# Expression Divergence of Chemosensory Genes between Drosophila sechellia and Its Sibling Species and Its Implications for Host Shift

報告人：

108753102 資科碩一 吳映函

108753109 資科碩一 陳庭軒

Meng-Shin Shiao, Jia-Ming Chang, Wen-Lang Fan, Mei-Yeh Jade Lu, Cedric Notredame, Shu Fang, Rumi Kondo, and Wen-Hsiung Li

# Abstract

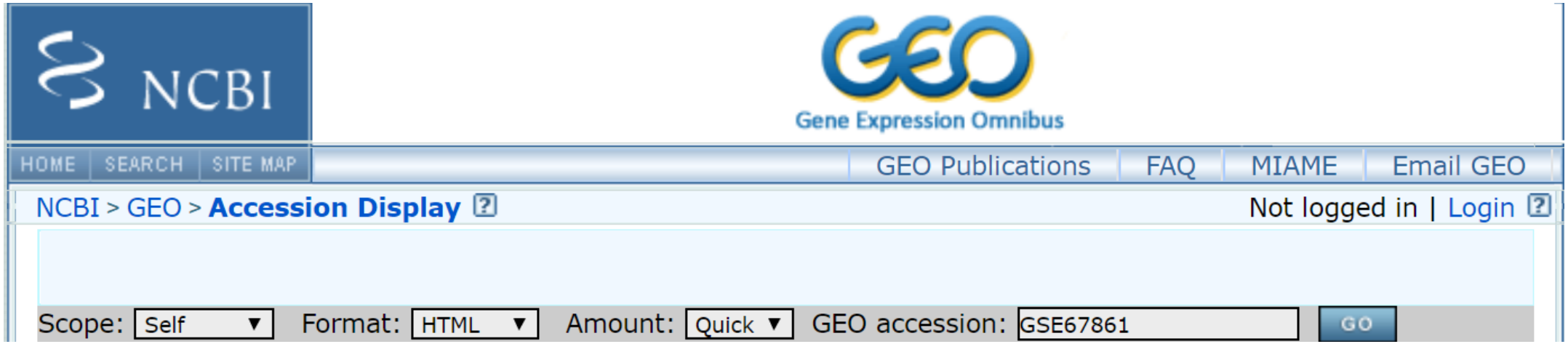

- We wanted to know whether gene expression, particularly chemosensory genes, has diverged between D. sechellia and its two sibling species.
- we found a higher percentage of chemosensory genes differentially expressed in the D. sechellia lineage(7.8%) than in the D. simulans lineage (5.4%)
- Our observations suggest that the host shift of D. sechellia was associated with the enrichment of differentially expressed, particularly upregulated, chemosensory genes.

# Materials and Methods

- We chose the most closely related generalist species, **D. simulans**, as a comparison and D. melanogaster as the outgroup generalist species.
- From D. melanogaster 3 to **D. sechellia** and D. mauritiana.
- The orthologous gene set (OGS) was manually curated by excluding genes duplicated in any of the species and only single copy genes in all three species were selected.
- Or22a has two distinct gene IDs in D. simulans (FBgn0068650 and FBgn0194492) and in D. sechellia (FBgn0171736 and FBgn0259897), whereas Or22b has two FlyBase IDs in D. simulans (FBgn0068649 and FBgn0194493).

# Dataset

- NCBI GEO
  - GSE67587
  - GSE67861
  - GSE67862



# Data Accessibility

- GSE67587 for D. sechellia (Taiwan)
- GSE67861 for D. sechellia (Japan)
- GSE67862 for D. simulans (Japan)

# Dataset

Samples (6)
Less...

GSM1650068 Dsec male TW rep1
GSM1650069 Dsec male TW rep2
GSM1650070 Dsec male TW rep3
GSM1650071 Dsec female TW rep1
GSM1650072 Dsec female TW rep2
GSM1650073 Dsec female TW rep3

Samples (6)
Less...

GSM1657327 Dsec male JP rep1
GSM1657328 Dsec male JP rep2
GSM1657329 Dsec male JP rep3
GSM1657330 Dsec female JP rep1
GSM1657331 Dsec female JP rep2
GSM1657332 Dsec female JP rep3

Samples (6)
Less...

GSM1657333 Dsim male JP rep1
GSM1657334 Dsim male JP rep2
GSM1657335 Dsim male JP rep3
GSM1657336 Dsim female JP rep1
GSM1657337 Dsim female JP rep2
GSM1657338 Dsim female JP rep3

# GSE67587 for D. sechellia (Taiwan)

| Samples | Run | # of Bases(G) | Size(Gb) |
|---|---|---|---|
| GSM1650068 Dsec male TW rep1 | SRR1952772 | 6.4G | 4.1Gb |
| GSM1650069 Dsec male TW rep2 | SRR1952773 | 5.9G | 3.7Gb |
| GSM1650070 Dsec male TW rep3 | SRR1952774 | 6.2G | 3.9Gb |
| GSM1650071 Dsec female TW rep1 | SRR1952775 | 7.3G | 4.6Gb |
| GSM1650072 Dsec female TW rep2 | SRR1952776 | 6.7G | 4.2Gb |
| GSM1650073 Dsec female TW rep3 | SRR1952777 | 7.0G | 4.4Gb |

# GSE67861 for D. sechellia (Japan)

| Samples | Run | # of Bases(G) | Size(Gb) |
|---|---|---|---|
| GSM1657327 Dsec male JP rep1 | SRR1973486 | 8.1G | 5.2Gb |
| GSM1657328 Dsec male JP rep2 | SRR1973487 | 7.5G | 4.7Gb |
| GSM1657329 Dsec male JP rep3 | SRR1973488 | 7.8G | 4.9Gb |
| GSM1657330 Dsec female JP rep1 | SRR1973489 | 6.1G | 3.9Gb |
| GSM1657331 Dsec female JP rep2 | SRR1973490 | 5.8G | 3.6Gb |
| GSM1657332 Dsec female JP rep3 | SRR1973491 | 6.0G | 3.8Gb |

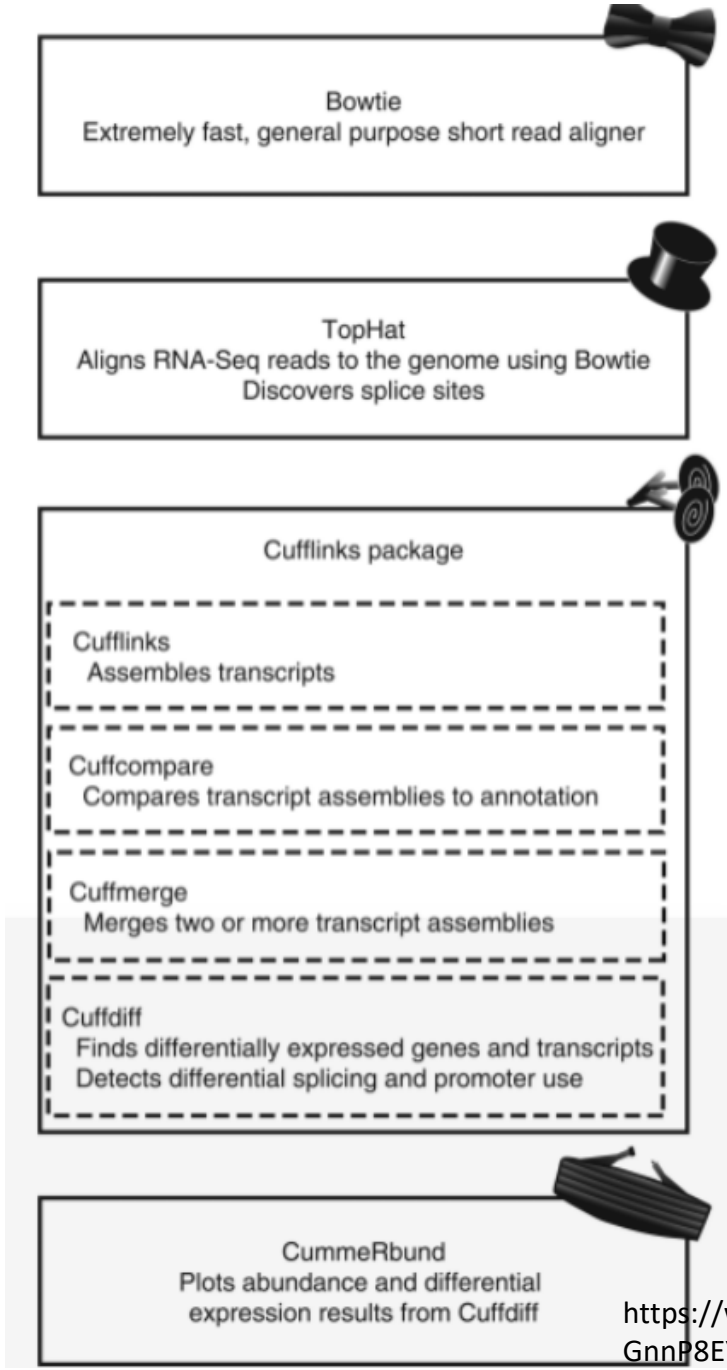
# GSE67862 for D. simulans (Japan)

| Samples | Run | # of Bases(G) | Size(Gb) |
|---|---|---|---|
| GSM1657333 Dsim male JP rep1 | SRR1973492 | 5.7G | 3.6Gb |
| GSM1657334 Dsim male JP rep2 | SRR1973493 | 5.3G | 3.3Gb |
| GSM1657335 Dsim male JP rep3 | SRR1973494 | 5.5G | 3.5Gb |
| GSM1657336 Dsim female JP rep1 | SRR1973495 | 7.7G | 5.0Gb |
| GSM1657337 Dsim female JP rep2 | SRR1973496 | 7.1G | 4.5Gb |
| GSM1657338 Dsim female JP rep3 | SRR1973497 | 7.4G | 4.7Gb |

# Table

| | A | B | C | D |
|---|---|---|---|---|
| 1 | #gene | Dmel | Dsec | Dsim |
| 2 | 128up | FBgn0010339 | FBgn0176208 | FBgn0182597 |
| 3 | 14-3-3epsilon | FBgn0020238 | FBgn0170212 | FBgn0186839 |
| 4 | 14-3-3zeta | FBgn0004907 | FBgn0176067 | FBgn0184006 |
| 5 | 140up | FBgn0010340 | FBgn0180739 | FBgn0191925 |
| 6 | 18w | FBgn0004364 | FBgn0176867 | FBgn0067532 |
| 7 | 26-29-p | FBgn0250848 | FBgn0180299 | FBgn0186151 |
| 8 | 312 | FBgn0029514 | FBgn0169330 | FBgn0185324 |
| 9 | 4EHP | FBgn0053100 | FBgn0178382 | FBgn0189856 |
| 10 | 5-HT7 | FBgn0004573 | FBgn0167057 | FBgn0188297 |
| 11 | 7B2 | FBgn0041707 | FBgn0165752 | FBgn0191274 |
| 12 | A16 | FBgn0028965 | FBgn0180777 | FBgn0193504 |
| 13 | ACC | FBgn0033246 | FBgn0175616 | FBgn0181977 |
| 14 | AGO1 | FBgn0262739 | FBgn0178121 | FBgn0084546 |
| 15 | AIF | FBgn0031392 | FBgn0178594 | FBgn0194524 |
| 16 | AP-1gamma | FBgn0030089 | FBgn0168650 | FBgn0188509 |
| 17 | AP-1sigma | FBgn0030132 | FBgn0181204 | FBgn0192503 |

# Analysis steps

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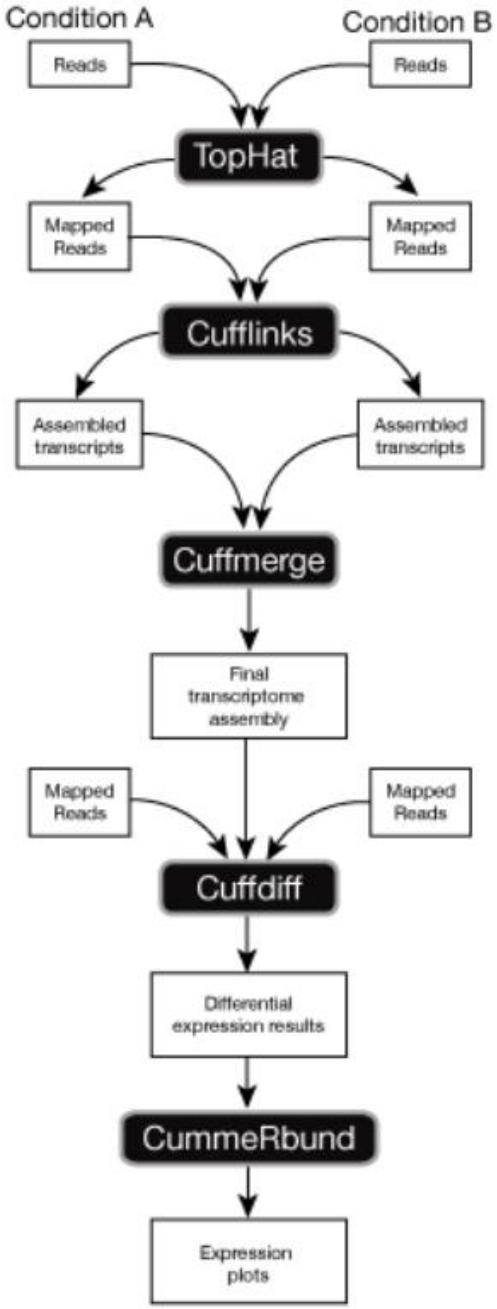
# Analysis steps

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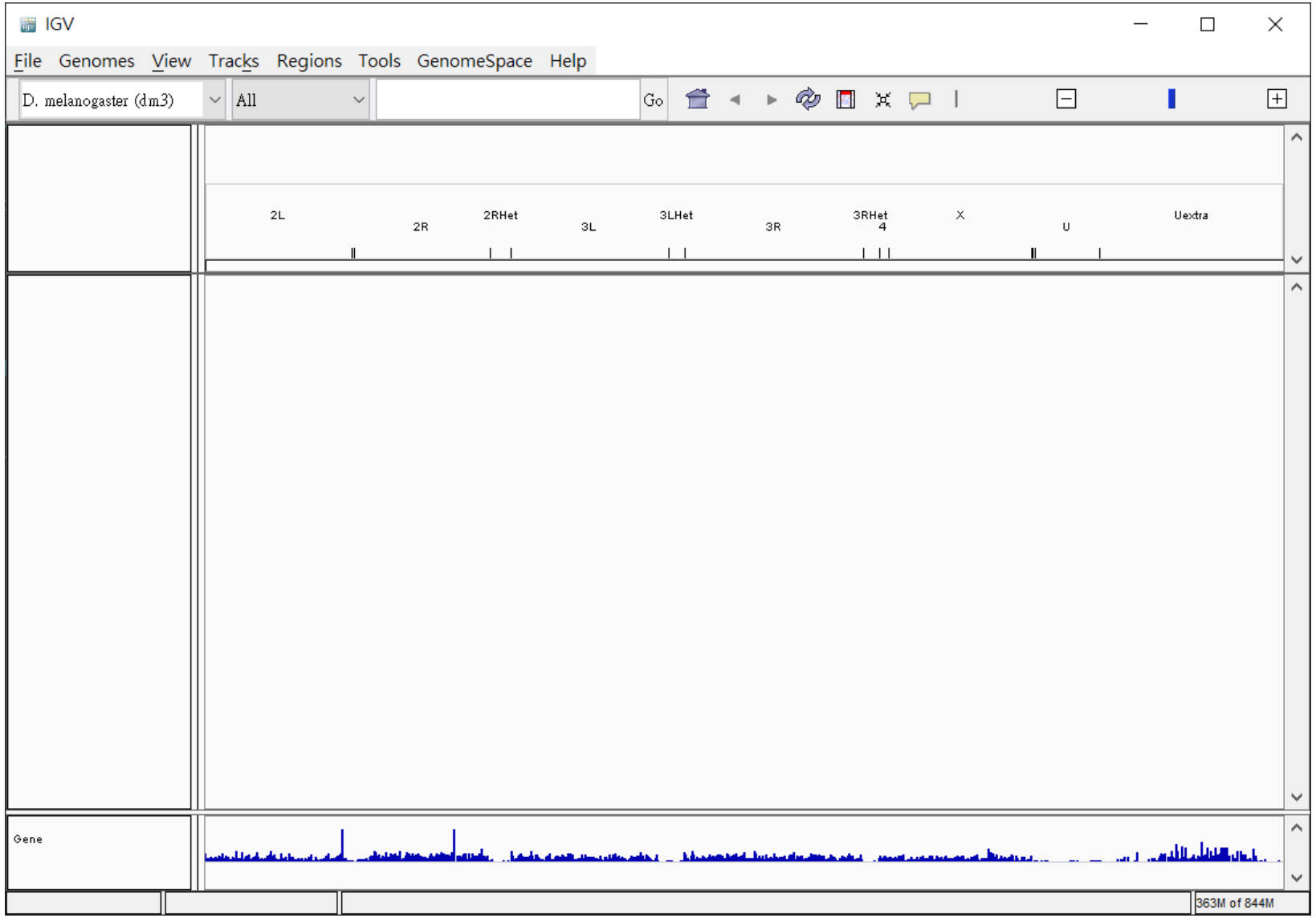
# IGV

- Tophat
- Samtools
- Cufflinks
- Cuffmerge
- Cuffdiff
- Use IGV
- CummeRbund

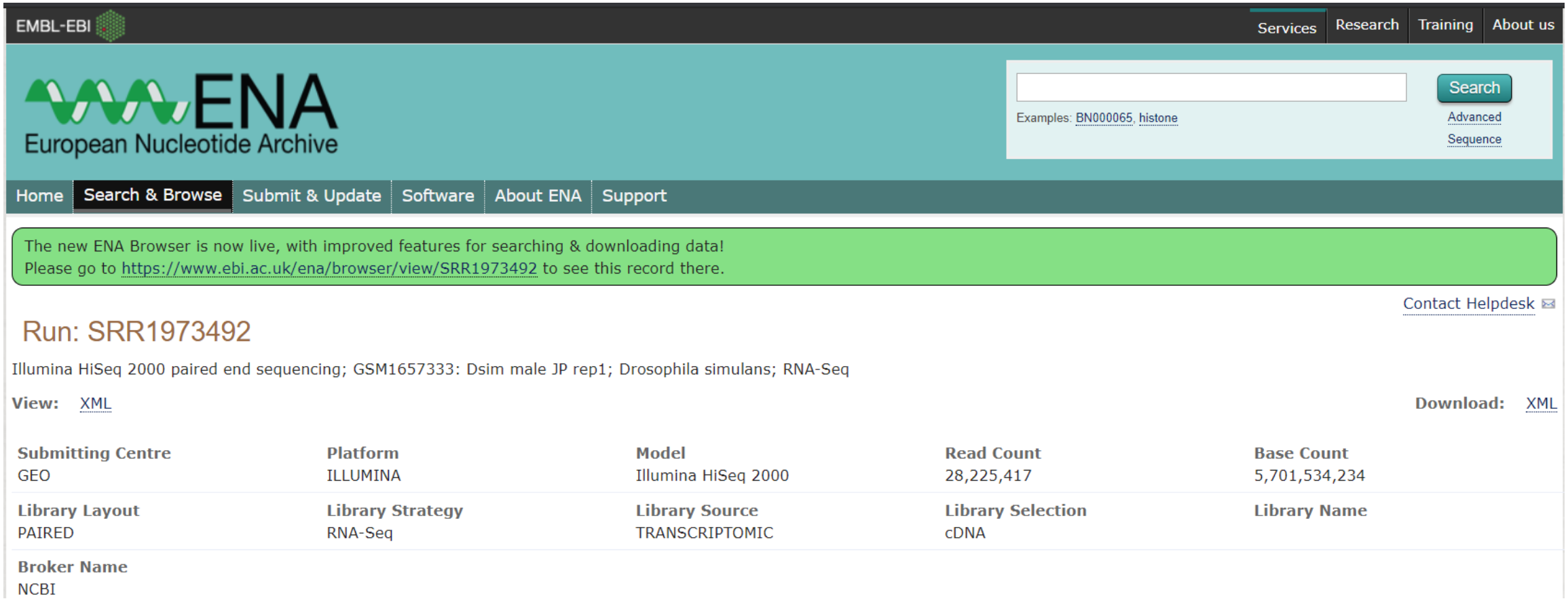


# Reference genomes

- Reference genomes version
  - r5.48 (D. melanogaster) (Dm3)
  - r1.3 (D. simulans) (droSim1)
  - r1.3(D. sechellia) (droSec1)

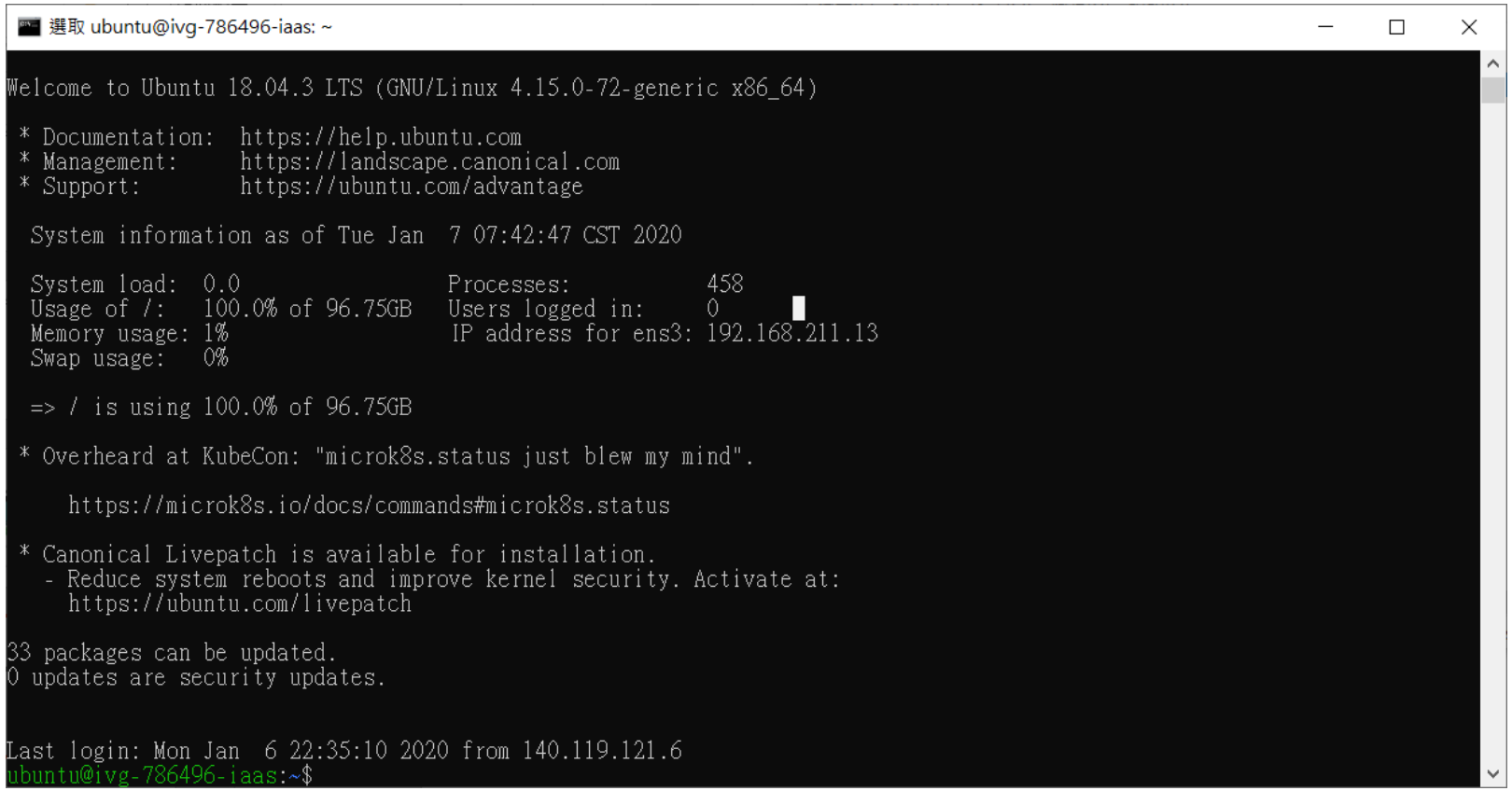
# Try

- Download data for many days



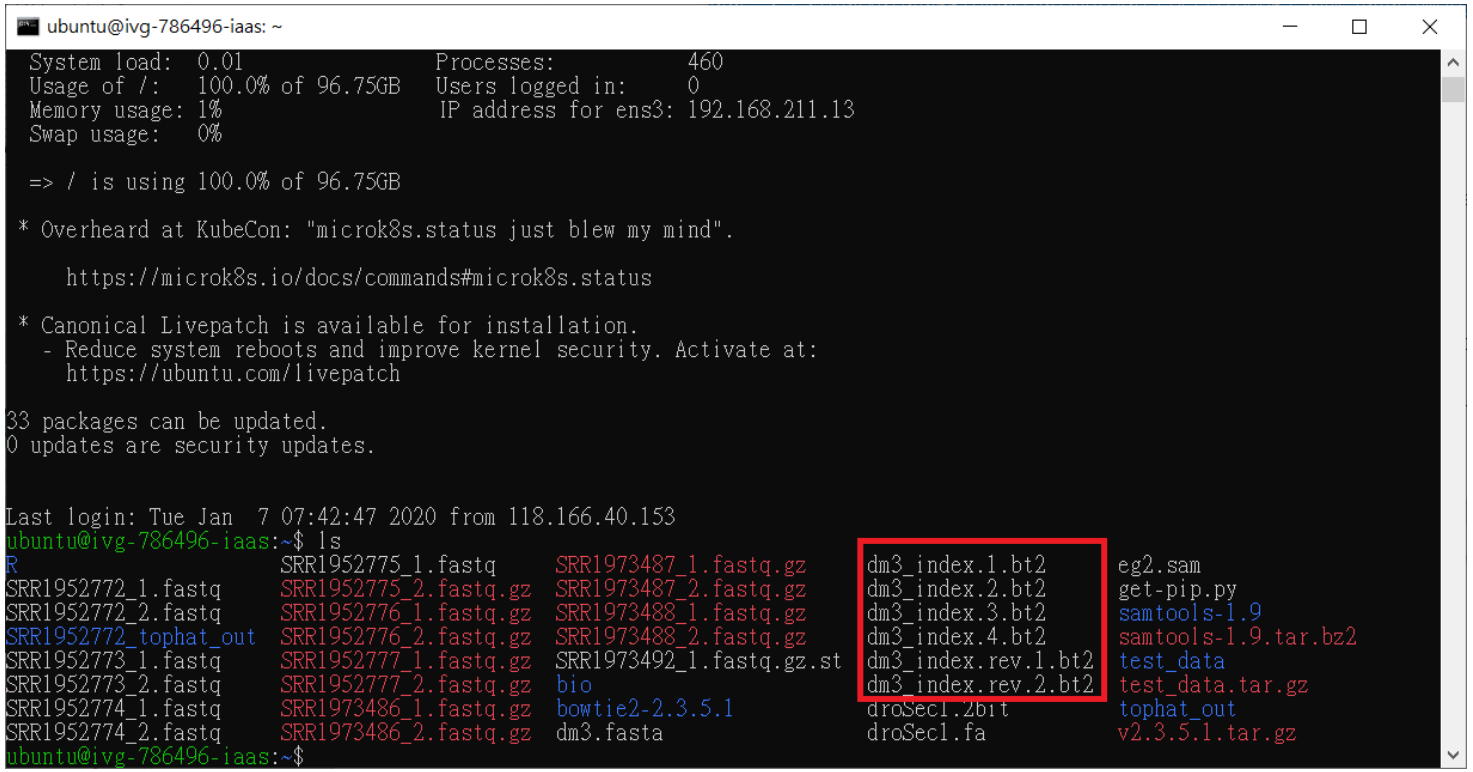
# Try

- **Ubuntu(R>3.6!!!!!!)**
- Oracle VM VirtualBox
- RMySQL
- Devtools
- Hmisc

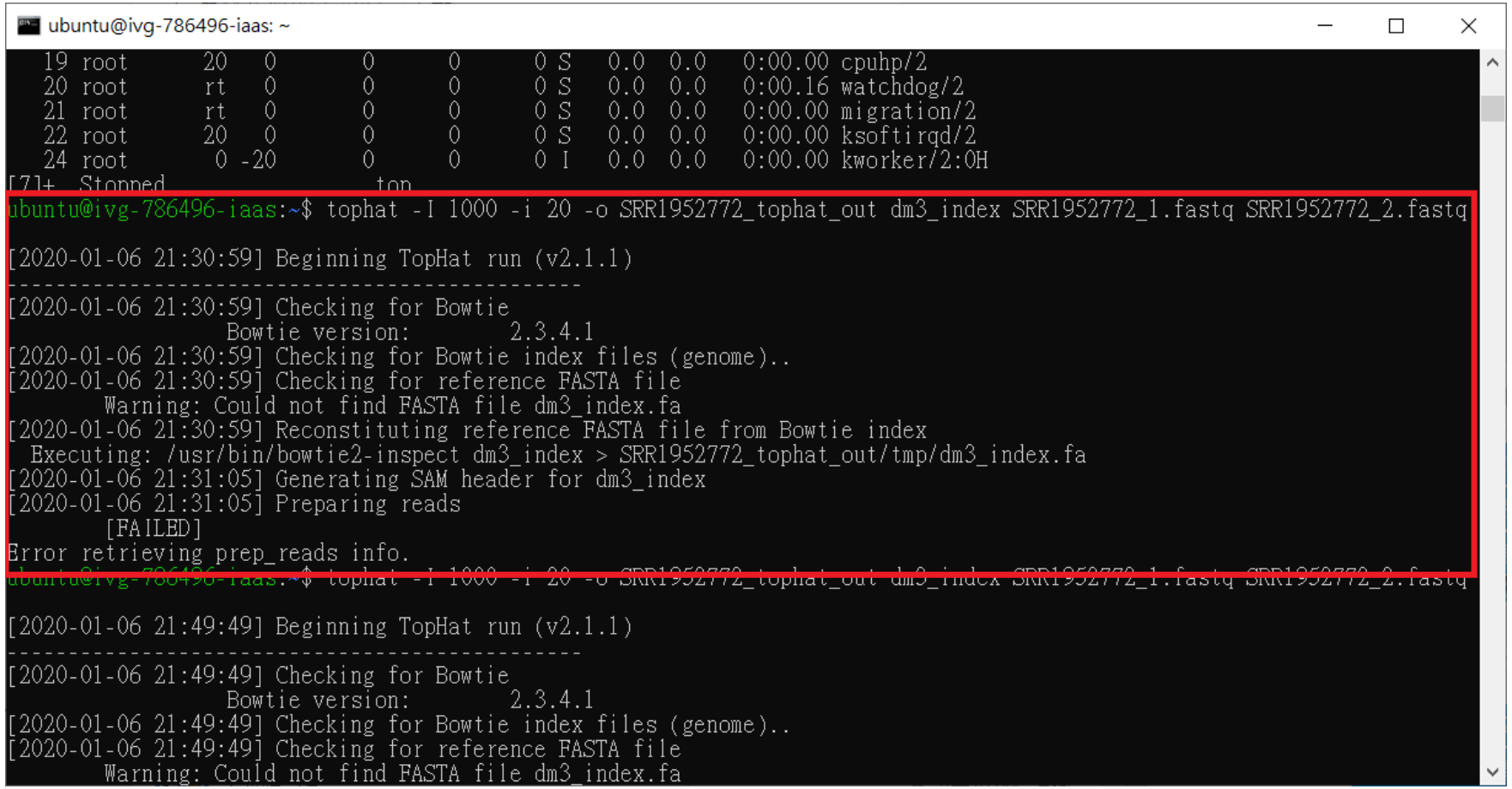


# packages

- Cufflinks
- Cuffmerge
- Cummerbund
- Tophat
- Bowtie2 (NEED Build Index)
- samtools



# Result


ubuntu@ivg-786496-iaas: ~
19 root 20 0 0 0 0 S 0.0 0.0 0:00.00 cpuhp/2
20 root rt 0 0 0 0 S 0.0 0.0 0:00.16 watchdog/2
21 root rt 0 0 0 0 S 0.0 0.0 0:00.00 migration/2
22 root 20 0 0 0 0 S 0.0 0.0 0:00.00 ksoftirqd/2
24 root 0 -20 0 0 0 I 0.0 0.0 0:00.00 kworker/2:0H
[7]+ Stopped top
ubuntu@ivg-786496-iaas:~$ tophat -I 1000 -i 20 -o SRR1952772_tophat_out dm3_index SRR1952772_1.fastq SRR1952772_2.fastq
[2020-01-06 21:30:59] Beginning TopHat run (v2.1.1)
[2020-01-06 21:30:59] Checking for Bowtie
Bowtie version: 2.3.4.1
[2020-01-06 21:30:59] Checking for Bowtie index files (genome)..
[2020-01-06 21:30:59] Checking for reference FASTA file
Warning: Could not find FASTA file dm3_index.fa
[2020-01-06 21:30:59] Reconstituting reference FASTA file from Bowtie index
Executing: /usr/bin/bowtie2-inspect dm3_index > SRR1952772_tophat_out/tmp/dm3_index.fa
[2020-01-06 21:31:05] Generating SAM header for dm3_index
[2020-01-06 21:31:05] Preparing reads
[FAILED]
Error retrieving prep_reads info.
[2020-01-06 21:49:49] Beginning TopHat run (v2.1.1)
[2020-01-06 21:49:49] Checking for Bowtie
Bowtie version: 2.3.4.1
[2020-01-06 21:49:49] Checking for Bowtie index files (genome)..
[2020-01-06 21:49:49] Checking for reference FASTA file
Warning: Could not find FASTA file dm3_index.fa

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