
Oyster River Protocol Documentation

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The Oyster River Protocol for (eukaryotic) transcriptome assembly is an actively developed, evidenced based method for optimizing transcriptome assembly. The manuscript corresponding to this protocol is here: <https://peerj.com/articles/5428/> In brief, the protocol assembles the transcriptome using a multi-kmer multi-assembler approach, then merges those assemblies into 1 final assembly.

Contact Information

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Some method you'd like me to benchmark? File an [issue](#)

1.1 1. Installing the software

In general, the ORP can be successfully and easily installed on Linux operating systems. OSX might work, but I have not tried and it is unsupported. Don't try this on Windows.

Here are the instructions for installation. Getting stuff installed will be the hard part (the included makefile should do most/all of the hard work, though). Once you have things installed, should be smooth sailing!

2.1 2. List of dependencies

Sorry there are so many. Assembly is complex.. The makefile should take care of this.

- Rcorrector, Trimmomatic, Trinity, SPAdes, TransABySS, MCL, Metis, OrthoFuser, BLAST, seqtk, BUSCO (make sure to install databases), TransRate (the ORP version packaged here).
- Python modules numpy, scipy, biopython, cvxopt.

2.2 3. *oyster.mk* Usage

After activating the *orp_v2* conda environment. this command will run the entire ORP in one shot! You can add the `--dry-run` flag to the end to see the individual commands that it will run, if you are curious. The *STRAND=RF* allows for strand specific assembly in version 2.1.0 of the ORP.

You must use the full PATH to the *oyster.mk* script for it to work

```
source activate orp_v2

/path/to/Oyster_River_Protocol/oyster.mk main \
STRAND=RF \
MEM=150 \
CPU=24 \
READ1=SRR2016923_1.fastq \
READ2=SRR2016923_2.fastq \
RUNOUT=SRR2016923
```

2.3 4. *strandeval.mk* Usage

After activating the *orp_v2* conda environment. this command will run the evaluate the strandedness of your assembly in ORP version 2.1.0. It should help you understand if you have assembled the reads using the proper flags. You can add the `--dry-run` flag to the end to see the individual commands that it will run, if you are curious. The evaluation script was modified from a similar script in the Trinity distribution (<https://github.com/trinityrnaseq/trinityrnaseq/wiki/Examine-Strand-Specificity>).

See *strandexamine* for some help in interpreting the results.

You must use the full PATH to the *strandeval.mk* script for it to work

```
source activate orp_v2

/path/to/Oyster_River_Protocol/strandeval.mk main \
ASSEMBLY=assembly.fasta \
CPU=24 \
READ1=SRR2016923_1.fastq \
READ2=SRR2016923_2.fastq \
RUNOUT=SRR2016923
```

2.4 5. *report.mk* Usage

After activating the *orp_v2* conda environment. this command will generate a transcriptome assembly report, in ORP version 2.1.0. You can add the `--dry-run` flag to the end to see the individual commands that it will run, if you are curious. It can be run on an assembly generated by any method.

** The `LINEAGE=` flag must be specified, and the database you specify must be in `/path/to/Oyster_River_Protocol/busco_dbs`. The Eukaryotic database is there by default.

```
source activate orp_v2

/path/to/Oyster_River_Protocol/report.mk main \
ASSEMBLY=assembly.fasta \
CPU=24 \
LINEAGE=eukaryota_odb9
READ1=SRR2016923_1.fastq \
READ2=SRR2016923_2.fastq \
RUNOUT=SRR2016923
```

2.5 6. Changelog

Version 2.1

- Strand specific libraries are now assembled properly, this is enabled by adding the `STRAND=` flag. Both `RF` and `FR` are options, tho `RF` is the most common option.
- There is a new tool, *strandeval.mk*, which helps you evaluate the strandedness of your assembly.
- There is a new tool, *report.mk*, which generates an assembly report for you.
- There is a new tool, *quant.mk*, which facilities the quantitation procedure.
- Typing *oyster.mk help*, *report.mk help*, *strandeval.mk help* will print a help message.

Version 2.0

- The final assembly is now called *\$RUNOUT.ERP.fasta*.
- Shannon has been removed, and TransABySS has been added in its place. MANY users (and myself) have struggled with the RAM use and runtime of Shannon. TransABySS is much faster, and uses much less RAM.
- Diamond is leveraged for transcript recovery. It had been noted by some users that a few “real” transcripts were getting lost during the OrthoFuser steps.. Diamond, which is run after, recovers those.
- The use of LinuxBrew has been removed, in favor of conda. Dependencies are now managed by conda. You will need to launch the *orp_v2* conda environment before assembling.
- cd-hit-est is now run as default.