

Using RAMPAGE to identify and annotate promoters in insect genomes

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Abstract. Application of Transcription Start Site (TSS) profiling technologies, coupled with large-scale next-generation sequencing (NGS) has yielded valuable insights into the location, structure and activity of promoters across diverse metazoan model systems. In insects, TSS profiling has been used to characterize the promoter architecture of *Drosophila melanogaster* [1] and subsequently was employed to reveal widespread transposon-driven alternative promoter usage in the fruit fly [2].

In this chapter we discuss the computational analysis of the experimental data derived from one TSS profiling method, RAMPAGE (RNA Annotation and Mapping of Promoters for Analysis of Gene Expression), that can be used for the precise, quantitative identification of promoters in insect genomes. We demonstrate this using the software tools GoRAMPAGE [3] and TSRchitect [4], providing detailed instructions with the aim of taking the user from raw reads to processed results.

Keywords: *cis*-regulatory regions, promoter architecture, transcription initiation, transcription start sites (TSSs)

1 Introduction

1.1 TSS Profiling Identifies Promoters at Genome-Scale

The promoter, which is defined in eukaryotes as the genomic region bound by RNA Polymerase II immediately prior to transcription initiation [5], is the primary locus of the regulation of gene expression. The identification of promoter regions is necessary for understanding the *cis*-regulatory signals controlling gene expression in an organism, and is also important for genome annotation. However, despite the rapid accumulation of genome sequences across metazoan and arthropod diversity, accurate annotation of promoter regions remains sparse. This is because—absent empirically-defined information—precisely identifying

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sequence motifs that demarcate the promoter is unreliable. In contrast with current *in silico* approaches, direct mapping of TSSs identifies the location of the core promoter. Cap Analysis of Gene Expression (CAGE) [6], one of the first methods devised to identify 5'-ends of mRNAs at large-scale, involves selective capture of 5'-capped transcripts, first-strand reverse-transcription and ligation of a short oligonucleotide (CAGE tag).

CAGE was initially utilized by the FANTOM (Functional Annotation of the Mammalian Genome) consortium to identify promoter architecture in human and mouse [7], providing the first glimpse of the global landscape of transcription initiation. At the onset of the next-generation sequencing (NGS) era, CAGE was coupled with massively-parallel sequencing to define 5'-mRNA ends at large scale. This advance provided more extensive coverage of the expressed transcriptome and provided increased sensitivity for quantitative measurements of promoter activity.

1.2 Promoter Architecture of *Drosophila melanogaster*

Hoskins and colleagues [1] performed CAGE in *D. melanogaster* as part of the modENCODE consortium, identifying promoters at large-scale and characterizing the promoter architecture of an insect genome for the first time. The authors found that TSS distributions at *Drosophila* promoters exhibit a range of shapes that can be generally grouped into two major classes: *peaked* and *broad*. This confirmed the original finding of Rach and colleagues [8], which was done using publicly-available expressed sequence tags (ESTs). Peaked promoters have a single, major TSS position occupying a narrow genomic region, whereas broad promoters lack a single, major TSS and contain TSSs across a wider region [8, 9]. The authors also showed a strong association between promoter class and motif composition (consistent with previous findings [8, 10]). Peaked promoters were associated with positionally-enriched *cis*-regulatory motifs including TATA, Initiator (Inr) and DPE (Downstream Promoter Element), while broad promoters contained an enrichment of less-well characterized motifs, including *Ohler6* and *Ohler7* [11]. The existence of at least two promoter classes appears to be conserved among metazoans and has been reported (using TSS profiling methods) in insects, cladocerans [12], fish [13] and mammals [14, 9].

1.3 Promoter Structure of Insects

Beyond *D. melanogaster*, few investigations have utilized TSS profiling in insect genomes. As a consequence, what is known about promoter architecture in insects is largely restricted to the *Drosophila* genus. As part of the modENCODE effort, CAGE was performed in multiple tissues and developmental stages of the *Drosophila pseudoobscura*. TSSs were found to be highly similar between species: 81% of TSSs of aligned, CAGE-identified TSSs from *D. pseudoobscura* were positioned within 20nt of their counterparts in *D. melanogaster*. An enrichment of

the CA dinucleotide was detected at the TSS ($[-1, +1]$), and the motifs corresponding to TATA, Inr and DPE were positioned at the same locations relative to the TSS in both species.

The only other insect species for which TSS profiling has been applied is the Tsetse fly (*Glossina morsitans morsitans*) [15]. Using TSS-seq (specifically Oligo-capping; for details see [16]), the authors identified 3134 promoters associated with 1424 genes. The authors found a preference for CA and AA dinucleotides at the TSSs and observe the major core promoter elements observed in *Drosophila*: TATA, Inr, DPE, in addition to MTE (Motif Ten Element). As in *D. melanogaster*, peaked promoters were more likely to contain TATA and Inr than broad promoters. While the taxonomic sampling of species for TSS profiling has been limited, the existing studies are sufficient to provide a general picture of insect promoter architecture. A major demarcation between the promoter architecture of insects and mammals appears to be the large fraction of mammalian promoters found in CpG islands [15]. CpG island promoters (CPIs) form the largest class of promoter in mammals [17]; by contrast, CPIs are not known to exist as a class in invertebrates.

1.4 Paired-end TSS Profiling with RAMPAGE

The most recent major methodological advance in TSS Profiling is RAMPAGE [2, 18], a protocol for 5'-cDNA sequencing that combines cap trapping and template-switching with paired-end sequence information (see Figure 1). As with CAGE and other TSS profiling methods, RAMPAGE reads are aligned, to obtain TSSs and clustered to identify Transcription Start Regions (TSRs), which are enrichments of TSSs consistent with promoters (Figure 2a). A key advantage of generating paired-end sequence is transcript connectivity, which provides a direct link between a given 5'-end and its associated mRNA molecule [2] (Figure 2b). Because short or spurious RNAs are found within the transcriptome, transcript connectivity allows the TSSs (and thus promoters) of full-length mRNAs to be unambiguously identified, which benefits genome annotation and improves interpretation of transcript species.

Batut and colleagues [2] generated libraries from total RNA isolated from 36 stages across the life cycle of *D. melanogaster*, generating a comprehensive gene expression and promoter atlas for fruit fly and demonstrating the utility of RAMPAGE. RAMPAGE is currently being applied as part of the latest iteration of ENCODE to identify promoters in human, but as of this writing it has not been applied to any non-*Drosophila* insect model system.

In anticipation of the future application of TSS profiling into other insect model systems, we discuss in this chapter a well-documented protocol for the computational processing and analysis of RAMPAGE data, using selected libraries from Batut *et al.* [2]. This method consists of two parts: first, we discuss how to process, filter and align the sequenced RAMPAGE libraries to the *D. melanogaster* genome. Second, we show how to identify TSSs and promoters

from the aligned sequences and associate them with coding regions. In closing, we will consider further applications of this data and discuss the utility of reproducible workflows in bioinformatic analysis.

2 Materials

The example analyses described herein require a workstation capable of doing modern bioinformatics; minimally a reasonably-appointed laptop. An intermediate understanding of the Linux/Unix command line will be extremely useful, although we make efforts to explain the procedures with clarity. In addition, it will likely be necessary for the participant to have superuser privileges on the machine. If you do not have a machine (or have access to one) that meets these requirements, it is recommended that you consider cloud-based cyberinfrastructure, including Amazon Web Services (AWS; <https://aws.amazon.com/>), CyVerse (<http://www.cyverse.org/>) [19], or JetStream (<https://jetstream-cloud.org/>) [20]. The former is a well-known pay-per-use solution, while the latter two are NSF-funded resources that makes compute allocations freely available to the public.

2.1 Hardware

1. x86-64 compatible processors
2. 16GB RAM
3. 80GB+ hard disk space

2.2 Operating System

- 64 bit Linux (preferred) or Mac OS X (with Command Line Tools from XCode)

2.3 Software

Below is a list of the software packages required for this demonstration (*see Note 1*).

Sequence retrieval

1. SRA Toolkit [21] (<https://www.ncbi.nlm.nih.gov/sra/docs/toolkitsoft/>)

GoRAMPAGE

1. GoRAMPAGE [3] (<https://github.com/brendelGroup/GoRAMPAGE>)
2. fastq-multx [22] (<https://github.com/brwnj/fastq-multx>)
3. FASTX-Toolkit [23] (http://hannonlab.cshl.edu/fastx_toolkit/Index.html)
4. TagDust2 [24] (<https://sourceforge.net/projects/tagdust/>)
5. Samtools [25] (<http://www.htslib.org/doc/samtools.html>)

131 6. STAR [26] (<https://github.com/alexdobin/STAR>)

132 **TSRchitect**

- 133 1. R (v. 3.4 and up) [27] (<https://www.r-project.org/>)
- 134 2. Bioconductor (v. 3.5 and up) [28] (<http://bioconductor.org/>)
- 135 3. TSRchitect [4] (<http://bioconductor.org/packages/release/bioc/html/TSRchitect.html>)
- 136 4. Various R package dependencies (see **Methods**)

137 **2.4 Demonstration**

138 We created an online demonstration (demo) to serve as a companion to this
 139 chapter, which contains both scripts and select files to assist you in completing
 140 this tutorial. Please find the repository here:
 141 <https://github.com/brendelgroup/GoRAMPAGE/demo/MMB> (see **Note 2**).

142 **2.5 Installation of R packages**

143 For installation of the software listed above, please follow the instructions pro-
 144 vided by each respective package. Part of our analysis will require the use of R
 145 packages found in the Bioconductor suite [28] (see **Note 3**). To install Biocon-
 146 ductor, please type the following from an R console:

```
147 source("https://bioconductor.org/biocLite.R")
148 biocLite()
```

149 We will use the R package *TSRchitect* to identify promoters from aligned RAM-
 150 PAGE libraries. Prior to running the analysis, it will be necessary to install a
 151 series of prerequisite packages to *TSRchitect* from Bioconductor. Please install
 152 these packages, followed by *TSRchitect* (as before, from an R console):

```
153 source("https://bioconductor.org/biocLite.R")
154 biocLite(c("AnnotationHub", "BiocGenerics", "BiocParallel",
155 "ENCODEExplorer", "GenomicAlignments", "GenomeInfoDb",
156 "GenomicRanges", "IRanges", "methods",
157 "Rsamtools", "rtracklayer", "S4Vectors",
158 "SummarizedExperiment"))
159
160 biocLite("TSRchitect")
```

161 Finally, please confirm that *TSRchitect* has been installed correctly by loading
 162 it from your R console as follows:

```
163 library(TSRchitect) #loading TSRchitect
```

164 3 Methods

165 3.1 Retrieving the RAMPAGE sequence data from NCBI

166 To begin our analysis, we must download the RAMPAGE data to our worksta-
 167 tion. We will utilize tools provided by the SRA Toolkit, which should already
 168 be installed on your machine (see **Materials**). The command *fastq-dump* al-
 169 lows one to directly retrieve data from the GEO database using the appropriate
 170 identifier(s). While there are 36 RAMPAGE libraries in the Batut *et al.* pa-
 171 per, we will select a subset of these to analyze here. We will compare samples
 172 from selected embryonic (E01h-E03h) and larval (L1-L3) tissues, representing
 173 the beginning and end of embryonic development. For more information about
 174 the experiment and the available RAMPAGE libraries, please see the following
 175 link: <https://www.ncbi.nlm.nih.gov/Traces/study/?acc=SRP011193>.

176
 177 First, let's proceed with downloading the libraries from early embryonic tissues
 178 (see **See Note 4**). We will make a new folder (entitled "**fastq_files/**") to
 179 house these files.

```
180 mkdir fastq_files
181 cd fastq_files
182
183 fastq-dump --split-files SRR424683
184 fastq-dump --split-files SRR424684
185 fastq-dump --split-files SRR424685
```

186 We continue by downloading the data from late larval tissues.

```
187 fastq-dump --split-files SRR424707
188 fastq-dump --split-files SRR424708
189 fastq-dump --split-files SRR424709
```

190 Once the download of the aforementioned files are complete, you should see a
 191 total of 12 (6 \times 2) separate fastq files in your current working directory:

```
192 ls -l *.fastq | wc -l
```

193 3.2 Creating symlinks to the files

194 Our workflow expects fastq files that have the format "***.R1/R2.clipped.fq**".
 195 Rather than rename them, we can simply create brand new symbolic links (sym-
 196 links) to the files, as follows:

```
197 cd ..
198 mkdir -p output/reads/clipped
199 cd output/reads/clipped
200
201 #embryonic libraries
```

```

202 ln -s ../../../../fastq-files/SRR424683_1.fastq E01h.R1.clipped.fq
203 ln -s ../../../../fastq-files/SRR424683_2.fastq E01h.R2.clipped.fq
204 ln -s ../../../../fastq-files/SRR424684_1.fastq E02h.R1.clipped.fq
205 ln -s ../../../../fastq-files/SRR424684_2.fastq E02h.R2.clipped.fq
206 ln -s ../../../../fastq-files/SRR424685_1.fastq E03h.R1.clipped.fq
207 ln -s ../../../../fastq-files/SRR424685_2.fastq E03h.R2.clipped.fq
208
209 #larval libraries
210 ln -s ../../../../fastq-files/SRR424707_1.fastq L1.R1.clipped.fq
211 ln -s ../../../../fastq-files/SRR424707_2.fastq L1.R2.clipped.fq
212 ln -s ../../../../fastq-files/SRR424708_1.fastq L2.R1.clipped.fq
213 ln -s ../../../../fastq-files/SRR424708_2.fastq L2.R2.clipped.fq
214 ln -s ../../../../fastq-files/SRR424709_1.fastq L3.R1.clipped.fq
215 ln -s ../../../../fastq-files/SRR424709_2.fastq L3.R2.clipped.fq
216
217 cd ../../.. #returning to the output directory

```

218 3.3 Downloading genomic data from *D. melanogaster*

219 Now that we have the fastq files from the RAMPAGE libraries downloaded and
 220 named appropriately, we now must retrieve the genome assembly and rRNA se-
 221 quences from *D. melanogaster*. The genome assembly is required for aligning the
 222 RAMPAGE reads, and the rRNA sequences are required to filter out matching
 223 reads in the sequenced RAMPAGE libraries. Because our sample is intended to
 224 contain only capped RNAs, any rRNA sequences we observe in these RAMPAGE
 225 libraries are contaminants that must be removed.

226
 227 Please make note of the rRNA sequences, found in the file "Dmel_rRNA.fasta",
 228 from the folder `additional_files` folder in the demo (see **Note 5**).

229
 230 We will then download a version of the *D. melanogaster* genome assembly from
 231 ENSEMBL (www.ensembl.org) [29]. To retrieve the genome assembly, please do
 232 the following:

```

233 mkdir genome
234 cd genome
235 wget ftp://ftp.ensembl.org/pub/release-78/fasta/
236 drosophila_melanogaster/dna/Drosophila_melanogaster.BDGP5.dna.toplevel.fa.gz
237 #uncompressing the file
238 gzip -d Drosophila_melanogaster.BDGP5.dna.toplevel.fa.gz
239 cd ..

```

240 3.4 Filtering and alignment of RAMPAGE reads using 241 GoRAMPAGE

242 At this stage we are ready to commence with the rRNA filtering and alignment
 243 of the RAMPAGE libraries. We will use GoRAMPAGE, a tool we developed, to

perform these tasks in a concerted workflow. GoRAMPAGE runs TagDust [24] to remove rRNA and low-complexity reads and STAR [26] to align RAMPAGE (or other paired-end) reads to a given genome assembly.

Setting up the GoRAMPAGE job. Please refer to the script "GoRAMPAGE_script_MMB.sh" and (using a text editor) provide the appropriate paths to the genome assembly, output directory (see above) and rRNA sequences (see **Note 6**). GoRAMPAGE jobs can optionally be run in parallel (see **Note 7**). The script can be executed as follows:

```
#vi GoRAMPAGE_script_MMB.sh #updating with a text editor
./GoRAMPAGE_script_MMB.sh
```

If everything is working correctly you should start to see the results of the job being written to the file "errScript". You can inspect the progress during the run using the *less* command.

```
less -S errScript
```

Should the run fail before completion, any associated error messages will be printed to the errScript file. Once the job is complete, you should see the message "GoRAMPAGE job is complete!" appear on the command-line terminal.

Inspecting the rRNA filtering results. To evaluate the results from Step 3 (rRNA filtering), please navigate to the top level of the "output" directory and open the file "LOGFILES". You'll see the recorded progress of the program Tagdust and a record of the results. We notice that (for the L3h library) 1046448 of reads (78.1%) were "extracted", meaning that slightly more than 20% of reads were removed because of matches with ribosomal sequences. The removed reads from all libraries are found in the "dusted_discard" directory, and the extracted reads are found in the current directory. Due to their sheer abundance within cells, ribosomal RNA sequences are an inevitable contaminant within TSS profiling libraries. For analysis purposes, it is important that these sequences be removed, which is what has been completed here. Since this step was conducted appropriately, we can proceed to the next step.

Evaluating the alignments. The folder "alignments/" in your GoRAMPAGE output folder will now contain 6 .bam files, each representing the distinct RAMPAGE libraries selected for our analysis. Typing "ls -l" from the command line will show that these files are symlinks to the original alignment files found in the "STARoutput/" directory. "STARoutput/", as its name suggests, contains the output from the STAR alignment, and this includes the alignment files "*.sortedByCoord.out.bam", and four additional log files. The files with the suffix "*.STAR.Log.final.out" each contain a summary of the alignment, such as the number of input reads, the percentage of uniquely-mapped reads and the percentage of unmapped reads. An inspection of these log files indicates that

the alignments have similar mapping rates (~70-80%), a reasonable outcome for our purposes.

Now that our RAMPAGE libraries are filtered and aligned, we can commence with the second half of our analysis.

3.5 Promoter identification from aligned RAMPAGE libraries

We can now use the prepared alignment files to identify TSSs and promoters from the selected RAMPAGE libraries. There are currently several tools available for this purpose. *CAGEr*, developed by Haberle [30], was utilized to perform TSS identification as part of the FANTOM5 efforts. We will use *TSRchitect* in this demonstration, since it was specifically designed to analyze paired-end TSS profiling datasets, and also because it is more flexible with respect to model system (*i.e.* it does not require a corresponding *BSGenome* [31] package). The latter feature will be helpful when analyzing the non-*D. melanogaster* TSS profiling datasets that we expect to be generated in the near future.

Setting up the Analysis. *TSRchitect*, the package we'll use for this analysis, is an R package available in the Bioconductor suite of genomics tools [28]. It makes use of existing packages and data structures within this environment, where available, to identify promoters from sequence alignments. Since you have already installed *TSRchitect* and its dependencies (see section 2.3), we are set to proceed.

There are two general ways one can choose to run *TSRchitect*. The first is interactively *i.e.* typing the instructions directly into an R console. While this is a perfectly acceptable way to run analyses using package, for larger jobs it will likely be more efficient (and likely more reproducible) to run a dedicated R script. We have provided sample scripts to make it easier for you to set up an R script. The two scripts are identical with a single exception: one is set up to run in parallel ("*TSRchitect_parallel_MMB.R*"), while the other is written to run in serial ("*TSRchitect_serial_MMB.R*"). Please select the script that best suits your computing resources. In the section to follow, we will go through the output of the analysis. For further details on how to use *TSRchitect*, please see its documentation at its Bioconductor page found here: <https://www.bioconductor.org/packages/release/bioc/html/TSRchitect.html>.

Running the Analysis. To run *TSRchitect* using the batch script, provide full paths for the variables "BAMDIR" and "DmAnnot" in the script provided (see **Note 8**). *BAMDIR* should be a path to the subdirectory "alignments/" in RAMPAGE output directory you specified earlier, and *DmAnnot* should be a full path to the *D. melanogaster* gene annotation listed above.

323 Once this is complete, we can run the batch script from the Linux command-line
 324 as follows:

```
325 R CMD BATCH TSRchitect_parallel_MMB.R #or use 'serial script
326 #assumes variables BAMDIR and DmAnnot have already been set
327 bg #puts this job in the background
```

328 Once the job is underway, you can monitor its progress by looking at the contents
 329 of the .Rout file (in this case, "TSRchitect_parallel_MMB.Rout").

330 **Reviewing the *TSRchitect* script.** Before we evaluate the results (which
 331 will have been written to your working directory after running the batch script),
 332 there are some important aspects of the analysis to review. We discuss these for
 333 informational purposes only; it will not necessary to perform these commands
 334 separate from the batch script provided. First, we must initialize the *tssObject*
 335 (which stores the information about the experiment) appropriately (*see Note 9*).

336

337 The inputs in this case are BAM files (*inputType*="bam"); *TSRchitect* also ac-
 338 cepts input in BED format.

```
339 DmRAMPAGE <- loadTSSobj(experimentTitle = "RAMPAGE Tutorial", \
340   inputDir=BAMDIR, inputType="bam", isPairedEnd=TRUE, \
341   sampleNames=c("E1h","E2h", "E3h", "L1", "L2", "L3"), \
342   replicateIDs=c(1,1,1,2,2,2))
```

343 A critical step in our analysis is identifying TSRs from the aligned TSS data;
 344 to do this we use the function *determineTSR*. We have selected the job to run
 345 on 4 cores in this example (*n.cores*=4). Please enter the number of cores ap-
 346 propriate for your system. Because we want to identify TSRs from every one
 347 of the selected RAMPAGE libraries, we specify *tssSet*="all". The parameter
 348 *tagCountThreshold* was set to 25, meaning that only TSSs supported by 25 or
 349 more 5' RAMPAGE reads will be included within a TSR. Setting *writeTable* to
 350 "TRUE" means that the identified TSRs from each set will be written to the
 351 working directory.

```
352 DmRAMPAGE <- determineTSR(experimentName=DmRAMPAGE, n.cores=4, \
353   tsrSetType="replicates", tssSet="all", tagCountThreshold=25, \
354   clustDist=20, writeTable=TRUE)
```

355 *TSRchitect* can incorporate the tag abundances from each of the samples and
 356 append them to the list of identified TSRs. This is useful for downstream analysis
 357 of differential expression.

```
358 DmRAMPAGE <- addTagCountsToTSR(experimentName=DmRAMPAGE, \
359   tsrSetType="replicates", tsrSet=1, tagCountThreshold=10, \
360   writeTable=TRUE)
```

361 We can use *TSRchitect* to import an annotation file (or, alternatively, use an
 362 existing one from *AnnotationHub*) and use it to associate our set of identified
 363 TSRs with coding genes. We can specify the maximum distances (both up-
 364 and downstream) between the TSR and the annotation using the arguments
 365 *upstreamDist* and *downstreamDist*.

```
366 DmRAMPAGE <- importAnnotationExternal(experimentName=DmRAMPAGE, \
367   fileType="gff3", annotFile=DmAnnot)
368
369 DmRAMPAGE <- addAnnotationToTSR(experimentName=DmRAMPAGE, \
370   tsrSetType="replicates", tsrSet=1, \
371   upstreamDist=1000, downstreamDist=200, feature="gene", \
372   featureColumnID="ID", writeTable=TRUE)
```

373 Now we have generated a set of identified TSSs, TSRs from all 6 RAMPAGE
 374 libraries, and have associated the identified TSRs with annotated genes. Next, we
 375 will merge the libraries into two samples according to condition: early embryonic
 376 (E1h, E2h, E3h) and late larval (L1, L2, L3) using the information we provided
 377 when we initialized the *tssObject* at the start of this section. After merging, we
 378 identify promoters i) within the merged samples and ii) within the entire dataset
 379 combined, and associate with the *D. melanogaster* gene annotation as described
 380 previously (not shown).

```
381 #merging the sample data into two groups
382 DmRAMPAGE <- mergeSampleData(DmRAMPAGE)
383
384 # ... identifying TSRs from the merged samples:
385 DmRAMPAGE <- determineTSR(experimentName=DmRAMPAGE, \
386   n.cores=4, tsrSetType="merged", \
387   tssSet="all", tagCountThreshold=40, \
388   clustDist=20, writeTable=TRUE)
```

389 **Evaluating the results** Our analysis using *TSRchitect* is now complete. A
 390 snapshot of a representative sample of small set of aligned RAMPAGE libraries
 391 is shown in Figure 3. Your working directory should now contain the following:

- 392 – TSSs from each sample *e.g.* TSSset-1.txt: (6)
- 393 – TSRs from each sample (in both .txt and .tab formats): (12)
- 394 – TSRs from each merged group (in both .txt and .tab formats): *e.g.* TSRsetMerged-
 395 1.txt: (4)
- 396 – TSRs from the combined set of TSSs: TSRsetCombined.tab: (1)

397 Let's briefly review the files (*see* **Note 10**). We can quickly obtain the counts
 398 on the command line, as follows:

```
399 wc -l *.tab
400 8377 TSRset-1.tab
```

```

401 6159 TSRset-2.tab
402 4814 TSRset-3.tab
403 17924 TSRset-4.tab
404 11851 TSRset-5.tab
405 3242 TSRset-6.tab
406 13986 TSRsetCombined.tab
407 7344 TSRsetMerged-1.tab
408 12126 TSRsetMerged-2.tab
409 85823 total

```

410 We will see that we have identified between roughly 3,200 and 18,000 TSRs
411 within the individual RAMPAGE samples, which is attributable to the dif-
412 ferences in library sizes. We detect 7,344 TSRs within the early embryonic
413 samples ("TSRsetMerged-1.tab") and 12,126 TSRs in the late larval samples
414 ("TSRsetMerged-2.tab"). Within the combined samples ("TSRsetCombined.tab")
415 we find 13,986 TSRs, which is similar to the number reported by Hoskins *et. al.*
416 [1].

417
418 In addition to identifying the position of a given TSRs, *TSRchitect* records other
419 useful information about its properties. The *width* of a TSR refers the span of
420 the genomic region it occupies (in bp), and the *Shape Index* (SI) is measure of
421 the relative peakedness of the TSR. We can see an example of this in the file
422 "TSRsetMerged-1.txt".

seq	start	end	strand	nTSSs	tsrWidth	shapeIndex	featureID
2L.67043.67044.+			2L	67043	67044 +	270 2	1 NA
2L.74089.74115.+			2L	74089	74115 +	341 27	0.13 NA
2L.94739.94752.+			2L	94739	94752 +	1650 14	0.55 FBgn0031
2L.102386.102386.+			2L	102386	102386 +	284 1	2 FBgn0031

428 3.6 Summary

429 The workflow provided here is intended to serve as a useful entry point for the
430 analysis of TSS profiling data in insects. On the computational side, we have
431 provided an open source set of tools so that the uninitiated genome scientist
432 can begin to analyze RAMPAGE (or other forms of TSS profiling data) quickly.
433 While the analysis centered on *D. melanogaster* via the use of public datasets,
434 it is anticipated that this will assist groups who may be interested in performing
435 TSS profiling in their preferred insect model system. The application of TSS
436 profiling technology across a more representative sample of insect diversity will
437 improve our understanding of the positions and general structure *cis*-regulatory
438 regions in this phylum.

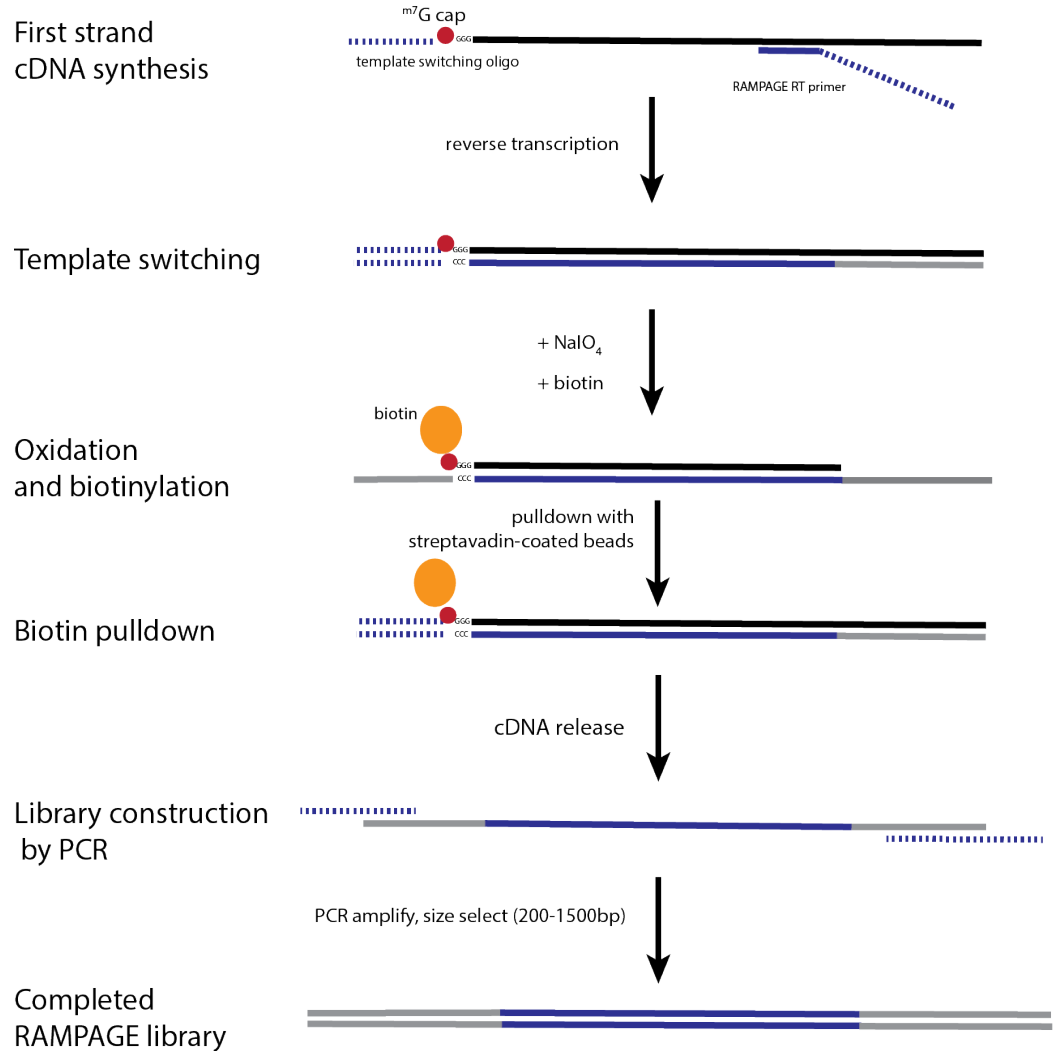


Fig. 1. A brief summary of the RAMPAGE protocol. Starting with high-quality total RNA, first-strand cDNA synthesis is initiated using a cap-bound oligonucleotide and a custom RAMPAGE RT primer, creating a double-stranded DNA-RNA hybrid molecule. Next, the 5'-m7G cap is oxidized, bound with biotin and pulled down with streptavidin-coated beads. The single-stranded cDNA molecules is released and the final RAMPAGE library construction is completed with PCR using custom oligonucleotides, followed by size-selection. This illustration was adapted from [18].

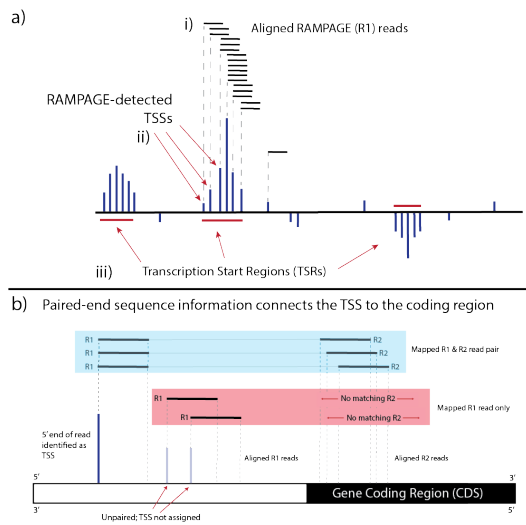


Fig. 2. An overview of promoter identification using RAMPAGE. a) RAMPAGE reads are aligned to the genome. The 5'-most genomic coordinate from each properly-paired R1 read is estimated as a TSS. The abundance of mapped 5'-ends at a given TSS is a measure of its abundance. TSSs above a minimum threshold will be clustered into TSRs. b) RAMPAGE-derived Paired-end sequence information provides a connection between a 5'-mRNA end and a gene coding region. Only properly-paired R1 reads (*i.e.* with an aligned R2 read) are identified as TSSs and then included in the downstream clustering procedure described in part a).

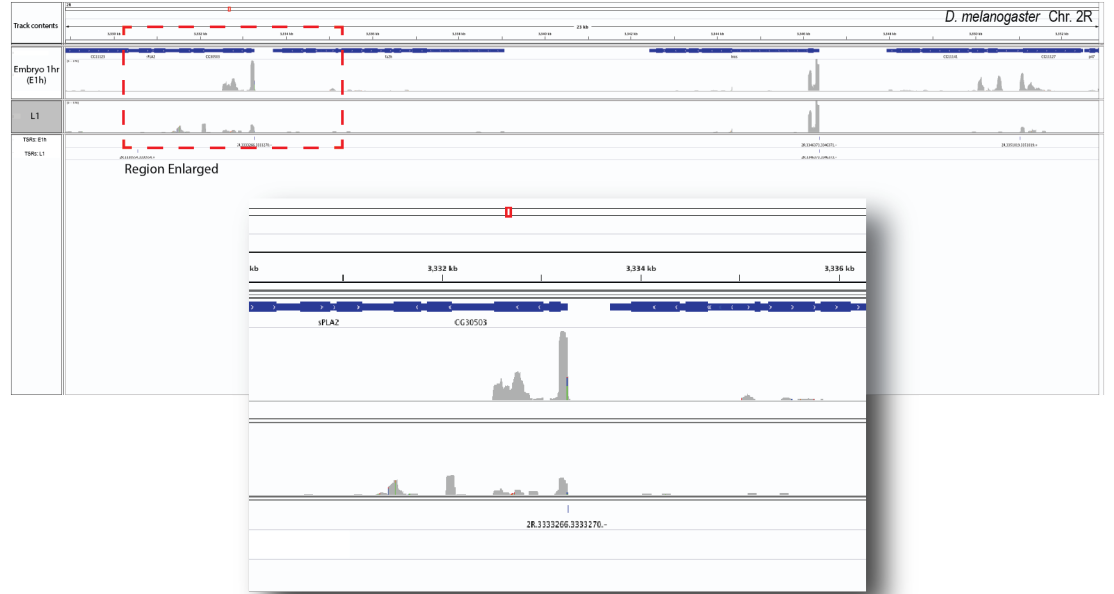


Fig. 3. An overview of the TSS profiling information provided by RAMPAGE. A representative visualization of RAMPAGE peaks (*i.e.* clusters of properly-aligned RAMPAGE reads) within an arbitrarily-selected genomic region of *D. melanogaster* chromosome 2R is shown, along with the corresponding gene annotation within this region. RAMPAGE data from two RAMPAGE libraries from Batut *et al* [2] are shown, which were generated from RNA isolated from developmental stages E1h and L1 *see Methods*. For each library, the abundance of RAMPAGE reads that align to a given site within the genome is represented by density plots (shown in gray). Gene models are shown in blue, where the thickened line represents exons and thin lines represent introns. The locations of TSRs identified by *TSRchitect* are shown in the two tracks from the bottom of the image. A single region, highlighted with the red dashed line is enlarged (the *Inset*) to show further detail of a selected gene and RAMPAGE signals. In some cases, the expression of 5'-ends between the two samples is roughly equivalent, whereas in others the observed signal is substantially higher (*see Inset*). The original images are screenshots generated in the Integrated Genomic Viewer (IGV; <http://software.broadinstitute.org/software/igv/>) [32]. Where necessary, additional annotation was added using Adobe Illustrator.

449 4 Figures

440 5 Notes

- 441 1. Please consult the GoRAMPAGE documentation found here:
 442 <https://github.com/BrendelGroup/GoRAMPAGE>.
 443 Installation instructions for the prerequisites of GoRAMPAGE (which in-
 444 cludes some of the items listed) are found at the following link:
 445 <https://github.com/BrendelGroup/GoRAMPAGE/tree/master/src>.
 446 2. On Linux, the installation of a few packages are necessary in order to install
 447 Bioconductor packages using *biocLite()*.
 448 To install them using Ubuntu:

```
449 apt-get install libssl-dev
450 apt-get install libcurl4-openssl-dev
451 apt-get install libxml2-dev
```

452 If you do not Ubuntu, use the commands necessary to install the above
 453 packages on your Linux distribution.

- 454 3. You can clone the entire GoRAMPAGE repository (which includes the con-
 455 tents of the demo) to your workspace on the command line using git, as
 456 follows:

```
457 git clone https://github.com/brendelgroup/GoRAMPAGE/
458 cd demo/MMB
```

459 The "scripts/" folder in the demo contains code for you to run the two major
 460 workflows described in this chapter. The "additional_files/" folder con-
 461 tains the following files which are necessary for the analysis: i) a fasta file con-
 462 taining ribosomal RNA sequences for *D. melanogaster* (*Dmel_rRNA.fasta*)
 463 and ii) a gene annotation for *D. melanogaster*
 464 (*Drosophila_melanogaster.BDGP5.78.gff*).

- 465 4. Since these fastq files are paired-end, we use the argument *-split-files* to
 466 generate separate files for each read pair.
- 467 5. If you are running this on a cluster with a job scheduler you'll need to add
 468 the necessary headers to the top of the script and submit the job in the
 469 appropriate manner.
- 470 6. The rRNA sequences were retrieved separately from Genbank at NCBI [33].
- 471 7. For parallel execution, GoRAMPAGE uses the Linux package *GNU parallel*
 472 [34]. Please see the GoRAMPAGE documentation for more information.
- 473 8. To do this, please edit the batch script *TSRchitect_serial_MMB.R* with a
 474 text editor of your choice.
- 475 9. Because the samples provided derive from related developmental stages, we
 476 will merge them for annotation purposes using the argument *replicateIDs*,
 477 (though it must be emphasized that they are not replicates).

10. All of *TSRchitect*'s output files are labeled according to the order that they are loaded onto the *tssObject*. For example, *TSSset-1.txt* corresponds to the first RAMPAGE dataset (in our case E1h), and *TSSset-2.txt* corresponds to the second RAMPAGE dataset (for this example E2h), and so on. You can check which datasets are loaded on the *tssObject* by simply entering it on an R console. Please see the *TSRchitect* documentation for more information.

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Disclosure Declaration

The authors declare that they have no competing interests.

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7 Checklist of Items to be Sent to Volume Editors

Here is a checklist of everything the volume editor requires from you:

☐ The final L^AT_EX source files

☐ A final PDF file

- 663 ☐ A copyright form, signed by one author on behalf of all of the authors of the
664 paper.
- 665 ☐ A readme giving the name and email address of the corresponding author.