

## **srdb.management**

+mgmt: VARCHAR(40) = PRIMARY KEY  
+country: VARCHAR(50)  
+managementauthority: VARCHAR(200)



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## **srdb.taxonomy**

+tsn: INT = PRIMARY KEY  
+scientificname: VARCHAR(200)  
+kingdom: VARCHAR(200)  
+phylum: VARCHAR(200)  
+classname: VARCHAR(200)  
+ordername: VARCHAR(200)  
+family: VARCHAR(200)  
+genus: VARCHAR(200)  
+species: VARCHAR(200)  
+myersname: VARCHAR(20)  
+commonname1: VARCHAR(200)  
+commonname2: VARCHAR(200)  
+myersscientificname: VARCHAR(200)  
+myersfamily: VARCHAR(50)



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## **srdb.assessor**

- +assessorid: VARCHAR(40) = PRIMARY KEY  
- +mgmt: VARCHAR(40) = REFERENCES mgmt  
+country: VARCHAR(50)  
+assessorfull: VARCHAR(200)

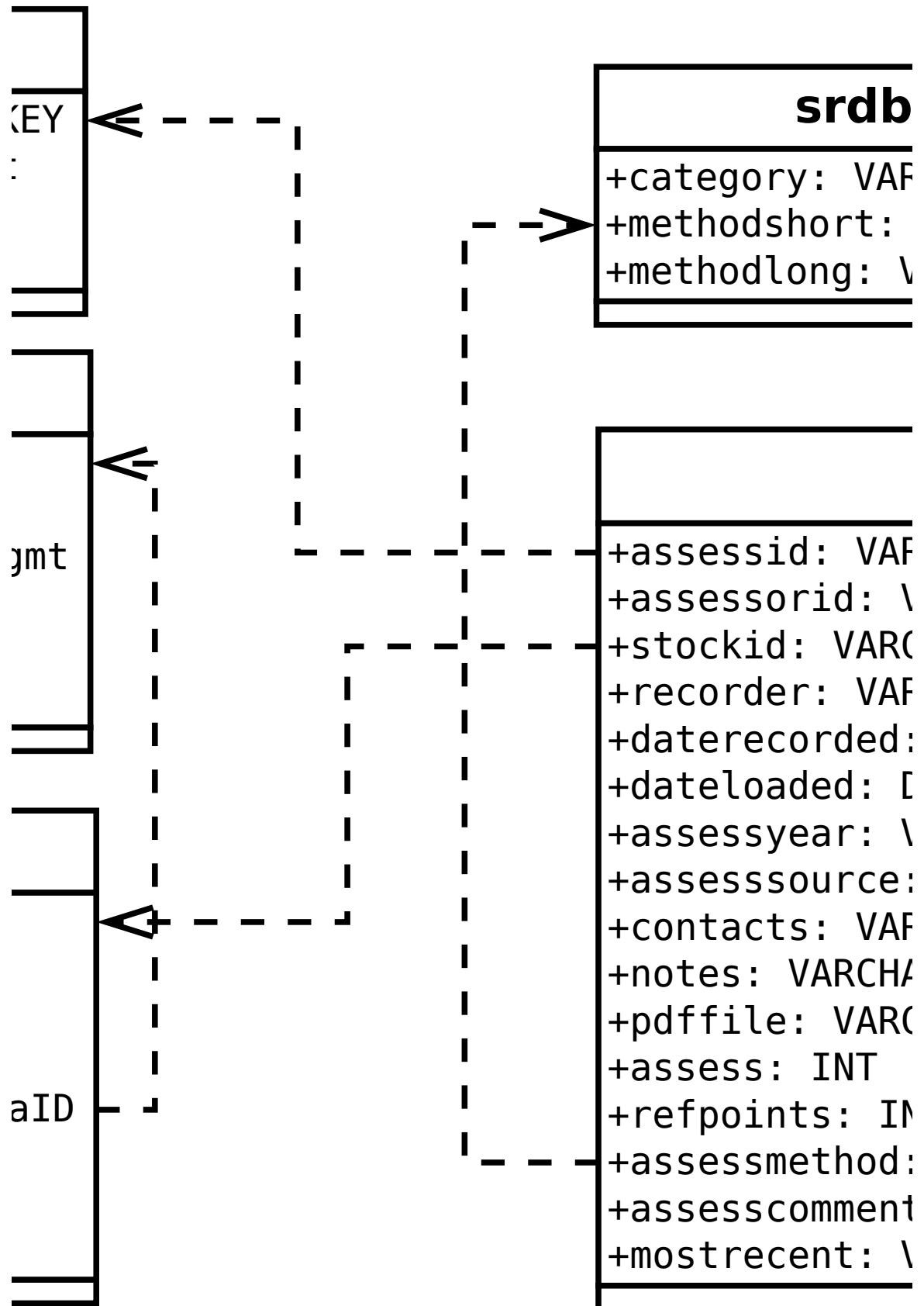
## **srdb.area**

+areaID: VARCHAR(70) = PRIMARY KEY  
+country: VARCHAR(50)  
- +areatype: VARCHAR(40) = REFERENCES mgmt  
+areacode: VARCHAR(25)  
+areaname: VARCHAR(100)  
+alternateareaname: VARCHAR(40)

## **srdb.stock**

- +stockid: VARCHAR(40) = PRIMARY KEY  
+tsn: INT = REFERENCES tsn  
+scientificname: VARCHAR(200)  
+commonname: VARCHAR(200)  
+areaID: VARCHAR(70) = REFERENCES area  
+stocklong: VARCHAR(200)  
+inMYERSdDB: INT  
+MYERSstockid: VARCHAR(40)

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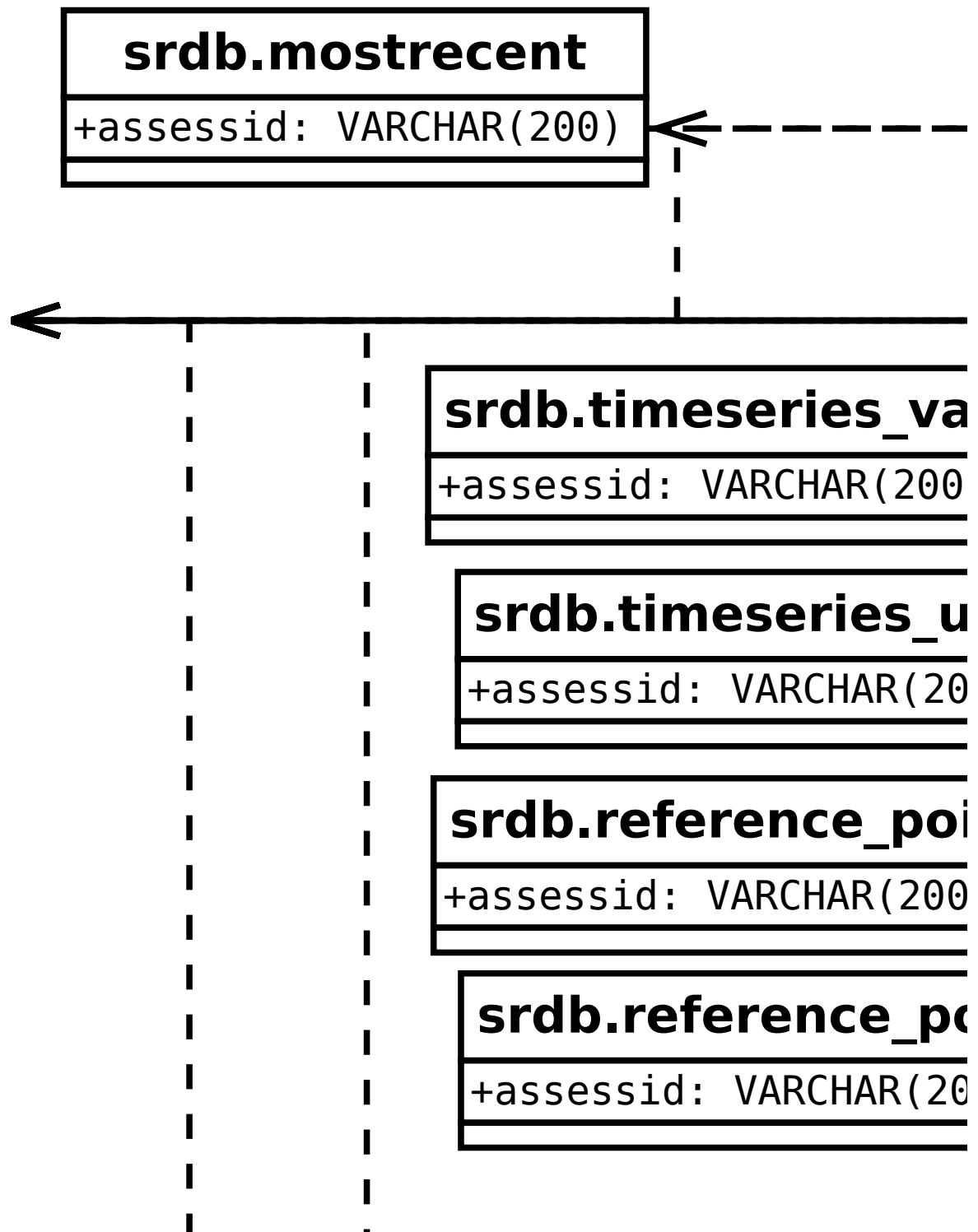


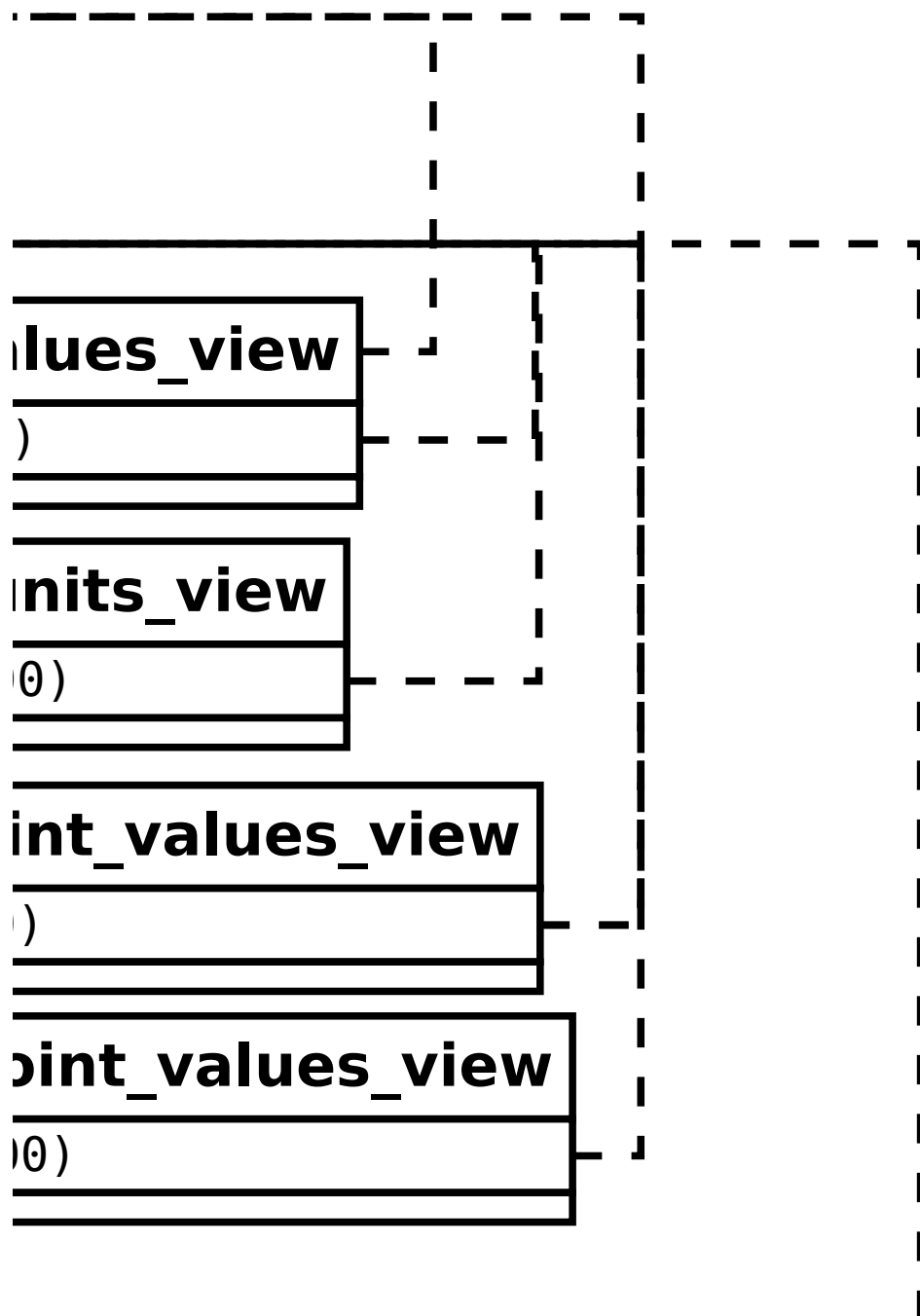
## **.assessmethod**

```
CHAR(100)  
  VARCHAR(20) = PRIMARY KEY  
  VARCHAR(200)
```

## **srdb.assessment**

```
CHAR(200)  
  VARCHAR(40) REFERENCES assessorid  
  CHAR(40) REFERENCES stockid  
  CHAR(40)  
  : DATE  
  DATE  
  VARCHAR(9)  
  : VARCHAR(300)  
  CHAR(300)  
  AR(1000)  
  CHAR(300)  
  
  NT  
  : VARCHAR(200) = REFERENCES methodshort  
  es: VARCHAR(1000)  
  VARCHAR(3)
```







<b>srdb.fishbasesaupcodes</b>
+scientificname: VARCHAR(200)



<b>srdب.لmetostocks</b>
+stockid: VARCHAR(40)

<b>srdب.لmerefs</b>
+lme_number: INT

+as
+b:
+b:
+b:

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## **srdb.bioparams**

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ssessid: VARCHAR(200) REFERENCES assessio  
loid: VARCHAR(40) = REFERENCES biounique  
iovalue: VARCHAR(100)  
ioyear: VARCHAR(10)

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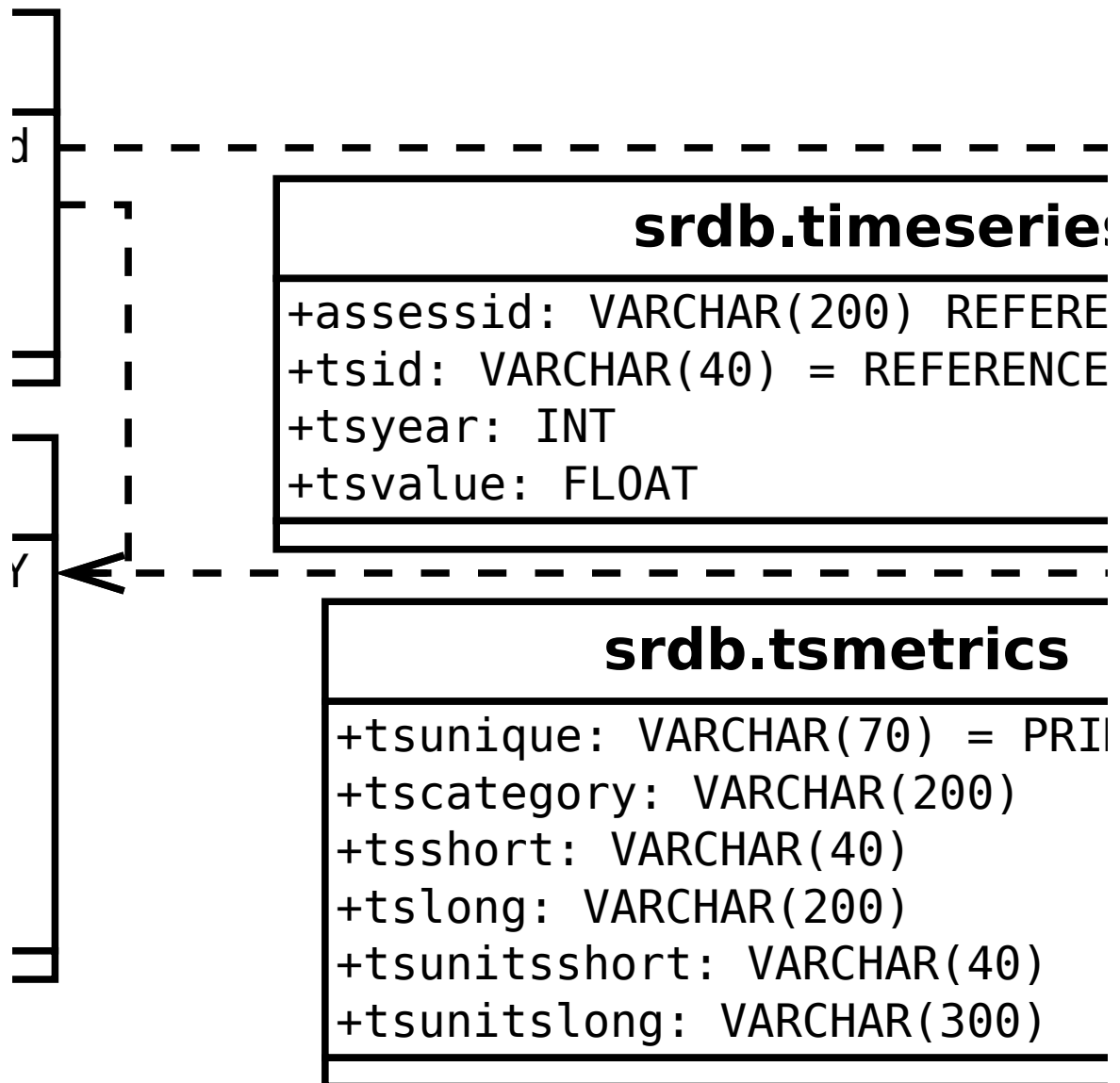
## **srdb.biometrics**

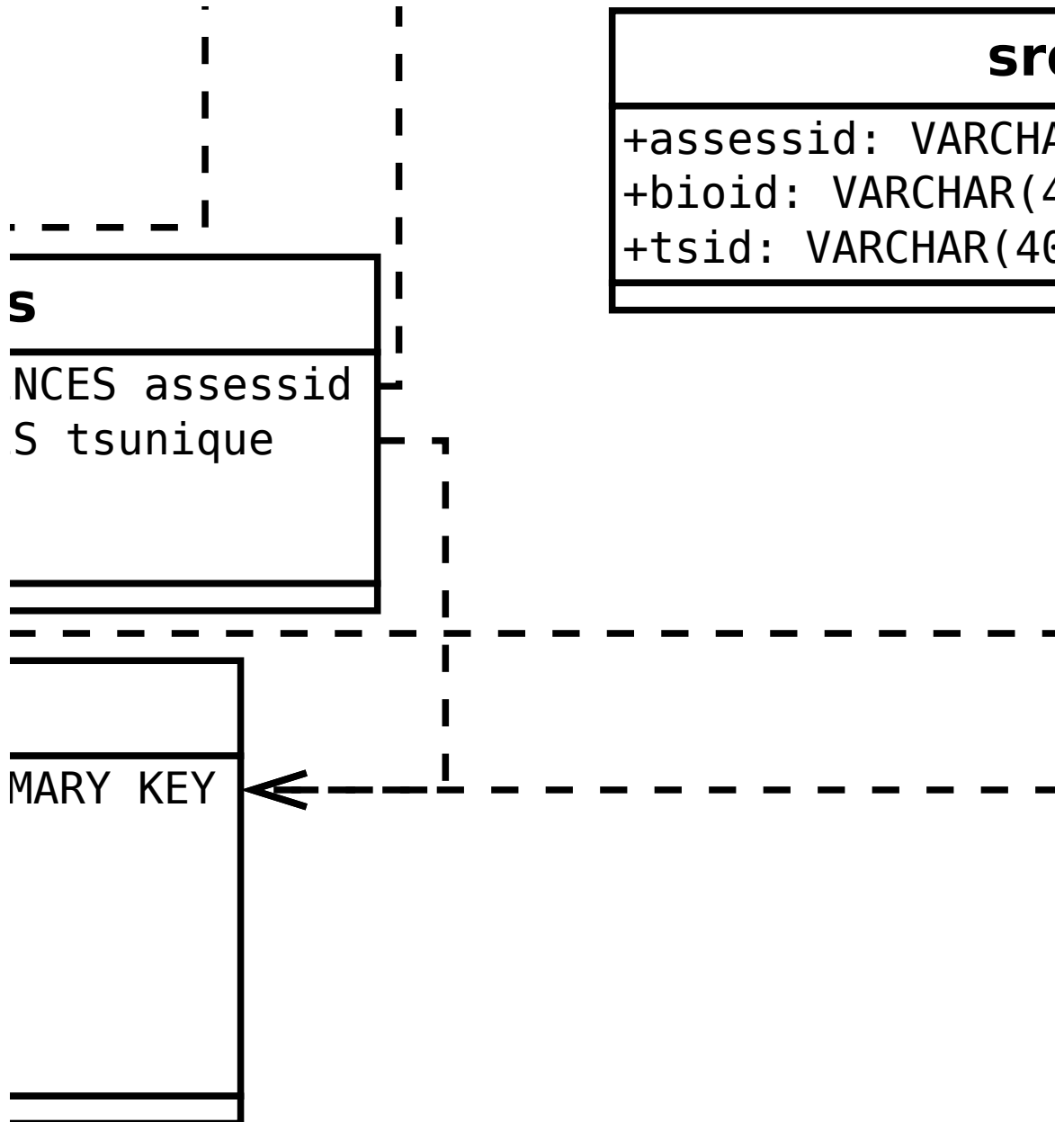
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+biounique: VARCHAR(70) = PRIMARY KEY  
+category: VARCHAR(100)  
+subcategory: VARCHAR(100)  
+bioshort: VARCHAR(40)  
+biolong: VARCHAR(300)  
+biounitsshort: VARCHAR(40)  
+biounitslong: VARCHAR(200)

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## db.brptots

AR(200)

40) = REFERENCES biunique

0) = REFERENCES tsunique



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+a

<b>rdb.tsrelative_explicit_view</b>
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ssessid: VARCHAR(200)
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