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Protocol status: Working

🌐 Repetitive element annotation protocol for the eastern banjo frog V.1

📁 In 1 collection

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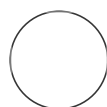
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ABSTRACT

This pipeline is the repetitive element annotation by using homology-based, *de novo* predictions and Tandem Repeats Finder to identify repetitive elements in the *Limnodynastes dumerilii dumerilii* genome assembly.

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1 The following sub-steps are the process for homology-based predictions to identify repetitive elements in the *Limnodynastes dumerilii dumerilii* genome assembly.

- 1.1 Identify known repetitive elements by aligning the *Limnodynastes dumerilii dumerilii* genome sequences against the Repbase-derived RepeatMasker libraries using RepeatMasker (v4.1.0).

Note

Use the parameters "-nolow -norna -no is" when running RepeatMasker.

- 1.2 Identify known repetitive elements by aligning the *Limnodynastes dumerilii dumerilii* genome sequences against the transposable element protein database using RepeatProteinMask (an application within the RepeatMasker package)

Note

Use the parameters "-noLowSimple -pvalue 0.0001 -engine ncbi" when running RepeatProteinMask.

2 The following sub-steps are the process for *de novo* predictions to identify repetitive elements in the *Limnodynastes dumerilii dumerilii* genome assembly.

- 2.1 Execute RepeatModeler (v2.0, RRID:SCR_015027) on the *Limnodynastes dumerilii dumerilii* assembly to build a *de novo* repeat library for this species.

2.2 Employ RepeatMasker (v4.1.0) to align the *Limnodynastes dumerilii dumerilii* genome sequences against the *de novo* library for repetitive element identification.

3 Identify tandem repeats in the *Limnodynastes dumerilii dumerilii* genome assembly by Tandem Repeats Finder (v4.09).

Note

Use the parameters "Match=2 Mismatch=7 Delta=7 PM=80 PI=10 Minscore=50 MaxPeriod=2000" when running Tandem Repeats Finder.