tagMeppr

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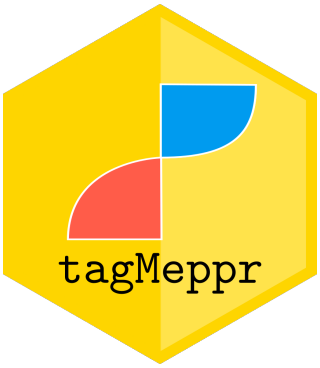
2019-08-22



Hi there! Welcome!

```
library(tagMeppr)
```

A hybrid reference genome

Remember: you only have to make a tagMepprIndex once per genome and protocol! This means that you can use it for however many samples for that protocol and organism (e.g. PiggyBac in human cells) you may have.

Loading a tagMepprIndex is easy with loadIndex().

```
reference_hg19_PB = loadIndex('BSgenome.Hsapiens.UCSC.hg19_PiggyBac_tagMeppRindex.fa.gz')
```

You can use print() on this tagMepprIndex, which gives you a lot of information:

```
print(reference_hg19_PB)
```

The tagMepprSample-object

Creating a new sample

```
C9 = newTagMeppr(F1 = 'clone9_FWD_R1.fq.gz',
                 F2 = 'clone9_FWD_R2.fq.gz',
                 R1 = 'clone9_REV_R1.fq.gz',
                 R2 = 'clone9_REV_R2.fq.gz',
                 name = "clone9",
                 protocol = 'PiggyBac')
```

This is the print:

```
print(C9)
```

Aligning

Omg. Mapping without leaving R! Please check if you have BWA and samtools intalled. Note no <- signs

```
align(exp = C9,
      ref = reference_hg19_PB,
      cores = 30,
      empericalCentre = T)
```

The object will be updated, which keeps your evironment tidy.

```
print(C1)
```

todo: - remove non-ttaa+pad from fasta - empirical center auto on 1K-Npad - fai: make internal w/ biostring