

# field missing, sequence preparation errors

I am a newbie here.

I am working on converting genome/gtf data to FASTA file format and using flux-simulator for that. The demo example from the flux-simulator works without any problem.

After that, I downloaded genome and gtf data from <http://hgdownload.soe.ucsc.edu/downloads.html>, <https://genome.ucsc.edu/cgi-bin/hgTables?command=start>.

But while running mouse(mm9) gtf, it does not work at all and shows the error:

```
[ERROR] Error while loading stats: Field 5 not found  
java.lang.IllegalArgumentException: Field 5 not found
```

I also tried to run flux simulator for "fly" genome.

I got this error:

```
[INFO] Loading default PCR distribution  
    preparing transcript sequences ** ERROR  
[ERROR] Error while preparing sequences:  
[ERROR] Error while fragmenting : Problems reading sequence chr2L: pos 22877860, len 82,  
check whether chromosomal sequence exists / has the correct size  
java.lang.RuntimeException: Problems reading sequence chr2L: pos 22877860, len 82,
```

Can you please tell how to solve these problems?