/ - root

data/ : write\_tome\_data() read\_tome\_gene\_data() read\_tome\_sample\_data()

exon/

dims read\_tome\_data\_dims()

i

p

x

exon\_lengths - a vector object

intron/

dims

i

p

x

intron\_lengths - a vector object

t\_exon/

dims read\_tome\_data\_dims(transpose = T)

i

p

x

t\_intron/

dims

i

p

x

total\_exon\_counts : read\_tome\_total\_counts(region = “exon”)

total\_intron\_counts : read\_tome\_total\_counts(region = “intron”)

dend/

[dend\_name : write\_tome\_dend() read\_tome\_dend()

desc : write\_tome\_dend\_desc()

gene\_meta/

gene/

[gene\_columns] - vector objects

desc - a data.frame object

gene\_names - a vector object : write\_tome\_data() read\_tome\_gene\_names()

log - a data.frame object

mapping/

[mapping\_name]/

memb - a data.frame object

desc - a data.frame object

projection/

[projection\_name] : write\_tome\_projection()

desc : write\_tome\_projection\_desc()

sample\_meta/

anno/ : write\_tome\_anno() read\_tome\_anno()

[anno\_columns] - vector objects

desc : write\_tome\_anno\_desc() read\_tome\_anno\_desc()

sample\_names : write\_tome\_data() read\_tome\_sample\_names()

stats/

count\_gt0 - a data.frame object : write\_tome\_stats()

count\_gt1 - a data.frame object : write\_tome\_stats()

count\_n - a data.frame object : write\_tome\_stats()

medians - a data.frame object : write\_tome\_stats()

sums - a data.frame object : write\_tome\_stats()

desc - a data.frame object : write\_tome\_stats\_desc()

tome\_meta/

citation - a data.frame object

desc - a data.frame object