

Astalavista-3.1 run with some error warnings

Dear professor,

When trying to use the astalavista (version 3.1) on our linux server, I encounter a problem as follow. It seems that the software got some errors but it finally run and get the result. I want to know why the ERROR warnings happened, and how to fix them.

```
[ytshen@IGDBTIANLAB bin]$ ./astalavista -t asta -i ~/analysis_data/cufflinks/2013-4-9/coty_default/parameter_choose/coty_u/transcripts.gtf
Astalavista v3.1 (Flux Library: 1.21)

[ERROR] Error while creating tool instance for barna.astalavista.AStalavista
java.lang.InstantiationException
    at sun.reflect.InstantiationExceptionConstructorAccessorImpl.newInstance(InstantiationExceptionConstructorAccessorImpl.java:48)
    at java.lang.reflect.Constructor.newInstance(Constructor.java:532)
    at java.lang.Class.newInstance0(Class.java:372)
    at java.lang.Class.newInstance(Class.java:325)
    at java.lang.Class.newInstance(Class.java:410)
    at barna.commons.launcher.Flux.findTools(Flux.java:104)
    at barna.commons.launcher.Flux.main(Flux.java:104)
[ERROR] Make sure the class exists and has a default constructor.
# started Thu Apr 11 15:55:26 SARST 2013
# CHR_SEQ null
# EDGE_CONFIDENCE 127
# EVENTS [AS1]
# EVENTS_ATR []
# EVENTS_DIMENSION 2
# EVENTS_FILE null
# HELP false
# INTRON_CONFIDENCE 127
# IN_FILE /home/ytshen/analysis_data/cufflinks/2013-4-9/coty_default/parameter_choose/coty_u/transcripts.gtf
# PAR_FILE null
# TMP_DIR /tmp
Checking GTF *[WARN] Unsorted in line 9 - cannot perform gene clustering: Gm01 . CUFF.1.1 @ 57470 after CUFF.3.1 @ 70963
sorting GTF file OK (00:00:02)
[WARN] skipped line Gm01 Cufflinks transcript 116434 127971 1000.0 + . transcript_id "CUFF.10.1": conf_hi "120.439768": conf_lo "89.847476": cov "14.781766"
: gene_id "CUFF.10": FPKM "105.1436219887": frac "1.000000":
Iterating Annotation ***** done. (00:00:01)
[INFO] took 3 sec.
[INFO] found 187 events.
AStalavista.
```

Thank you very much!

Yours sincerely,

Yanting Shen