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 of 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    "ENCODExplorer",  "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
```

3   Methods

3.1   Retrieving the RAMPAGE sequence data from NCBI

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

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

```
mkdir fastq_files
cd fastq_files

fastq-dump --split-files SRR424683
fastq-dump --split-files SRR424684
fastq-dump --split-files SRR424685
```

We continue by downloading the data from late larval tissues.

```
fastq-dump --split-files SRR424707
fastq-dump --split-files SRR424708
fastq-dump --split-files SRR424709
```

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

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

3.2   Creating symlinks to the files

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

```
cd ..
mkdir -p output/reads/clipped
cd output/reads/clipped

#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
```

3.3 Downloading genomic data from *D. melanogaster*

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

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

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

```
mkdir genome
cd genome
wget ftp://ftp.ensembl.org/pub/release-78/fasta/
drosophila_melanogaster/dna/Drosophila_melanogaster.BDGP5.dna.toplevel.fa.gz
#uncompressing the file
gzip -d Drosophila_melanogaster.BDGP5.dna.toplevel.fa.gz
cd ..
```

3.4 Filtering and alignment of RAMPAGE reads using GoRAMPAGE

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

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

Setting up the GoRAMPAGE job. Please refer to the script
248 "GoRAMPAGE_script_MMB.sh" and (using a text editor) provide the appropriate
249 paths to the genome assembly, output directory (see above) and rRNA sequences
250 (*see* **Note 6**). GoRAMPAGE jobs can optionally be run in parallel (*see* **Note**
251 **7**). The script can be executed as follows:

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

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

```
less -S errScript
```

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

Inspecting the rRNA filtering results. To evaluate the results from Step
262 3 (rRNA filtering), please navigate to the top level of the "output" directory
263 and open the file "LOGFILES". You'll see the recorded progress of the program
264 Tagdust and a record of the results. We notice that (for the L3h library) 1046448
265 of reads (78.1%) were "extracted", meaning that slightly more than 20% of
266 reads were removed because of matches with ribosomal sequences. The removed
267 reads from all libraries are found in the "dusted_discard" directory, and the
268 extracted reads are found in the current directory. Due to their sheer abundance
269 within cells, ribosomal RNA sequences are an inevitable contaminant within TSS
270 profiling libraries. For analysis purposes, it is important that these sequences be
271 removed, which is what has been completed here.
272 Since this step was conducted appropriately, we can proceed to the next step.

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

²⁸³ the alignments have similar mapping rates (70-80%), a reasonable outcome for
²⁸⁴ our purposes.

²⁸⁶ Now that our RAMPAGE libraries are filtered and aligned, we can commence
²⁸⁷ with the second half of our analysis.

²⁸⁸ **3.5 Promoter identification from aligned RAMPAGE libraries**

²⁸⁹ We can now use the prepared alignment files to identify TSSs and promoters
²⁹⁰ from the selected RAMPAGE libraries. There are currently several tools avail-
²⁹¹ able for this purpose. *CAGEr*, developed by Haberle [30], was utilized to perform
²⁹² TSS identification as part of the FANTOM5 efforts. We will use *TSRchitect* in
²⁹³ this demonstration, since it was specifically designed to analyze paired-end TSS
²⁹⁴ profiling datasets, and also because it is more flexible with respect to model sys-
²⁹⁵ tem (*i.e.* it does not require a corresponding *BSGenome* [31] package). The latter
²⁹⁶ feature will be helpful when analyzing the non-*D. melanagaster* TSS profiling
²⁹⁷ datasets that we expect to be generated in the near future.

²⁹⁸ **Setting up the Analysis.** *TSRchitect*, the package we'll use for this analy-
²⁹⁹ sis, is an R package available in the Bioconductor suite of genomics tools [28].
³⁰⁰ It makes use of existing packages and data structures within this environment,
³⁰¹ where available, to identify promoters from sequence alignments. Since you have
³⁰² already installed *TSRchitect* and its dependencies (see section 2.3), we are set
³⁰³ to proceed.

³⁰⁵ There are two general ways one can choose to run *TSRchitect*. The first is in-
³⁰⁶ teractively *i.e.* typing the instructions directly into an R console. While this
³⁰⁷ is a perfectly acceptable way to run analyses using package, for larger jobs
³⁰⁸ it will likely be more efficient (and likely more reproducible) to run a ded-
³⁰⁹ icated R script. We have provided sample scripts to make it easier for you
³¹⁰ to set up an R script. The two scripts are identical with a single exception:
³¹¹ one is set up to run in parallel (`"TSRchitect_parallel_MMB.R"`), while the
³¹² other is written to run in serial (`"TSRchitect_serial_MMB.R"`). Please select
³¹³ the script that best suits your computing resources. In the section to follow, we
³¹⁴ will go through the output of the analysis. For further details on how to use
³¹⁵ *TSRchitect*, please see its documentation at its Bioconductor page found here:
³¹⁶ https://www.bioconductor.org/packages/release/bioc/html/TSRchitect.html.

³¹⁷ **Running the Analysis.** To run TSRchitect using the batch script, provide
³¹⁸ full paths for the variables "BAMDIR" and "DmAnnot" in the script provided
³¹⁹ (*see* **Note 8**). *BAMDIR* should be a path to the subdirectory "alignments/" in
³²⁰ RAMPAGE output directory you specified earlier, and *DmAnnot* should be a
³²¹ 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:

```
R CMD BATCH TSRchitect_parallel_MMB.R #or use 'serial script
#assumes variables BAMDIR and DmAnnot have already been set
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.

```
DmRAMPAGE <- loadTSSobj(experimentTitle = "RAMPAGE Tutorial", \
 inputDir=BAMDIR, inputType="bam", isPairedEnd=TRUE, \
 sampleNames=c("E1h","E2h", "E3h", "L1", "L2", "L3"), \
 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.

```
DmRAMPAGE <- determineTSR(experimentName=DmRAMPAGE, n.cores=4, \
 tsrSetType="replicates", tssSet="all", tagCountThreshold=25, \
 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.

```
DmRAMPAGE <- addTagCountsToTSR(experimentName=DmRAMPAGE, \
tsrSetType="replicates",  tsrSet=1, tagCountThreshold=10, \
 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
```
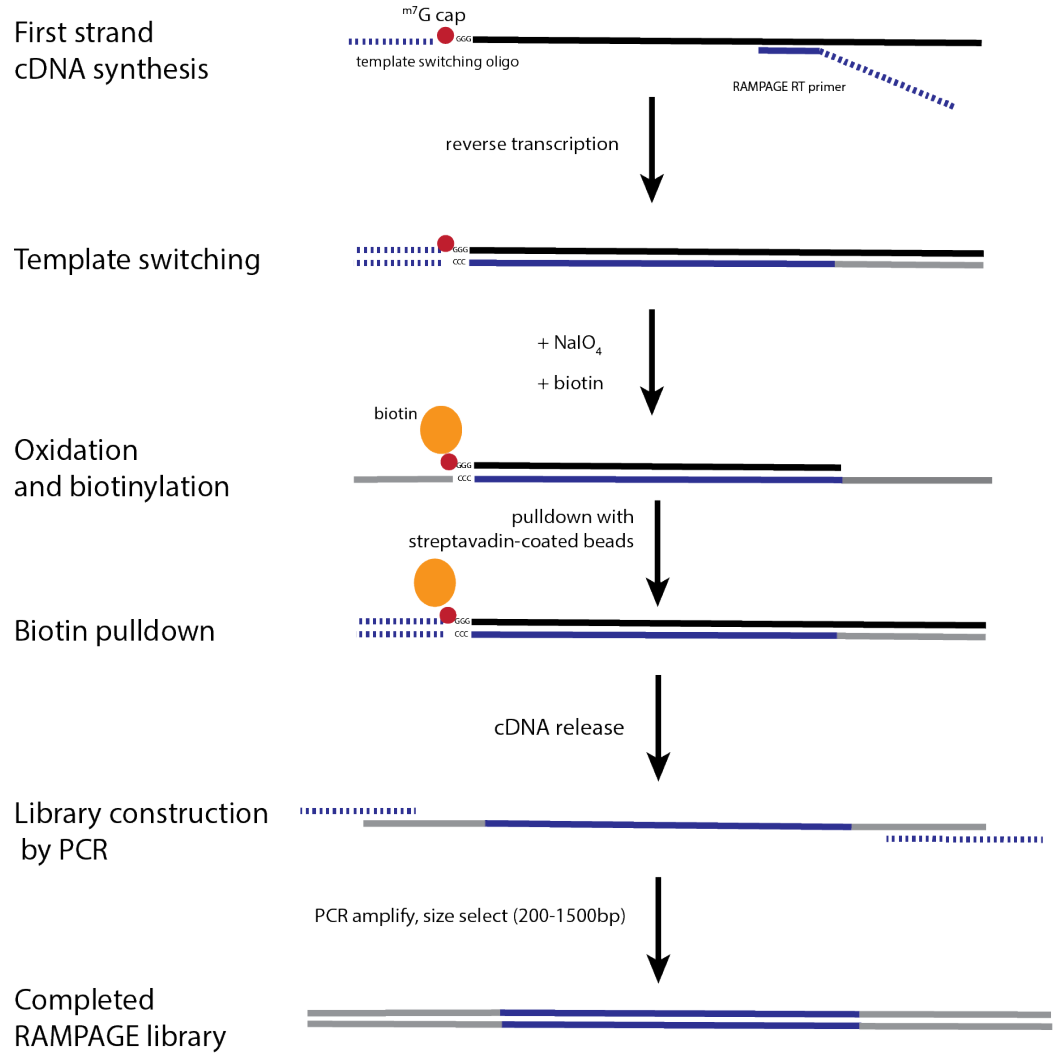
We will see that we have identified between roughly 3,200 and 18,000 TSRs within the individual RAMPAGE samples, which is attributable to the differences in library sizes. We detect 7,344 TSRs within the early embryonic samples ("TSRsetMerged-1.tab") and 12,126 TSRs in the late larval samples ("TSRsetMerged-2.tab"). Within the combined samples ("TSRsetCombined.tab") we find 13,986 TSRs, which is similar to the number reported by Hoskins *et. al.* [1].

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

3.6 Summary

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

First strand cDNA synthesis

^{m7}G cap

template switching oligo

RAMPAGE RT primer

reverse transcription

Template switching

GGG
CCC

+ NaIO$_4$

+ biotin

Oxidation and biotinylation

biotin

GGG
CCC

pulldown with streptavadin-coated beads

Biotin pulldown

GGG
CCC

cDNA release

Library construction by PCR

PCR amplify, size select (200-1500bp)

Completed RAMPAGE library

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 streptavadin-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].
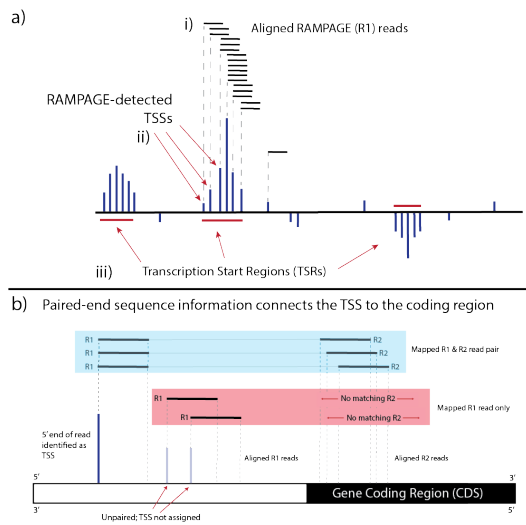
Fig. 2. An overview of promoter identification using RAMPAGE. a) RAMPAGE reads are aligned to the genome. The $5'$-most genomic coordinate from each properly-paired R1 read is estimated as a TSS. The abundance of mapped $5'$-ends at a given TSS is a measure of its abundance. TSSs above a minimum threshold 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*.
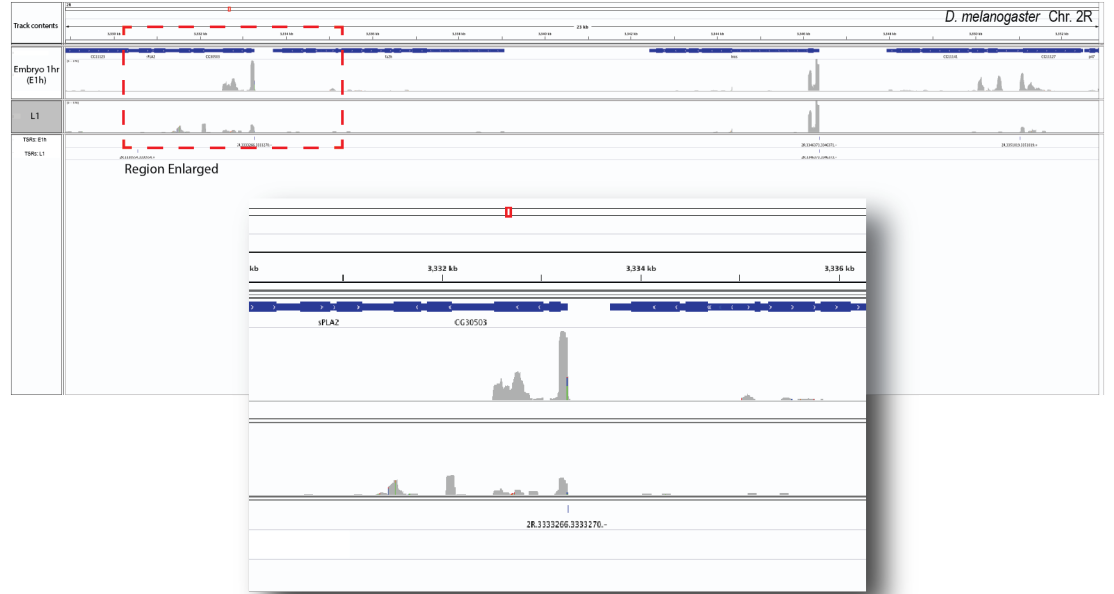
Fig. 3. An overview of the TSS profiling information provided by RAMPAGE. A representative visualization of RAMPAGE peaks (*i.e.* clusters of properly-aligned RAMPAGE reads) within an arbitrarily-selected genomic region of *D. melanogaster* chromosome 2R is shown, along with the corresponding gene annotation 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 RAMAPGE 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.

3.7   Figures

4   Notes

1. Please consult the GoRAMPAGE documentation found here:
   https://github.com/BrendelGroup/GoRAMPAGE.
   Installation instructions for the prerequisites of GoRAMPAGE (which includes some of the items listed) are found at the following link:
   https://github.com/BrendelGroup/GoRAMPAGE/tree/master/src.

2. On Linux, the installation of a few packages are necessary in order to install Bioconductor packages using *biocLite()*.
   To install them using Ubuntu:

```
apt-get install libssl-dev
apt-get install libcurl4-openssl-dev
apt-get install libxml2-dev
```

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

3. You can clone the entire GoRAMPAGE repository (which includes the contents of the demo) to your workspace on the command line using git, as follows:

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

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

4. Since these fastq files are paired-end, we use the argument *–split-files* to generate separate files for each read pair.

5. If you are running this on a cluster with a job scheduler you'll need to add the necessary headers to the top of the script and submit the job in the appropriate manner.

6. The rRNA sequences were retrieved separately from Genbank at NCBI [33].

7. For parallel execution, GoRAMPAGE uses the Linux package *GNU parallel* [34]. Please see the GoRAMPAGE documentation for more information.

8. To do this, please edit the batch script TSRchitect_serial_MMB.R with a text editor of your choice.

9. Because the samples provided derive from related developmental stages, we will merge them for annotation purposes using the argument *replicateIDs*, (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.

Acknowledgments

Disclosure Declaration

The authors declare that they have no competing interests.

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6   Checklist of Items to be Sent to Volume Editors

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

☐ The final LaTeX 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.