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**RNA-Seq analysis and de novo transcriptome assembly of Cry ...**  
Hevea brasiliensis, being the only source

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of commercial natural rubber, is an extremely economically important crop. In an effort to facilitate biological, biochemical and molecular research in rubber biosynthesis, here we report the use of next-generation massively parallel sequencing technologies and de novo transcriptome assembly to gain a comprehensive overview of the H.

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brasiliensis ...

## **De novo transcriptome assembly: A comprehensive cross ...**

CONCLUSION: Transcriptome assembly is a challenging computational task even if good solutions are already available to end-users, these solutions can still be improved while conserving the overall

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representation and quality of the assembly. The de novo RNA-Seq Assembly Pipeline (DRAP) is an easy to use software package to produce compact and ...

**RNA-Seq Based De Novo Transcriptome Assembly and Gene ...**



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Transcriptome analysis based on a de novo assembly of next generation RNA sequences is now performed routinely in many laboratories. The generated results, including contig sequences, quantification figures, functional annotations and variation discovery outputs are usually bulky and quite diverse. ...

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## **De novo transcriptome assembly - Wikipedia**

We describe Trans-ABYSS, a de novo short-read transcriptome assembly and analysis pipeline that addresses variation in local read densities by assembling read substrings with varying stringencies and then merging the

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resulting contigs before analysis.

Analyzing 7.4 gigabases of 50-base-pair paired-e ...

### **RNA-Seq de novo Assembly - docs.blast2go.com**

Introduction. De novo transcriptome assembly is one of the most frequent analyses performed in bioinformatics

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and it consists of reconstructing the transcriptome from RNA sequencing data, assembling short nucleotide sequences into longer ones without the use of a reference genome. This functionality is based on Trinity, a well-known de novo sequence assembler software developed at the Broad ...

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## **InsideDNA: RNA-Seq de novo assembly using Trinity**

TRINITY is a software package for conducting de novo (as well as the genome-guided version of) transcriptome assembly from RNA-seq data. The Trinity package also includes a number of perl scripts for generating statistics to assess assembly quality,

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and for wrapping external tools for conducting downstream analyses.

## **Rna Seq De Novo Assembly**

De novo transcriptome assembly is the de novo sequence assembly method of creating a transcriptome without the aid of a reference genome ... but RNA-seq

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can be strand-specific. Third, transcriptome assembly is more challenging because transcript variants from the same gene can share exons and are difficult to resolve ...

### **RNA-Seq de novo Assembly - BioBam**

The majority of the berry fruit species

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that were used for RNA sequencing and analysis (Table 1) lacked an available reference genome sequence, therefore, de novo assembly of the Illumina reads was carried out for each species using Trinity software. Ten transcriptomes were assembled from RNA-seq data derived from a single cDNA library corresponding to ripe/mature fruits for gene



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identification ...

## **github.com**

De novo assembly using Trinity Trinity is one of the most popular software package for efficient and robust de novo reconstruction of transcriptomes from RNA-Seq data. It consists of three software modules, Inchworm, Chrysalis

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and Butterfly, that run sequentially to process the sequencing reads.

### **de novo assembly | RNA-Seq Blog**

RNA-seq de novo assembly is one the most frequent type of sequence analysis in biology and bioinformatics. However, just as a complete genome assembly, RNA-seq assembly is not trivial and often

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requires large amount of RAM and CPUs. In this tutorial, we explain how to use one the most popular RNA-seq assemblers - Trinity.

### **TransLiG: a de novo transcriptome assembler that uses line ...**

Running Stringtie in De Novo Mode Note, to discover novel transcripts with

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Stringtie using the alignments we generated in the previous modules we will now run Stringtie in de novo mode. To use de novo mode do NOT specify either of the -G OR -e options. Extra options specified below -rf tells StringTie that our data is stranded and to use the correct strand specific mode (i.e. assume a ...

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## **RNAbrowse: RNA-Seq de novo assembly results browser**

The RNA sequencing study presented here generated the first de novo transcriptome assembly of castor semilooper, *Achaea janata* (Noctuidae: Lepidoptera), and compared gene expression signatures ...

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## **De novo assembly and analysis of RNA-seq data**

Introduction. De novo transcriptome assembly is one of the most frequent analyses performed in bioinformatics and it consists of reconstructing the transcriptome from RNA sequencing data, assembling short nucleotide

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sequences into longer ones without the use of a reference genome. This functionality is based on Trinity, a well-known de novo sequence assembler software developed at the Broad ...

### **RNA-seq, de novo transcriptome assembly and flavonoid gene ...**

RNA sequencing and de novo

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transcriptome assembly of *C. deserticola* fleshy stem. Stem of *C. deserticola* has been extensively used as a traditionally important tonic in China and Japan for many years. To obtain a global overview of gene expression in the *C. deserticola* fleshy stem, we collected *C.*

### **Best Practices for De Novo**



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### **Transcriptome Assembly with ...**

We would like to show you a description here but the site won't allow us.

### **RNA-seq analysis in de novo - GitHub**

STable - a novel approach to de novo assembly of RNA-seq data and its application in a metabolic model

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network based metatranscriptomic workflow August 6, 2018 Leave a comment 1,892 Views De novo assembly of RNA-seq data allows the study of transcriptome in absence of a reference genome either if data is obtained from a single organism...

### **De novo assembly using Trinity -**

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### **Gene-level RNA-Seq Data ...**

In this study, we presented a novel de novo assembler TransLiG for transcriptome assembly using short RNA-seq reads. Compared to the salient assemblers of same kind on both simulated and real datasets, TransLiG consistently performs the best in accuracy (including sensitivity and

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precision) and the number of correctly identified genes.

### **Compacting and correcting Trinity and Oases RNA-Seq de ...**

RNA-seq analysis in de novo. An integrated workflow for de novo analysis and DE gene assessment to conduct RNA-seq data analyses. This Workflow is

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developped in Louis Bernatchez' lab..  
WARNING. The software is provided "as is", without warranty of any kind, express or implied, including but not limited to the warranties of merchantability, fitness for a particular purpose and noninfringement.

### **RNA-Seq analysis and de novo**

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### **transcriptome assembly of ...**

Here, we present a large-scale comparative study in which 10 de novo assembly tools are applied to 9 RNA-Seq data sets spanning different kingdoms of life. Overall, we built >200 single assemblies and evaluated their performance on a combination of 20 biological-based and reference-free

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