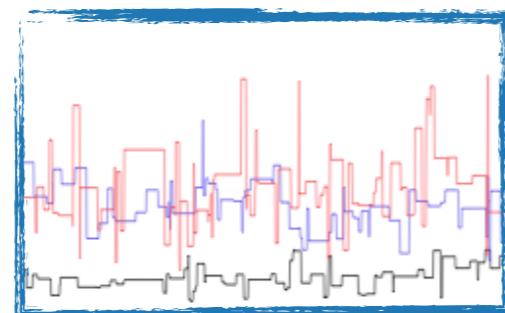
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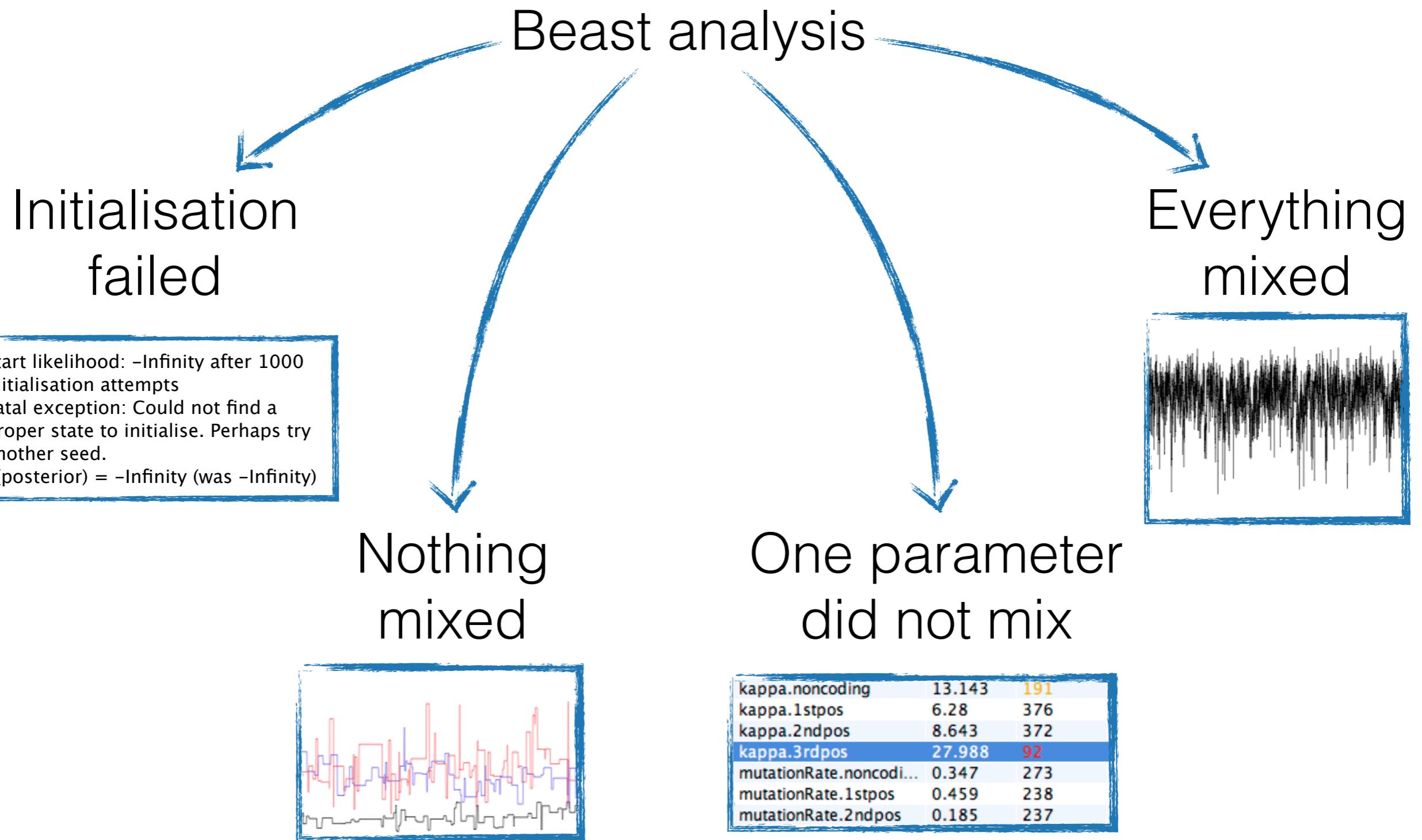
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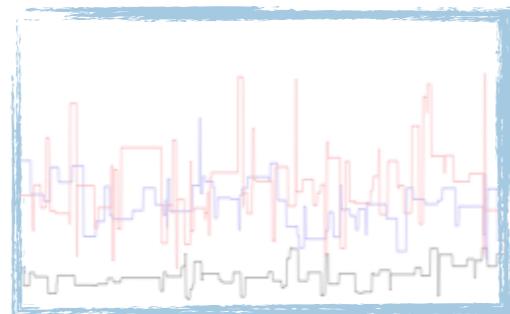
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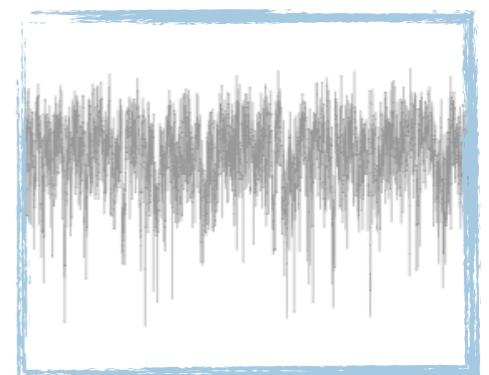
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# Failed initialisation

Start likelihood: -Infinity after 1000 initialisation attempts

Fatal exception: Could not find a proper state to initialise. Perhaps try another seed.

P(posterior) = -Infinity (was -Infinity)

P(prior) = -Infinity (was -Infinity)

P(BDMM) = -Infinity (was -Infinity)

P(ROPrior) = -0.5586849541070393 (was -0.5586849541070393)

P(rPrior) = -11.46042136866474 (was -11.46042136866474)

P(rateMatrixPrior) = -0.14088025499381485 (was -0.14088025499381485)

P(samplingProportionPrior) = -10.049507225748343 (was -10.049507225748343)

P(becomeUninfectiousRatePrior) = -0.7811241751317991 (was -0.7811241751317991)

java.lang.RuntimeException: Could not find a proper state to initialise. Perhaps try another seed.

at beast.core.MCMC.run(Unknown Source)

at beast.app.BeastMCMC.run(Unknown Source)

at beast.app.beastapp.BeastMain.<init>(Unknown Source)

at beast.app.beastapp.BeastMain.main(Unknown Source)

at beast.app.beastapp.BeastLauncher.main(Unknown Source)

Fatal exception: Could not find a proper state to initialise. Perhaps try another seed.

BEAST has terminated with an error. Please select QUIT from the menu.

Parameter prior is -Infinity

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**Example:**  $P(\text{rateMatrixPrior}) = -\text{Infinity}$  (was  $-\text{Infinity}$ )

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- Change seed;

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- Change seed;
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- Check for silly/incompatible priors;

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**Possible solutions:**

- Change seed;
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- Check for silly/incompatible priors;
- Check for underflow (too low values);

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**Possible solutions:**

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- Check for silly/incompatible priors;
- Check for underflow (too low values);
- Talk to the BEAST2 support group!

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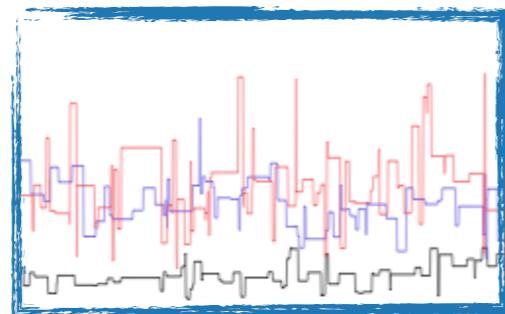
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Beast analysis

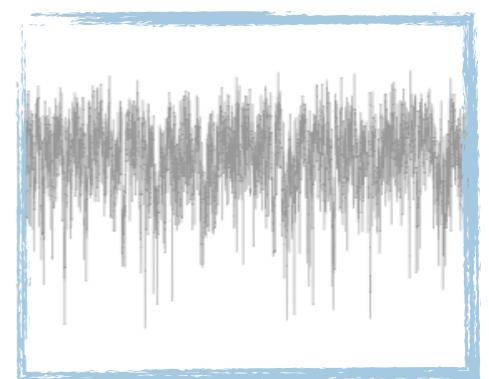
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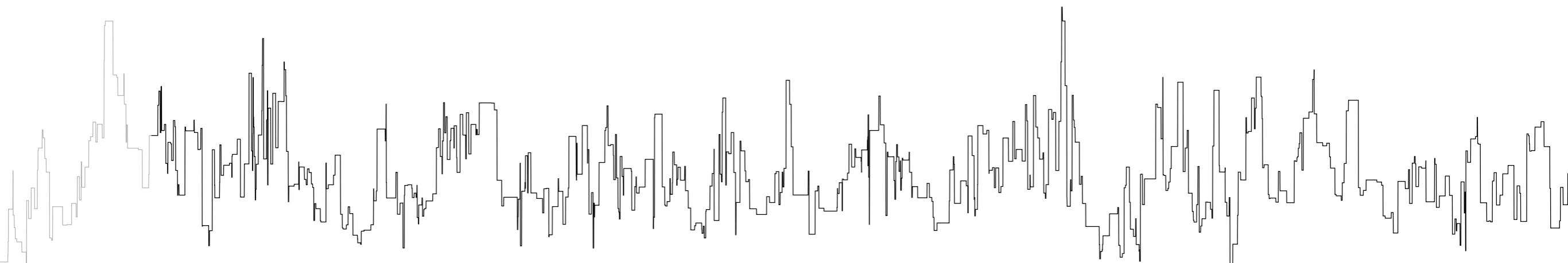
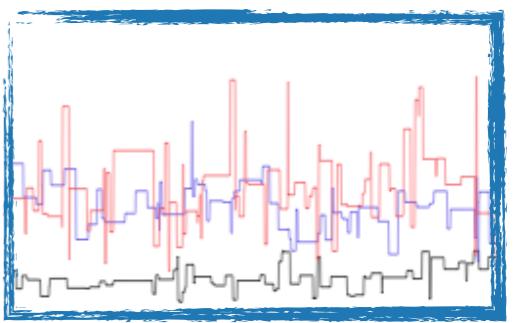
Everything mixed



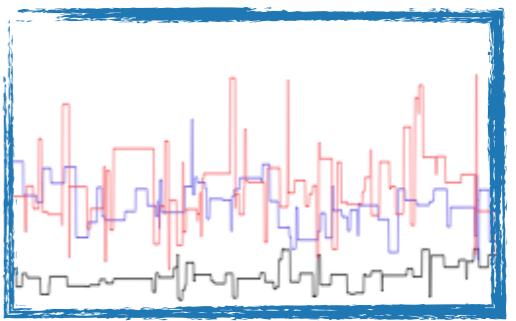
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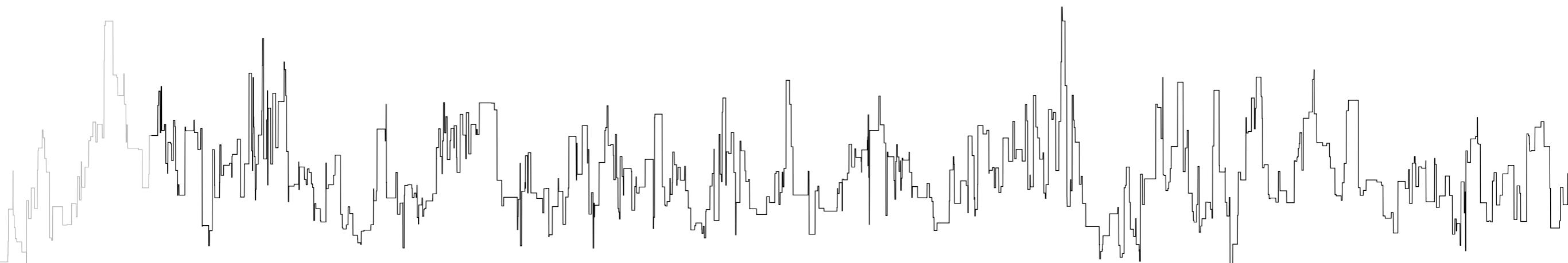
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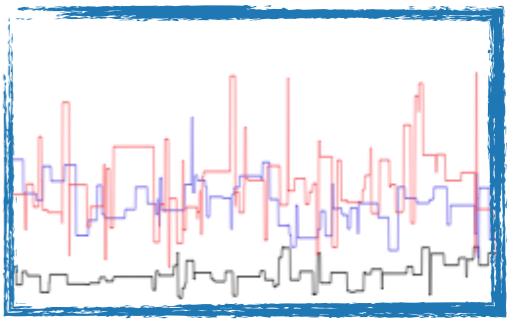
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Possible solutions:

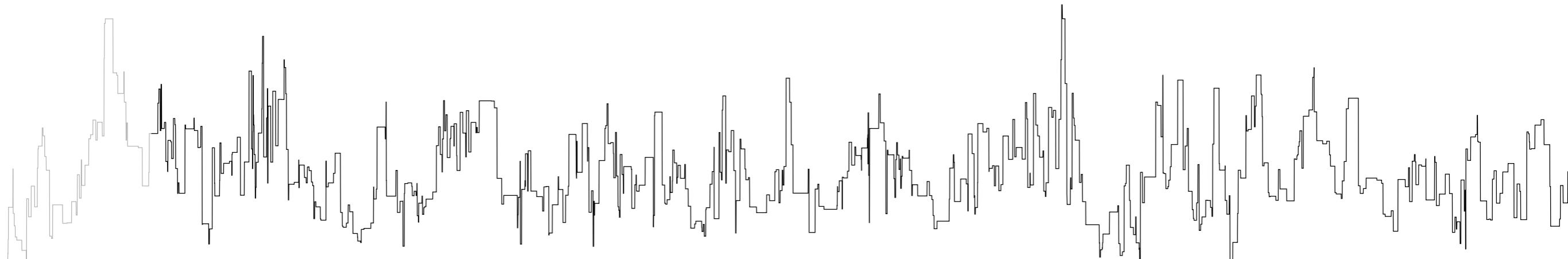


# Nothing mixed

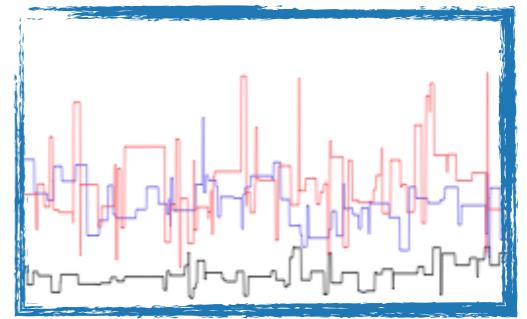


Possible solutions:

- Increase chain length;

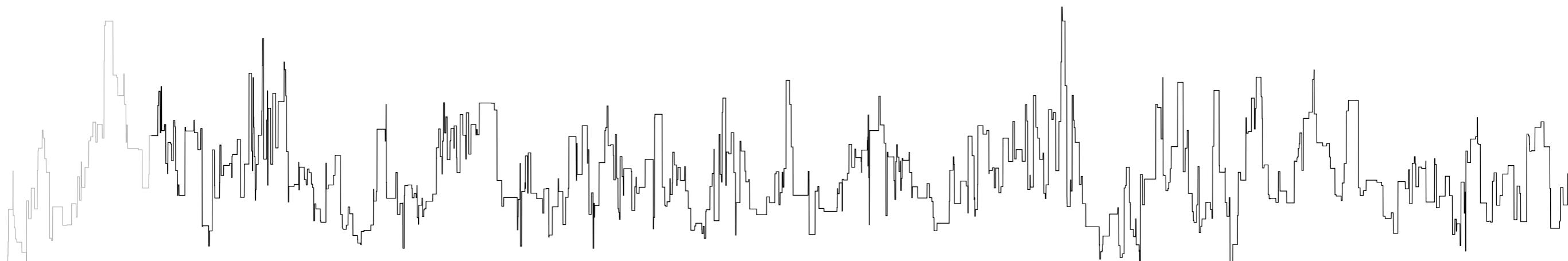


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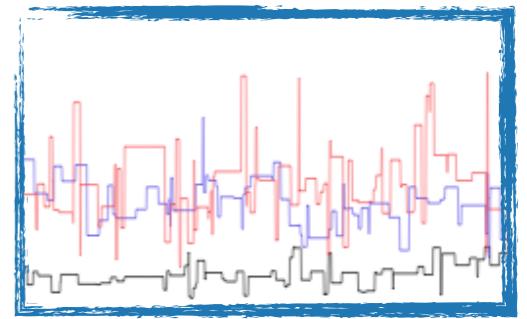


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- Increase chain length;
- Run multiple independent chains;

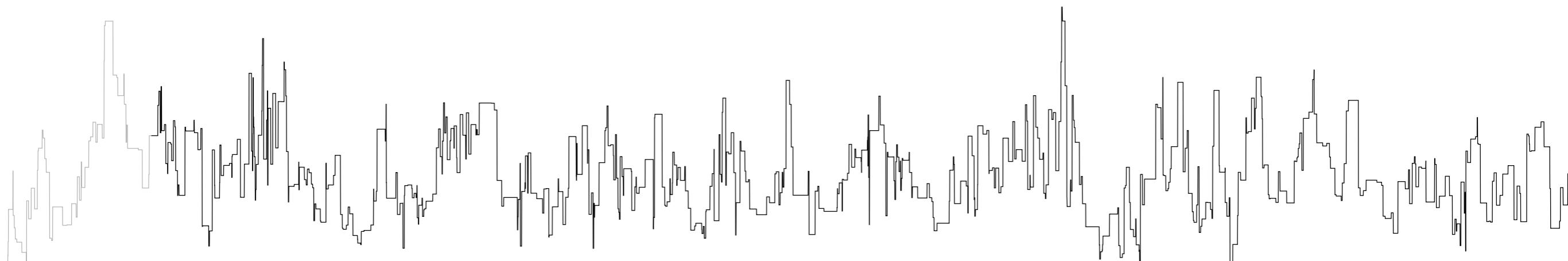


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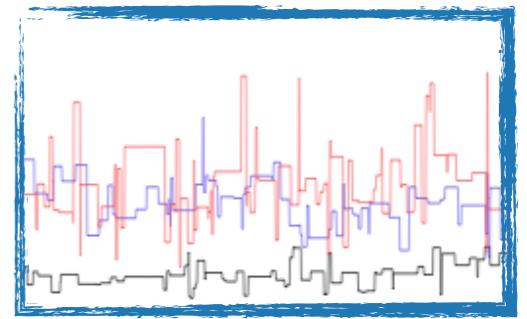


## Possible solutions:

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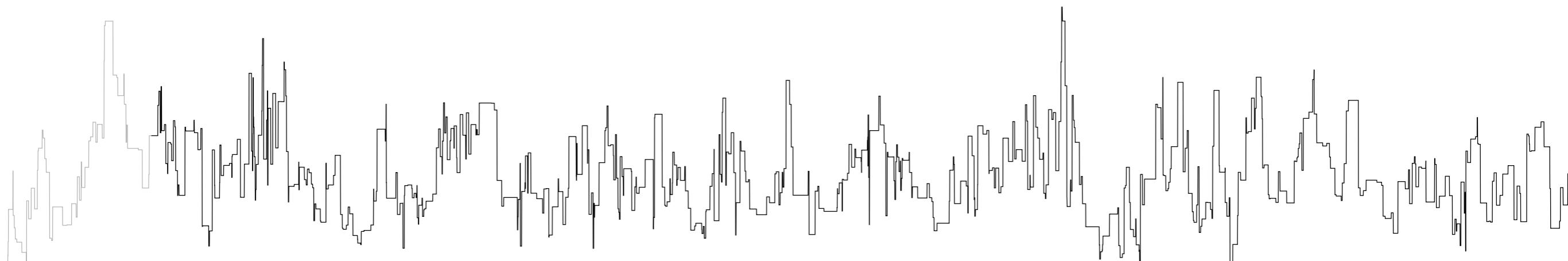


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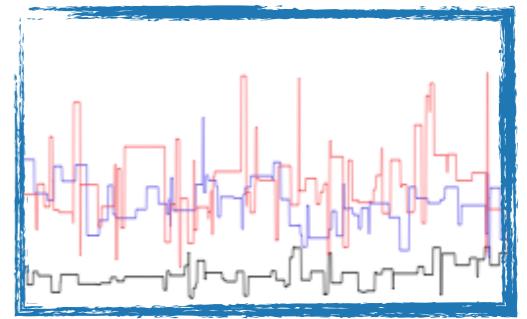


## Possible solutions:

- Increase chain length;
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- Check identifiability;

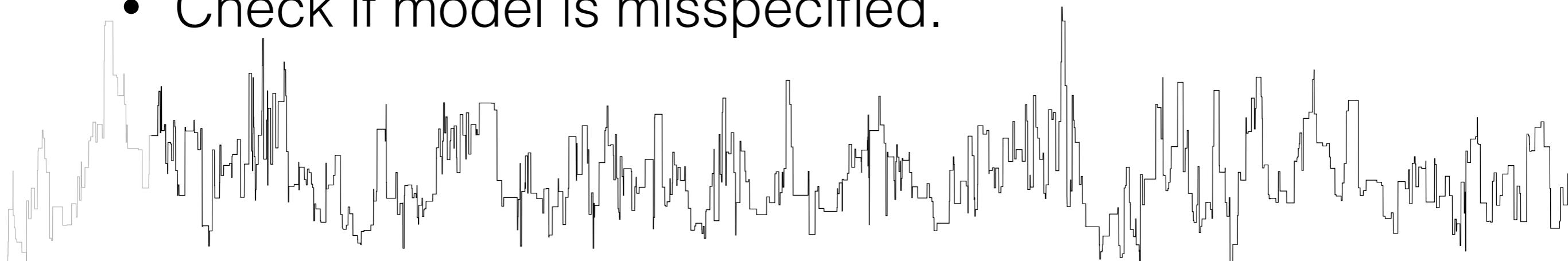


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## Possible solutions:

- Increase chain length;
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- Increase sampling frequency (if ACT permits);
- Check identifiability;
- Check if model is misspecified.



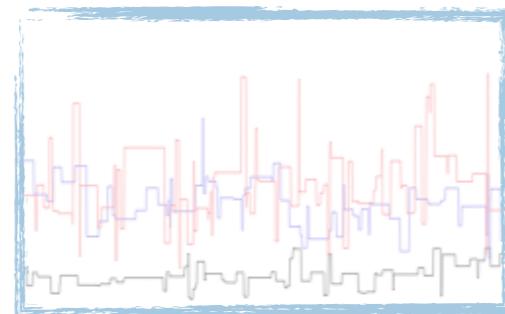
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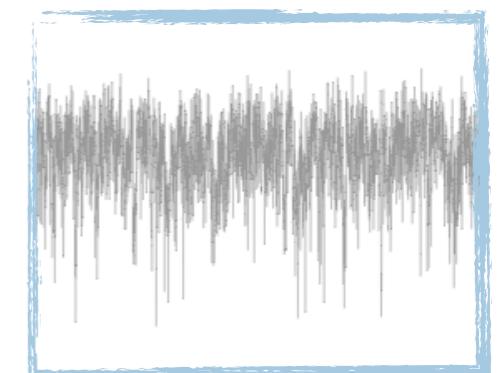
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- Tweak the operator weights:
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- Run longer (or combine several independent chains).

Only posterior not mixed

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Possible reasons:

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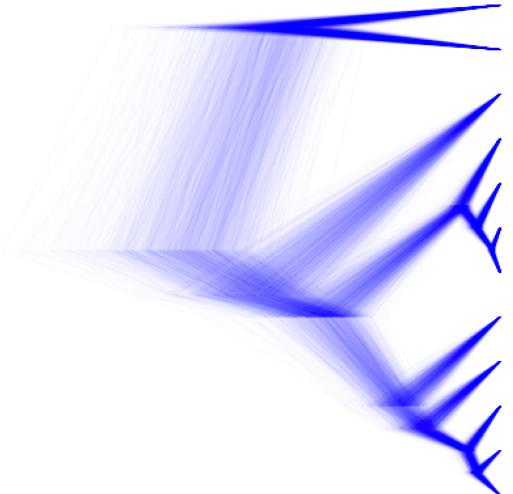
- Tree prior cares too much about a parameter the data says nothing about;

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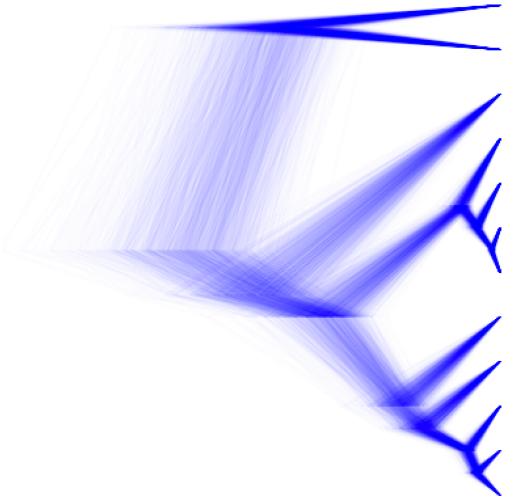
- Tree prior cares too much about a parameter the data says nothing about;
- Also one can always make a statistic that doesn't mix.

# Tree space mixing

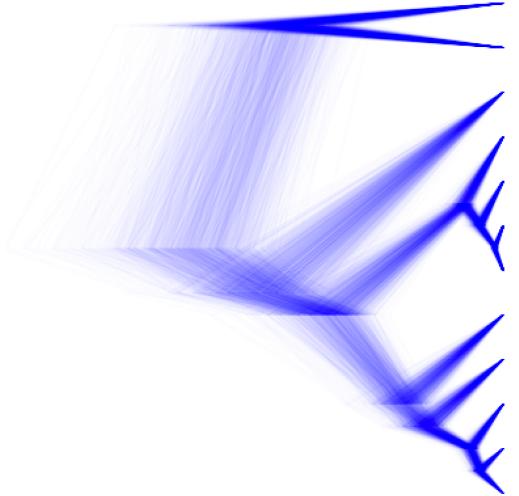


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Bad news:



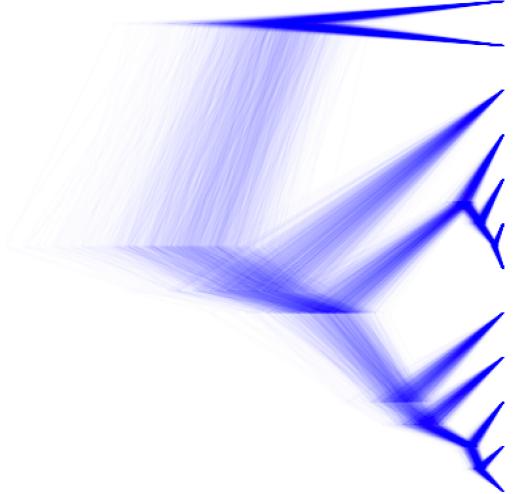
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Bad news:

At the moment we can not directly examine the ESS of the trees;

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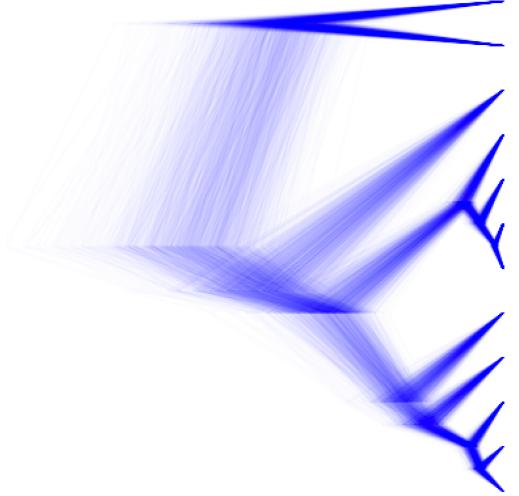


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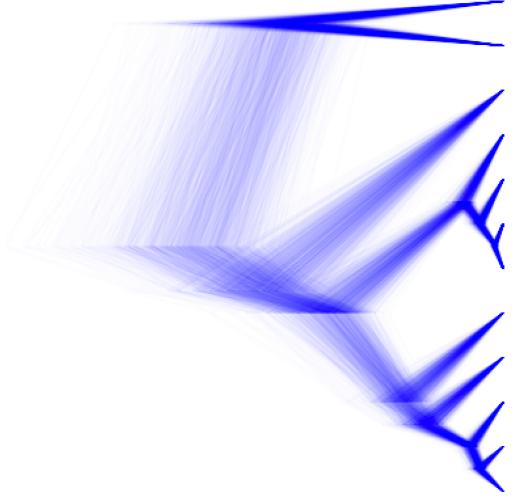
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At the moment we can not directly examine the ESS of the trees;

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Good mixing of the continuous parameters and likelihoods is indicative;

# Tree space mixing



Bad news:

At the moment we can not directly examine the ESS of the trees;

Good news:

Good mixing of the continuous parameters and likelihoods is indicative;

Can also use AWTY to see if the clade probabilities stabilised.

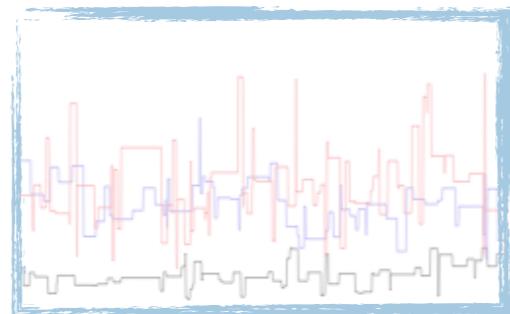
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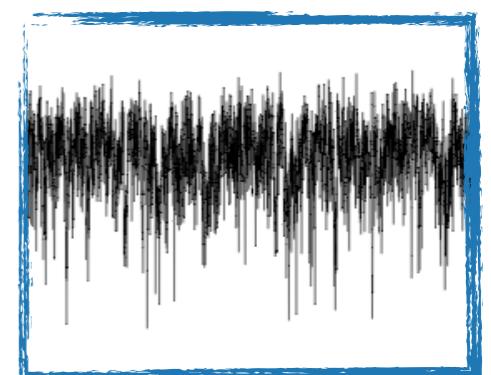
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Bayesian analysis always gives an answer!

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Bad news:

The answer is how uncertain we are.

# Troubleshooting time!



Roarrr!...

# Hacking XML

```
<run chainLength="1000000" id="mcmc" spec="MCMC" numInitializationAttempts="5000">
    <state id="state" storeEvery="5000">
        <parameter dimension="4" id="samplingProportion" lower="0.0" name="stateNode" upper="1.0" value="0 0.1 0 0.1"/>
        <parameter dimension="2" id="becomeUninfectiousRate" lower="0.0" name="stateNode" upper="Infinity" value="0.2 0.1"/>
        <parameter dimension="2" id="R0" lower="0.0" name="stateNode" upper="Infinity" value="2 1"/>
        <parameter dimension="2" name="stateNode" id="r" value="0.9"/>
        <stateNode idref="rateMatrix"/>
    </state>

    <distribution id="posterior" spec="CompoundDistribution">
        <distribution id="prior" spec="CompoundDistribution">
            <distribution R0="@R0" becomeUninfectiousRate="@becomeUninfectiousRate" id="BDMM"
                samplingProportion="@samplingProportion"
                spec="beast.evolution.speciation.BirthDeathMigrationModelUncoloured" tree="@tree" tiptypes="@tiptypes"
                removalProbability="@r" stateNumber="2" useRK="true" conditionOnSurvival="true">
                <parameter name="samplingRateChangeTimes" value="0. 4.36"/>
                <!-- latest sample time - earliest sample time = X -->
                <reverseTimeArrays spec="beast.core.parameter.BooleanParameter" value="false false true false"/>
                <migrationMatrix id="rateMatrix" spec='RealParameter' value="0.07 0" dimension="2" lower="0" upper="100"/>
                <frequencies id="geo-frequencies" spec='RealParameter' value="1 0" lower="0" upper="1" dimension="2"/>
            </distribution>
            <prior id="R0Prior" name="distribution" x="@R0">
                <LogNormal M="0" S="0.5" name="distr"/>
            </prior>
            <prior id="rPrior" name="distribution" x="@r">
                <Beta alpha="1" beta="99" name="distr"/>
            </prior>
            <prior id="rateMatrixPrior" name="distribution" x="@rateMatrix">
                <LogNormal M="-0.5" S="1.25" name="distr"/>
            </prior>
            <distribution spec="ExcludablePrior" xInclude="false true false true" id="samplingProportionPrior" name="distribution"
x="@samplingProportion">
                <Beta alpha="15" beta="35" name="distr"/>
            </distribution>
            <prior id="becomeUninfectiousRatePrior" name="distribution" x="@becomeUninfectiousRate">
                <Exponential mean="0.2" name="distr"/>
            </prior>
        </distribution>
    </distribution>

    <operator id="R0Scaler" parameter="@R0" scaleFactor="0.75" spec="ScaleOperator" weight="2"/>
    <operator id="becomeUninfectiousRateScaler" parameter="@becomeUninfectiousRate" scaleFactor="0.75" spec="ScaleOperator" weight="2"/>
    <operator id="samplingProportionScaler" parameter="@samplingProportion" scaleFactor="0.75" spec="ScaleOperator" weight="2"/>
    <operator id="rScaler" parameter="@r" scaleFactor="0.75" spec="ScaleOperator" weight="2"/>
    <operator id="updownBD" scaleFactor="0.9" spec="UpDownOperator" weight="2">
        <parameter idref="R0" name="up"/>
        <parameter idref="becomeUninfectiousRate" name="down"/>
    </operator>
```

# Cases for editing XML

- setting a starting tree;
- fixing the tree;
- need for excludable priors.

# Excludable priors

Excludable priors are only available in XML:

```
<distribution spec="BirthDeathMigrationModelUncoloured" ... >
    <migrationMatrix id="rateMatrix" spec='RealParameter' value="0.9 0"/>
    <!-- ... -->
</distribution>
<distribution spec="ExcludablePrior" xInclude="true false" id="rateMatrixPrior"
              name="distribution" x="@rateMatrix">
    <LogNormal M="-1" S="1.25" name="distr"/>
</distribution>
<!-- ... -->
```