

Expression calls from RNA-Seq data using BgeeCall R package



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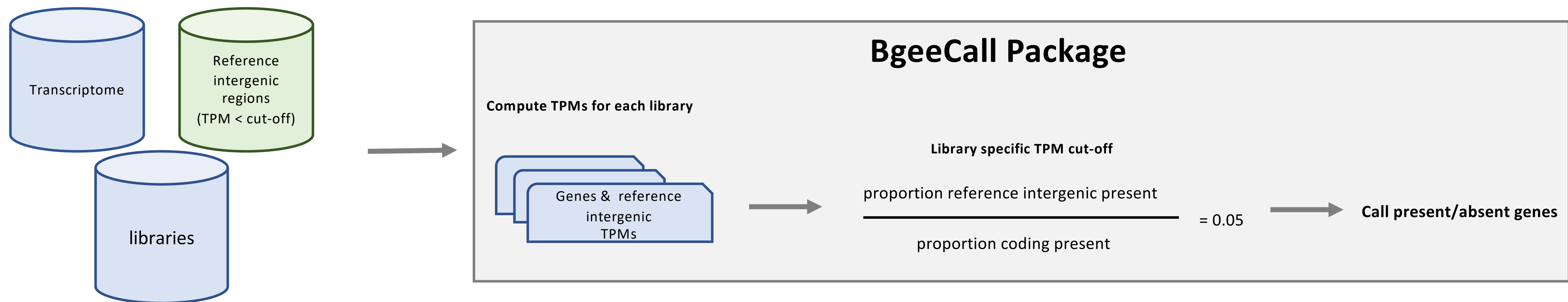
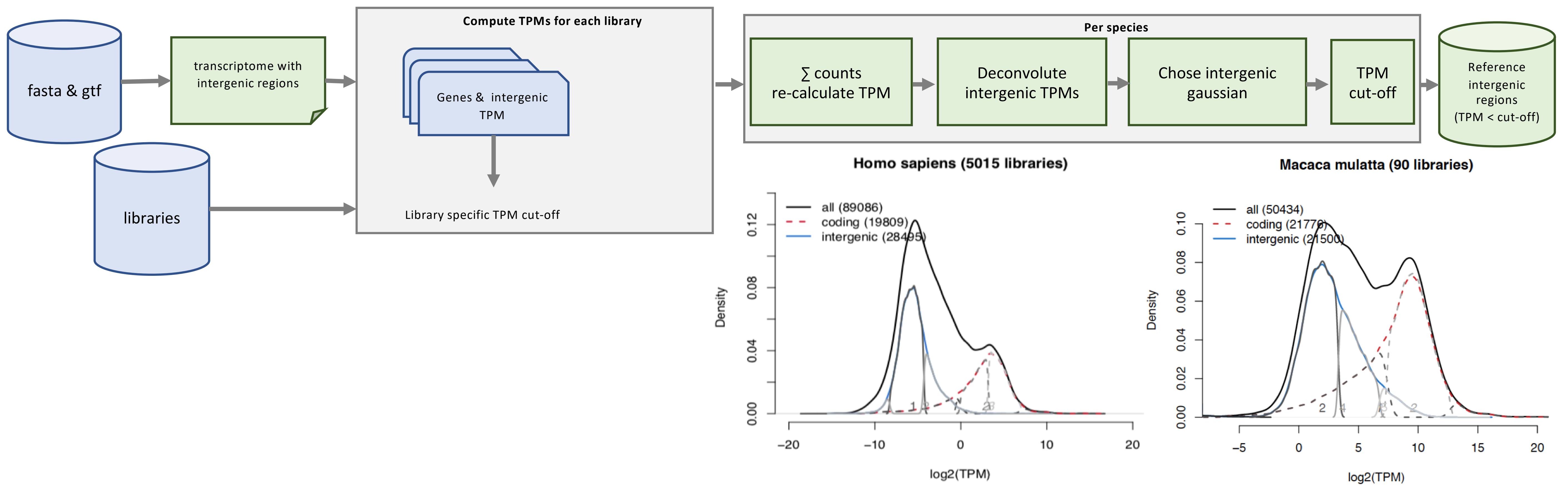
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BgeeCall allows researchers to classify in an accurate way the presence or absence of gene expression from their own RNA-Seq data. The approach integrated in the BgeeCall to make this classification is based on the set of reference intergenic regions.

Workflow

Use reference intergenic sequences to distinguish signal from noise in your RNA-Seq libraries



Summary

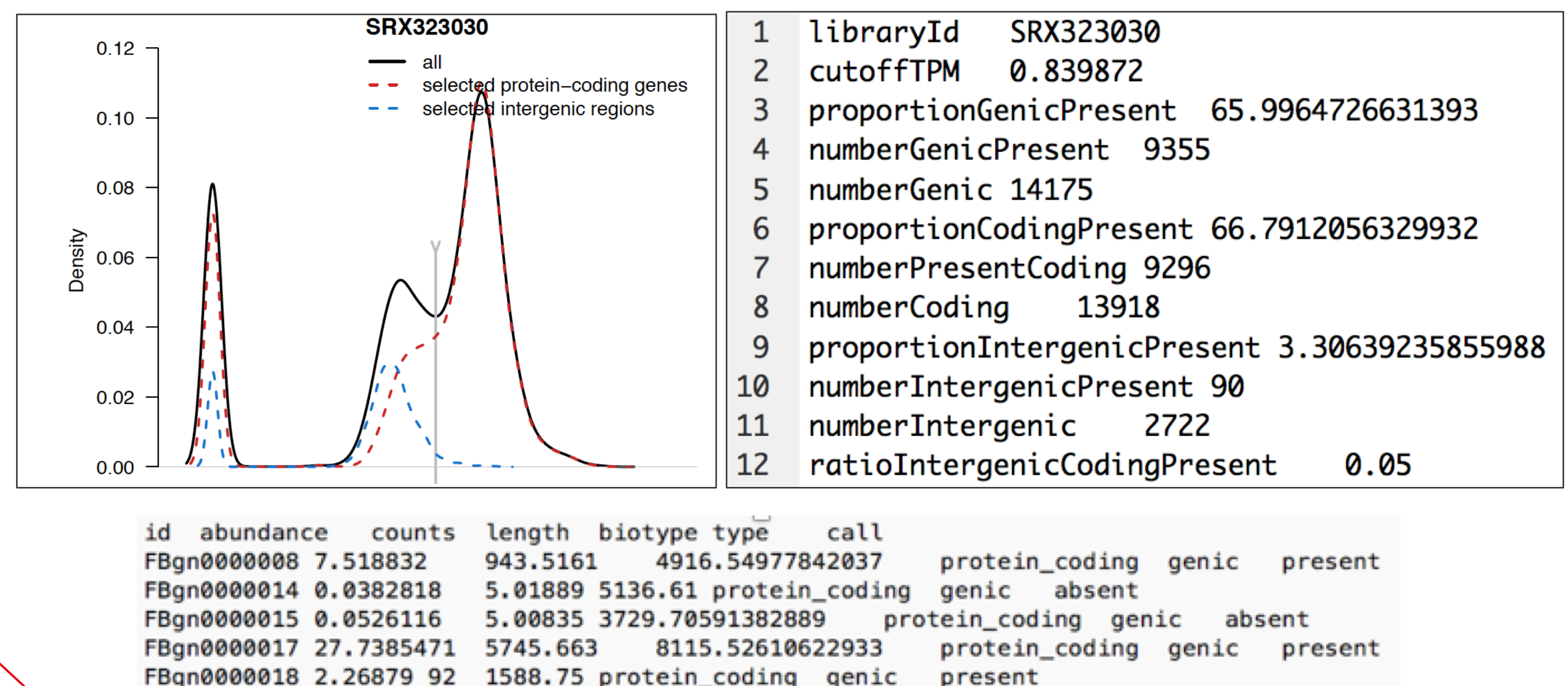
How to run BgeeCall

Use the reference intergenic regions from Bgee

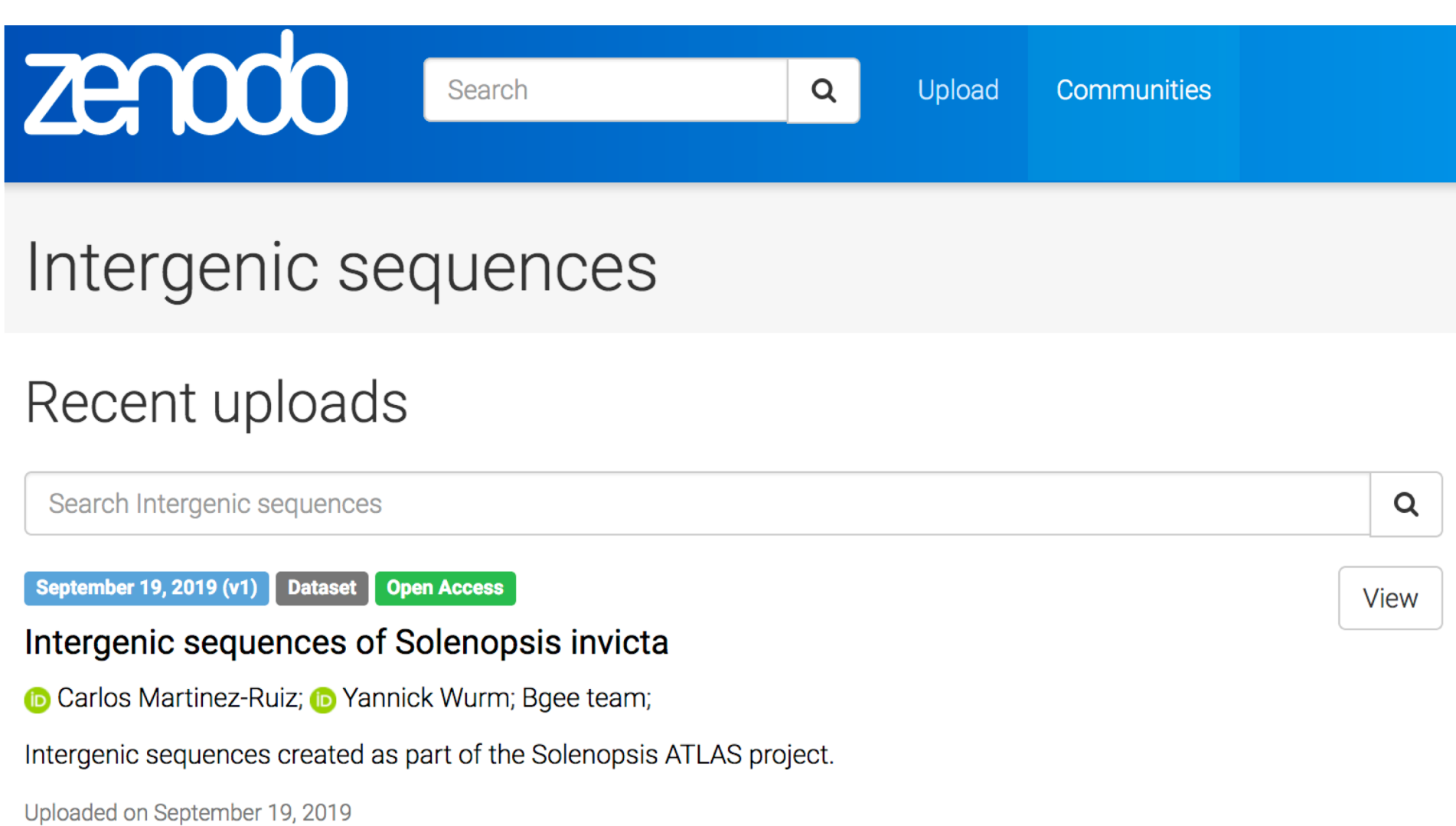
```
# init objects
user <- new("UserMetadata")

# edit attributes of the UserMetadata object
user@species_id <- "7227" # D. melanogaster
user <- setAnnotationFromFile(user, "path/to/annotation", "annot_name")
user <- setTranscriptomeFromFile(user, "path/to/transcriptome", "transcript_name")
user <- setRNASeqLibPath(user, "path/to/library/directory")

# generate present/absent calls
calls <- run_from_object(myUserMetadata = user)
```



Use the reference intergenic regions from the community



```
list_community_ref_intergenic_species()
## create a BgeeMetadata object using the community release
bgee <- new("BgeeMetadata", release = "community")
calls_output <- generate_calls_workflow(bgeeMetadata = bgee, userMetadata = user_BgeeCall)
```