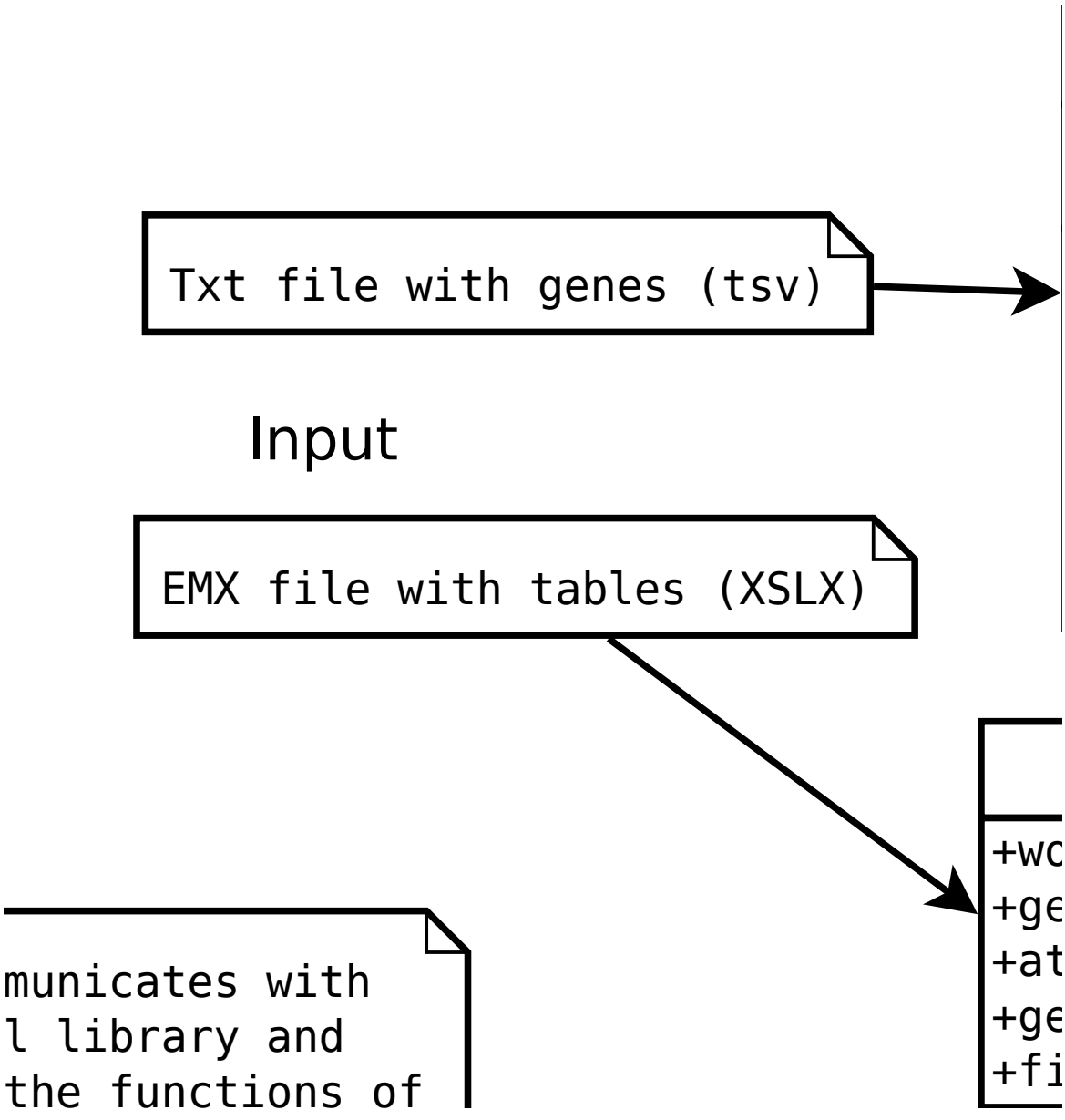
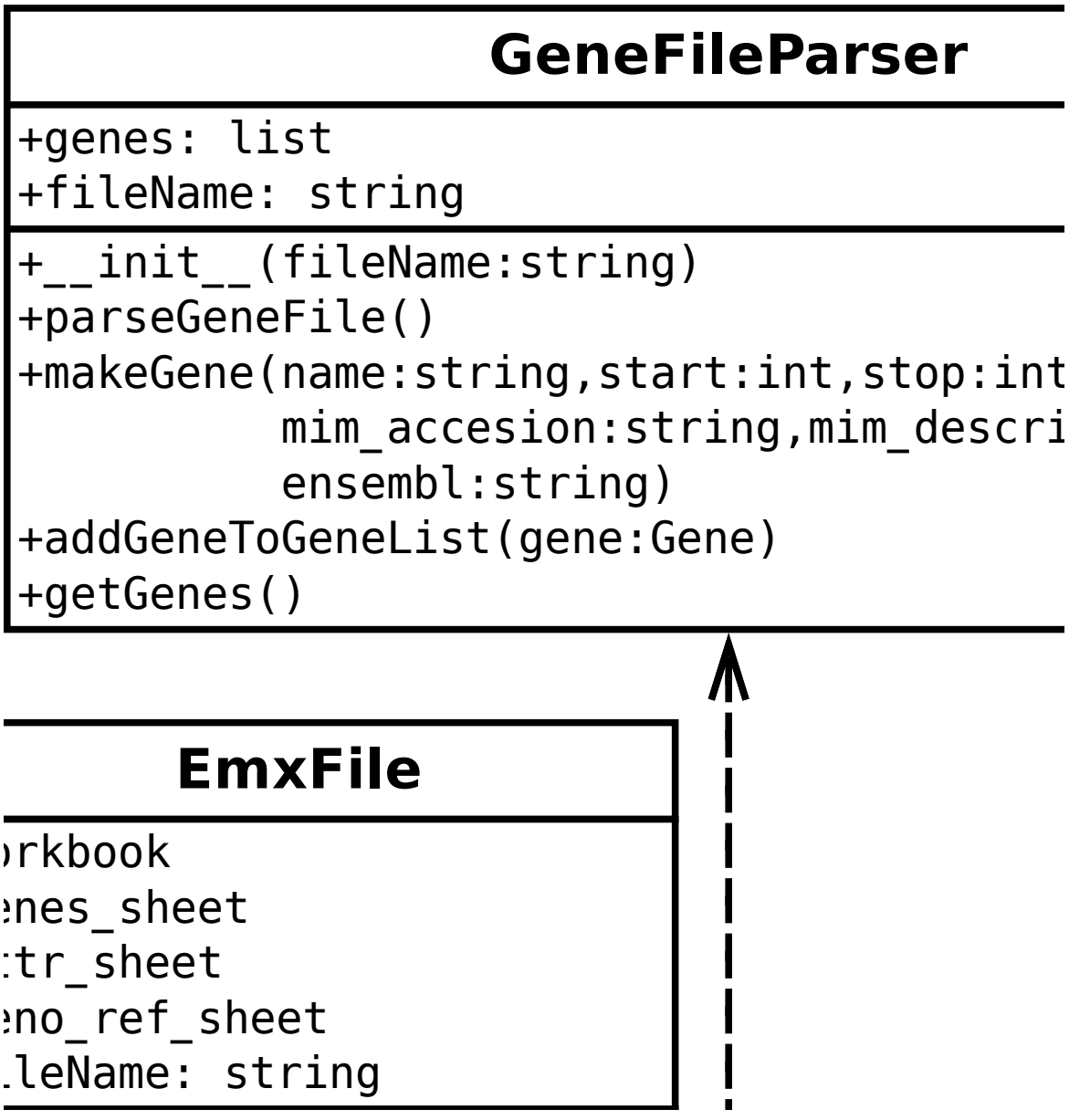
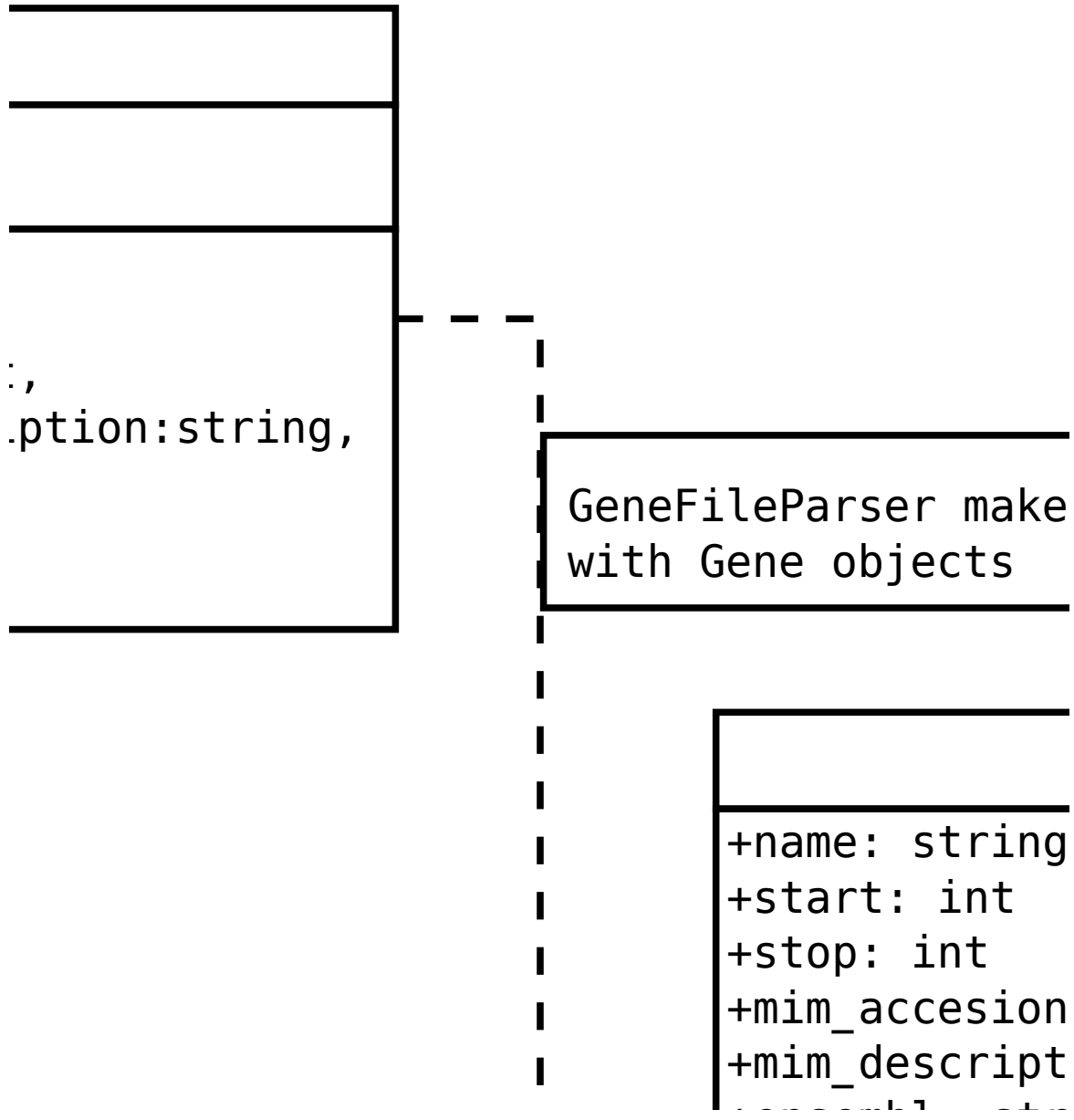
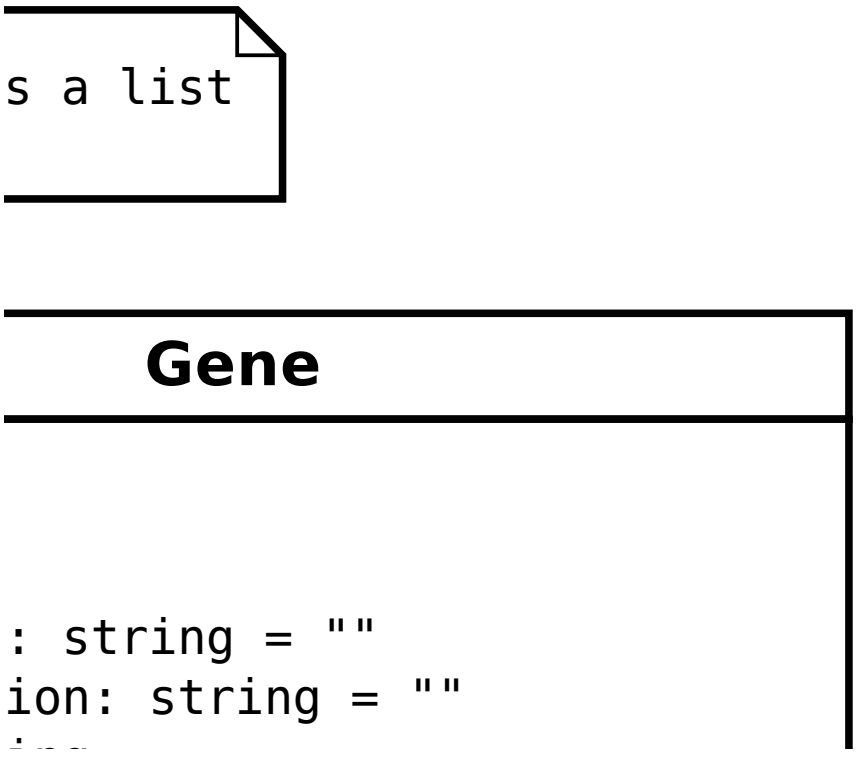
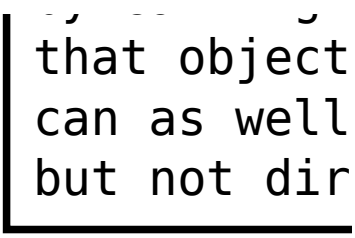
EmxFile com
the openpyx
by calling

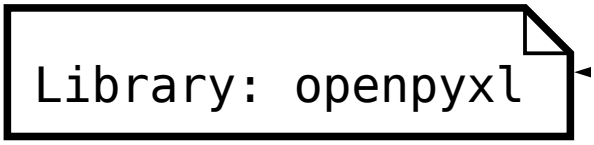

Txt file with genes (tsv)
Input
EMX file with tables (XSLX)
+wo
+ge
+at
+ge
+fi
municates with
l library and
the functions of

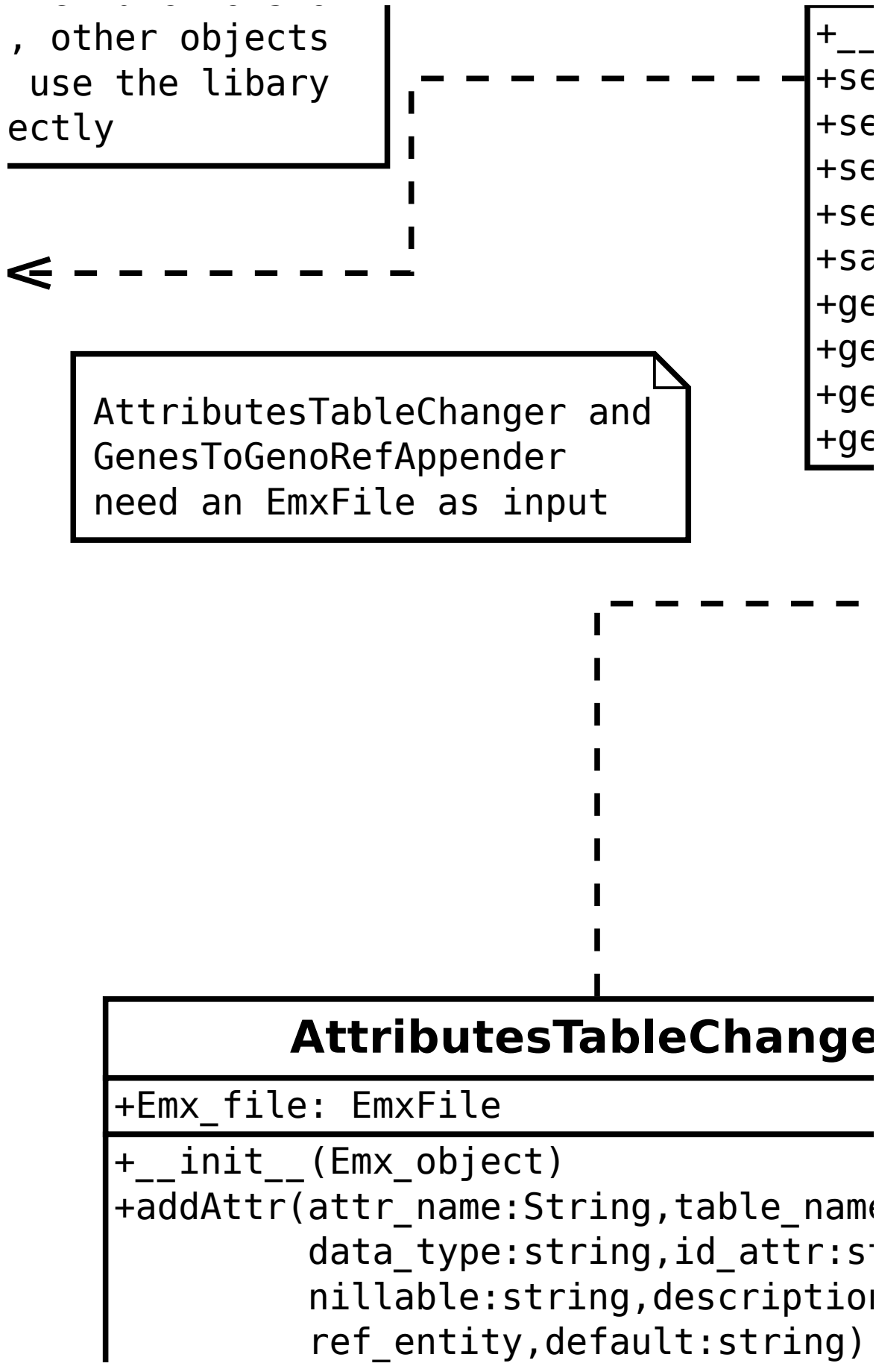

GeneFileParser
+genes: list
+fileName: string
+__init__(fileName:string)
+parseGeneFile()
+makeGene(name:string,start:int,stop:int
mim_accesion:string,mim_descri
ensembl:string)
+addGeneToGeneList(gene:Gene)
+getGenes()
EmxFile
rkbook
nes_sheet
tr_sheet
no_ref_sheet
leName: string

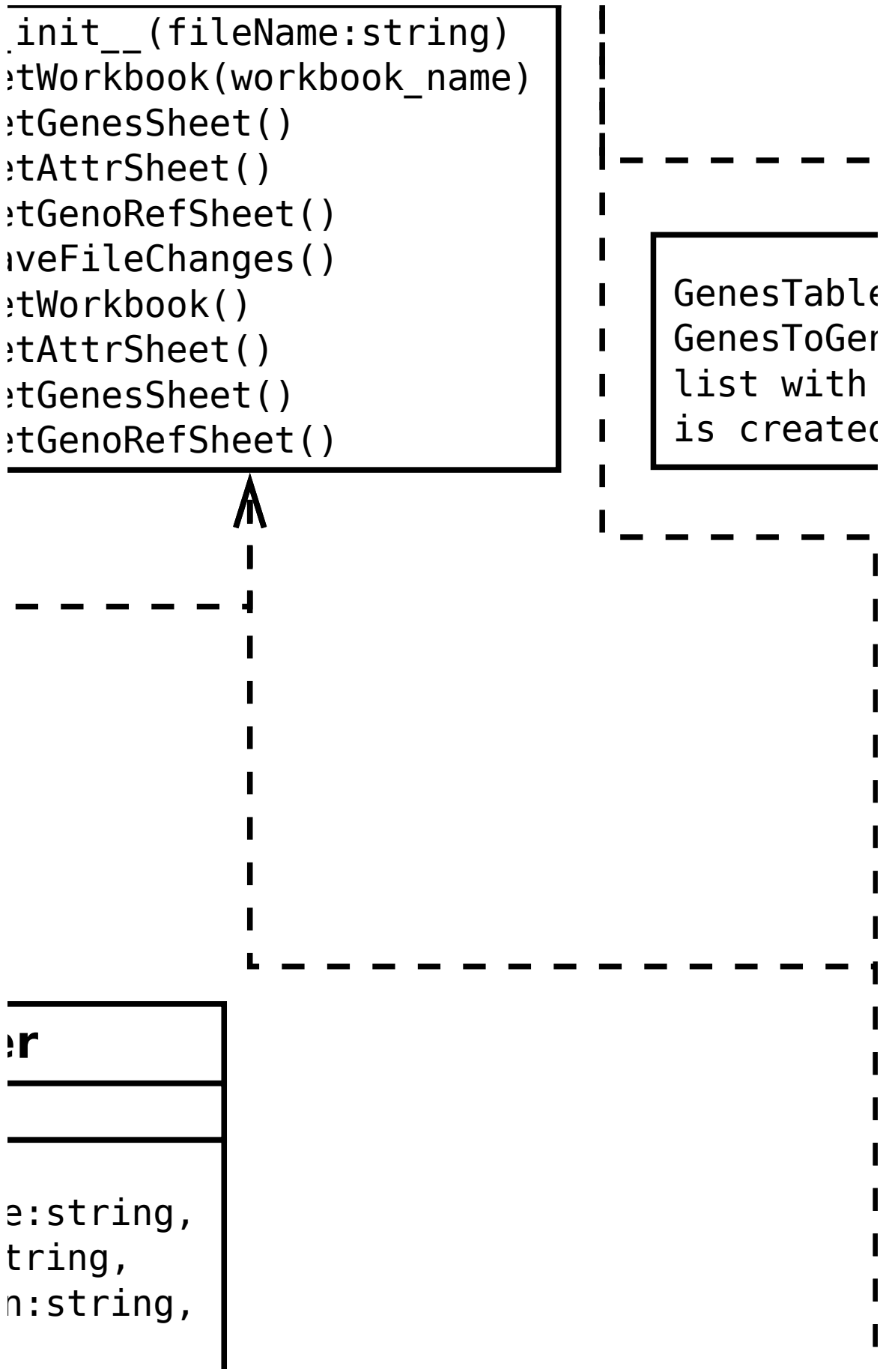

:,
.ption:string,
GeneFileParser make
with Gene objects
+name: string
+start: int
+stop: int
+mim_accesion
+mim_descript

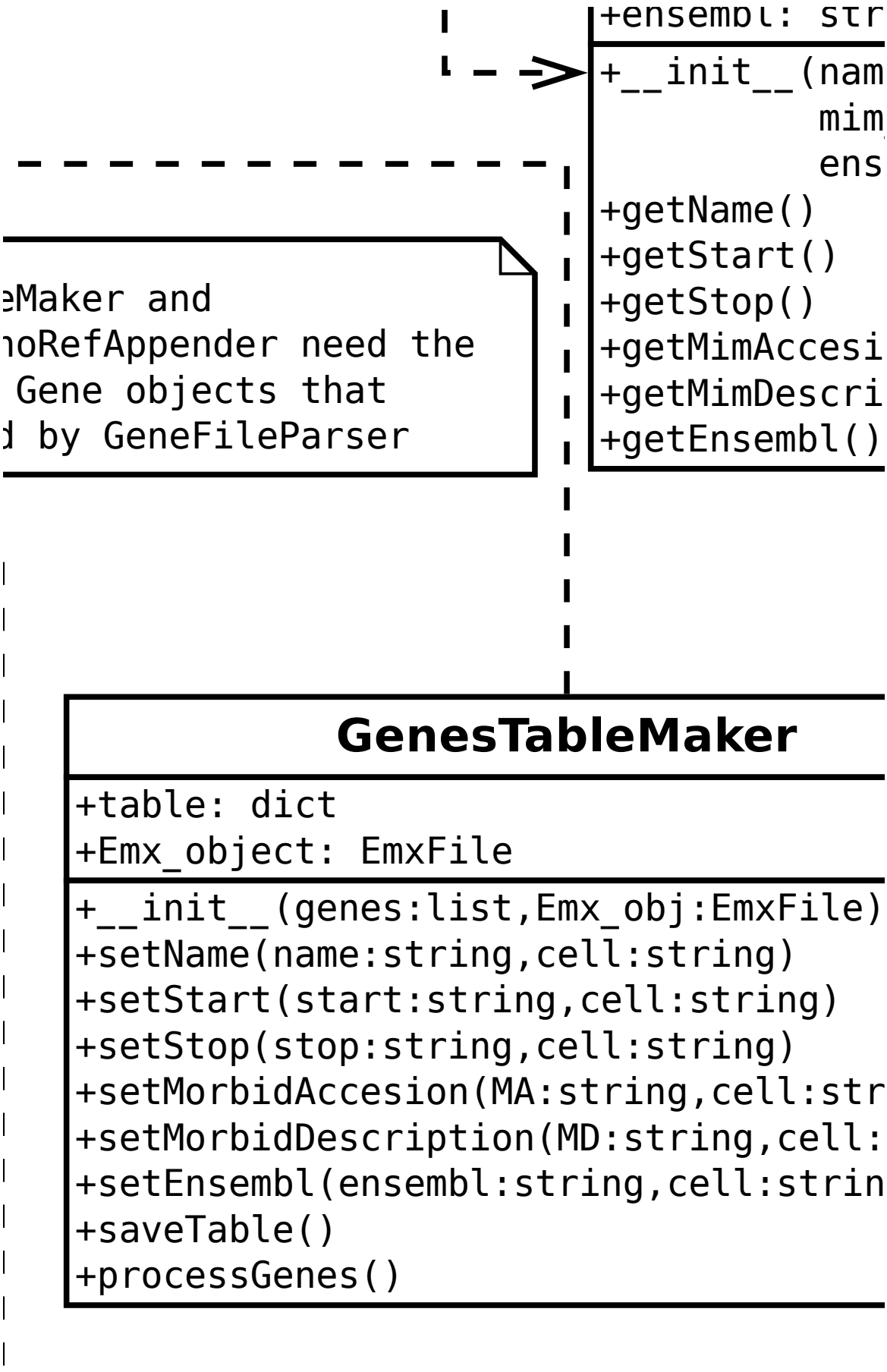

s a list
Gene
: string = ""
ion: string = ""

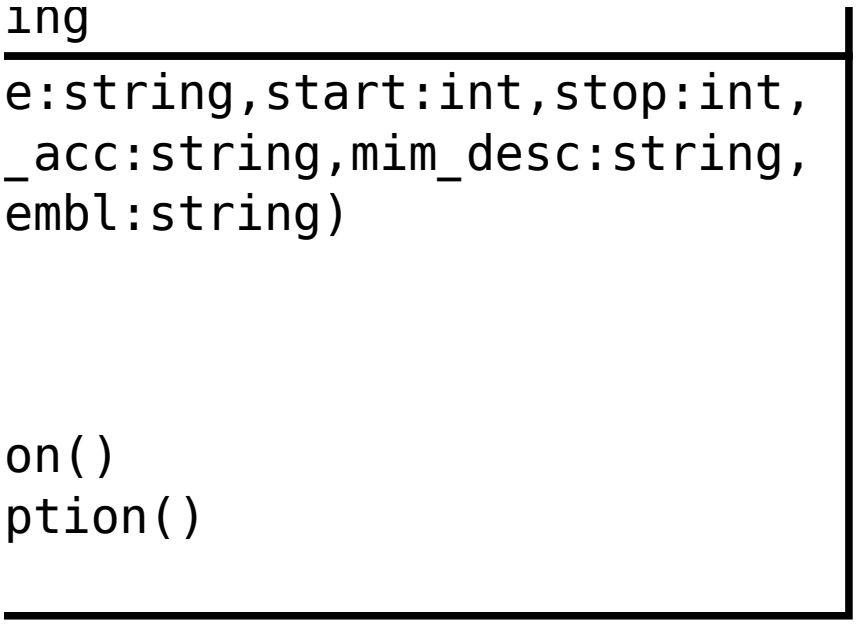

that object
can as well
but not dir

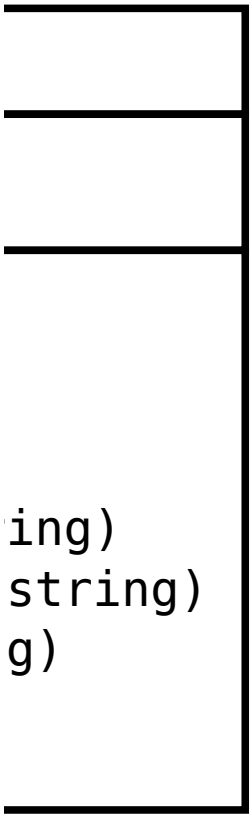

Library: openpyxl

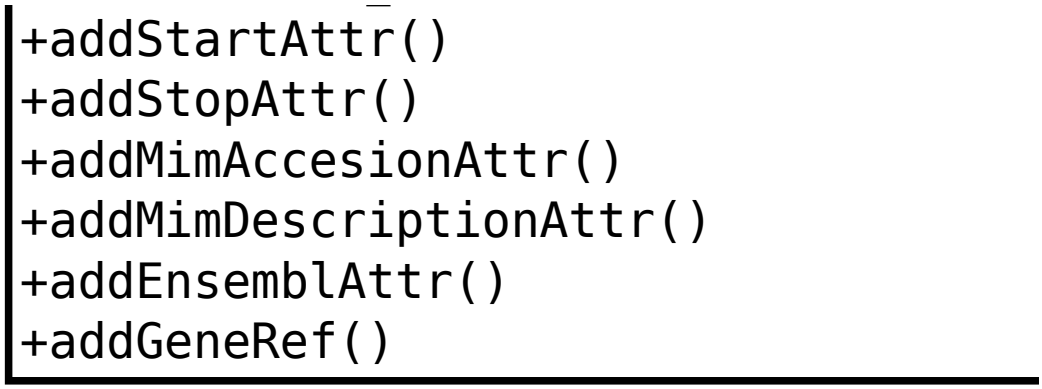

, other objects
use the libary
ectly
+__
+se
+se
+se
+se
+sa
+ge
+ge
+ge
+ge
AttributesTableChanger and
GenesToGenoRefAppender
need an EmxFile as input
AttributesTableChange
+Emx_file: EmxFile
+__init__(Emx_object)
+addAttr(attr_name:String,table_name
data_type:string,id_attr:st
nillable:string,description
ref_entity,default:string)

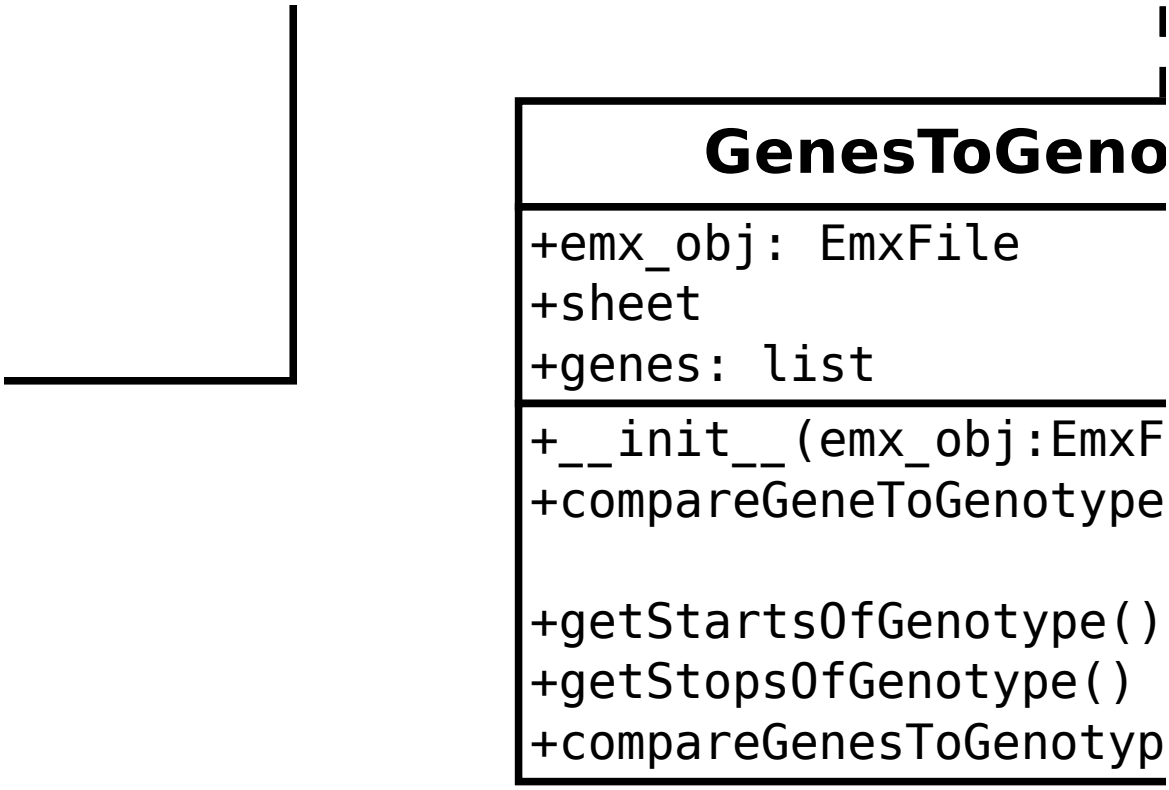

_init__(fileName:string)
etWorkbook(workbook_name)
etGenesSheet()
etAttrSheet()
etGenoRefSheet()
aveFileChanges()
etWorkbook()
etAttrSheet()
etGenesSheet()
etGenoRefSheet()
GenesTable
GenesToGe
list with
is created
er
e:string,
tring,
n:string,

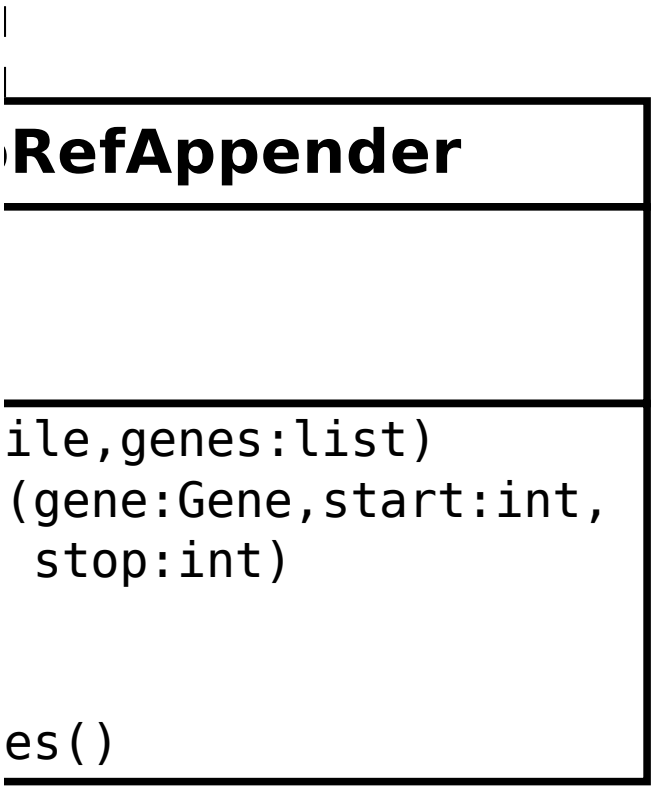

+ensembl: str
+__init__(nam
mim
ens
+getName()
+getStart()
+getStop()
+getMimAccesi
+getMimDescri
+getEnsembl()
eMaker and
noRefAppender need the
Gene objects that
d by GeneFileParser
GenesTableMaker
+table: dict
+Emx_object: EmxFile
+__init__(genes:list,Emx_obj:EmxFile)
+setName(name:string,cell:string)
+setStart(start:string,cell:string)
+setStop(stop:string,cell:string)
+setMorbidAccesion(MA:string,cell:str
+setMorbidDescription(MD:string,cell:
+setEnsembl(ensembl:string,cell:strin
+saveTable()
+processGenes()


ing
e:string,start:int,stop:int,
_acc:string,mim_desc:string,
embl:string)
on()
ption()


ing)
string)
g)


+addStartAttr()
+addStopAttr()
+addMimAccesionAttr()
+addMimDescriptionAttr()
+addEnsemblAttr()
+addGeneRef()


GenesToGeno
+emx_obj: EmxFile
+sheet
+genes: list
+__init__(emx_obj:EmxF
+compareGeneToGenotype
+getStartsOfGenotype()
+getStopsOfGenotype()
+compareGenesToGenotyp


RefAppender
ile,genes:list)
(gene:Gene,start:int,
stop:int)
es()