# MakeHub: Creating Individual Assembly Hubs for Display with the UCSC Genome Browser

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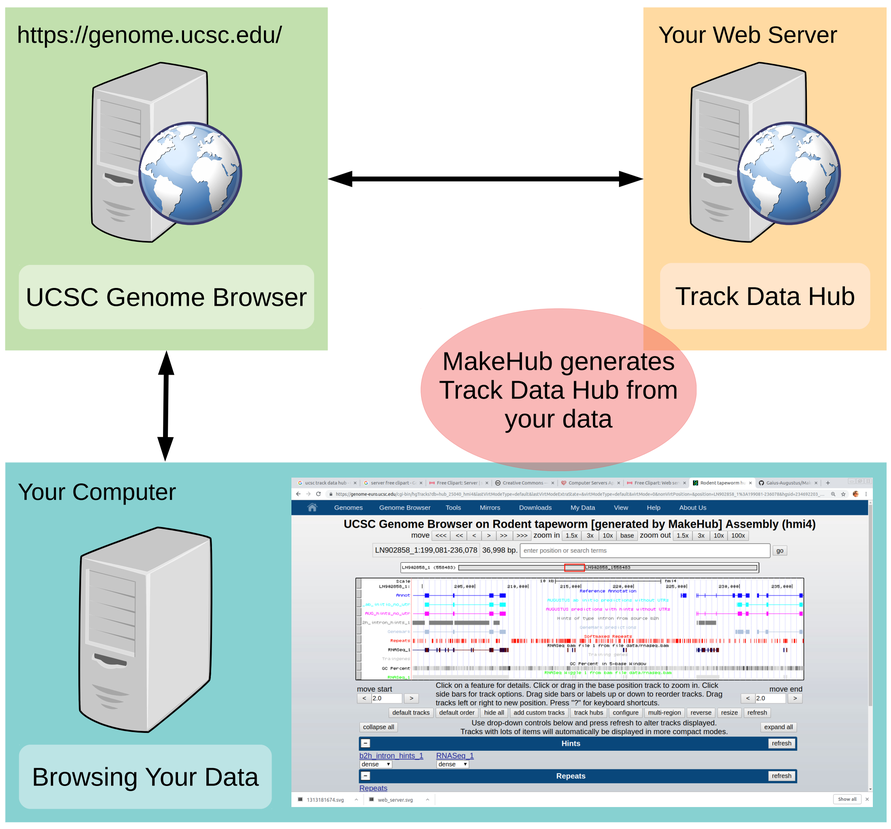
## Abstract

The UCSC Genome Browser [2] is one of the most powerful and most convenient tools for visualization of genomes with their annotation. Track data hubs [1] allow the display of externally hosted genomic data via publicly available UCSC Genome Browser instances. Creating your own assembly hub for a novel genome, however, is often a tedious task that involves many steps that are in part difficult for scientists without programming background.
MakeHub [3] has the goal to enable scientists to quickly and automatically generate assembly hubs of novel genomes, their annotation and informative RNA-Seq read alignments. Producing a complete assembly hub is a one-step process with MakeHub.
Implemented in Python, MakeHub utilizes tools provided by the UCSC Genome Browser group, SAMtools [4], and components of the gene Prediction tool AUGUSTUS [5]. MakeHub is integrated in the BRAKER [6,7] pipeline for fully automated and unsupervised RNA-Seq and/or protein based structural genome annotation. It is further compatible with the outputs of MAKER [8], GlimmerHMM[9], SNAP [10] and GeMoMa [11].

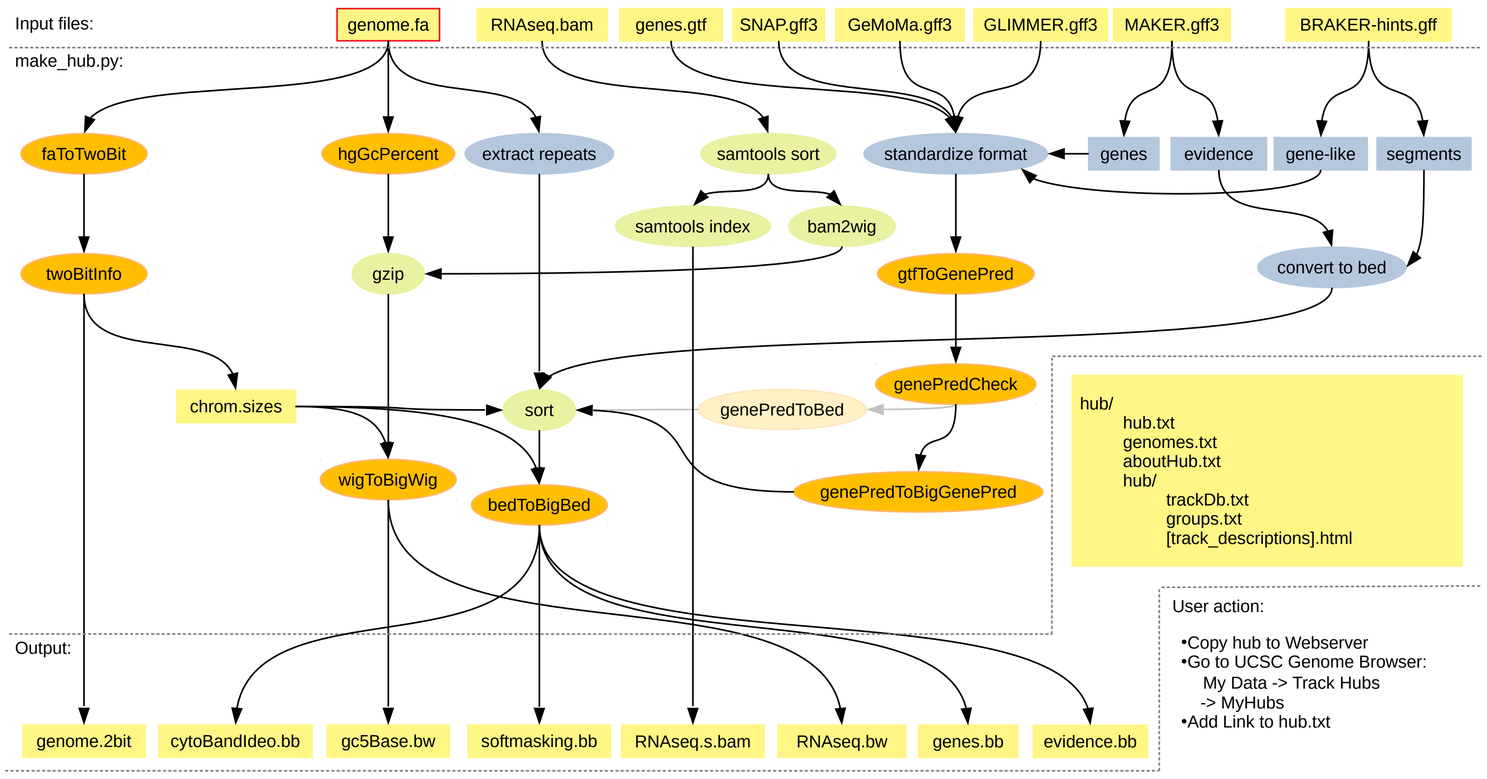
MakeHub is freely available at **https://github.com/Gaius-Augustus/MakeHub**.

## The Track Data Hub Principle




## MakeHub Creates Track Data Hubs

A single command invokes the MakeHub pipeline:




An example call that generates a hub with the following tracks:

- Repeats,
- Intron hints from RNA-Seq data,
- RNA-Seq coverage data,
- a gene model reference annotation,
- GeneMark-ET/EP [12, 13] predictions,
- training genes used to train AUGUSTUS,
- AUGUSTUS ab initio gene predictions,
- AUGUSTUS predictions with hints,
- base position,
- GC-content,
- restriction enzymes,
- perfect match to short sequence.

```
make_hub.py --short_label hmi4 --long_label "Rodent tapeworm" \
  --genome data/genome.fa --email katharina.hoff@uni-greifswald.de \
  --annot data/annot.gtf --bam data/rnaseq.bam \
  --braker_out_dir data --latin_name "Hymenolepsis microstoma" \
  --assembly_version GCA_000469805.2
```

## Software Dependencies

- Unix, e.g. Ubuntu Linux, including sort & gzip
- Python3
- Biopython
- UCSC Tools*:
  bedToBigBed, genePredCheck, faToTwoBit, gtfToGenePred, hgGcPercent, ixIxx, twoBitInfo, wigToBigWig, genePredToBed, genePredToBigGenePred
- SAMtools

*) will be downloaded automatically if missing

## Connecting Your Track Data Hub


## References

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## Acknowledgements

The international collaboration between the groups of Mark Borodovsky and Mario Stanke, supported by US National Institute of Health grant HG000783, gave rise to the development of MakeHub.