eCAMI Core Refactoring

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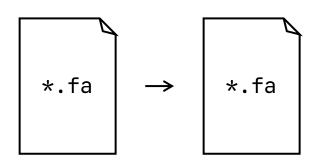
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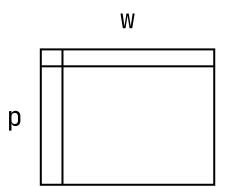
Git : github.com/ohshane71

Project Repository

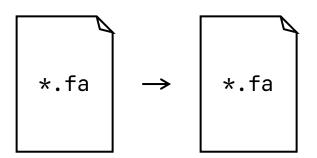
```
https://github.com/ohshane71/eCAMI/https://github.com/ohshane71/eCAMI/tree/dev
```

Pipeline

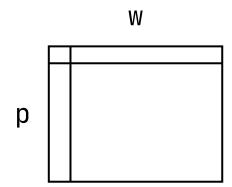




Pipeline



proteinI0



profast

proteinIO

File IO

Preprocessing

Shape Check

profast

Fit

Predict

Evaluate

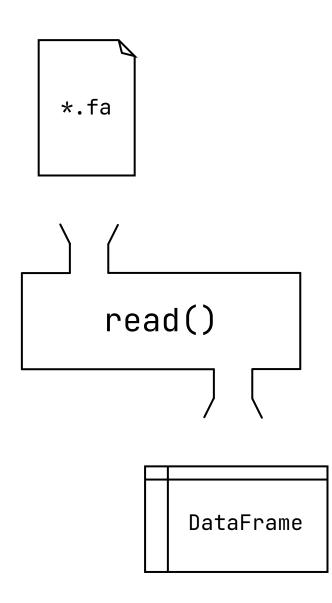
proteinI0

```
import proteinIO.fastaIO
import proteinIO.preprocessing
import proteinIO.protein
```

import proteinIO.fastaIO import proteinIO.preprocessing import proteinIO.protein

import proteinIO.fastaIO
import proteinIO.fastqIO
import proteinIO. IO

```
from proteinIO.fastaIO import *
read()
write()
```



DataFrame write() *.fa import proteinIO.fastaIO
import proteinIO.preprocessing
import proteinIO.protein

```
from proteinIO.preprocessing import *
manipulate_duplicates()
series2object()
shape()
```

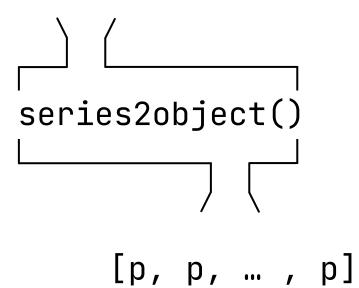
DataFrame manipulate_duplicates() DataFrame

manipulate_duplicates()

@param

keep='union'

>A9.9|GT5|GT5_1 MLSVVVPVYNEEKNVEELVK >A9.0|GT5|GT5_4|CBM48 MLSVVVPVYNEEKNVEELVK >A9.9|GT5_1|GT5_4|CBM48 MLSVVVPVYNEEKNVEELVK DataFrame



```
[p, p, ..., p]
      shape()
    { family dictionary }
```

Nested dictionary

```
"GH13":
 "_count" : 3,
 "_ex_count" : 1,
 "_elements" : [2, 7, 109],
     "_count" : 2,
     "_ex_count" : 2,
     "_elements" : [2, 109],
   },
```

import proteinIO.fastaIO
import proteinIO.preprocessing
import proteinIO.protein

from proteinIO.protein import *

Protein()

profast

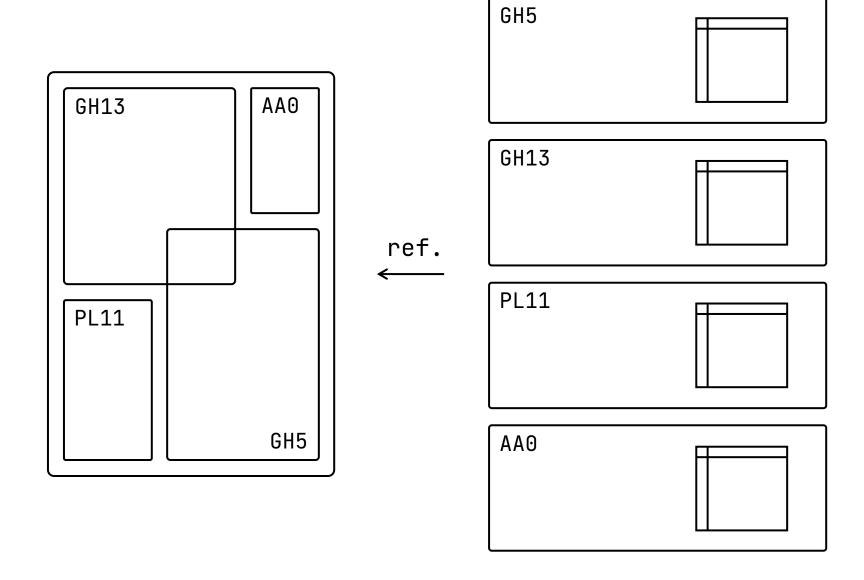
import profast.kmer.KMerClassifier

from profast.kmer.KMerClassifier import *

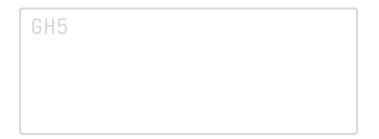
KMerClassifier()

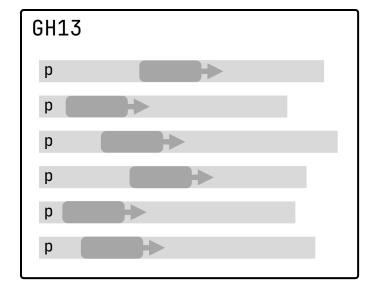
```
kmc = KMerClassifier()
kmc.alpha = 2
kmc.beta = 0.9
kmc.fit(X, shape, families, k)
kmc.X = [p, p, ..., p]
kmc.shape = { family dictionary }
kmc.families = ["GH5", "GH13", "PL11", "AA0"]|["*"]
          = 8
kmc.k
```

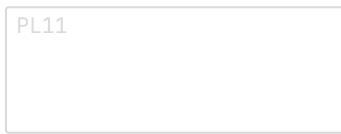
Multiprocessing



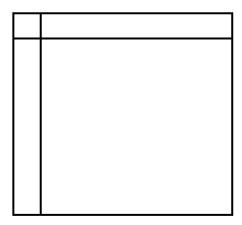
Threading











shared matrix per family

