Expression calls from RNA-Seq data using BgeeCall R package

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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" # O. melonogaster
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)
```

@bgeedb  http://bgee.org/  bgee@sib.swiss