# atlas-utils之过滤分类结果中线粒体和叶绿体来源的序列: filter

# 一、atlas-utils filter介绍

## 功能描述:

atlas-utils filter 过滤 USEARCH SINTAX/NBC 分类结果中线粒体和叶绿体来源的序列,可以指定匹配的分类学名称。

#### 命令行接口:

## 可选参数:

```
1-t 字符串 过滤分类学中d:Bacteria或者d:Archaea或者其他物种,默认为空;2多个分类学目标可设置如: d:Archaea,p:Firmicutes3-r输出过滤后的OTU ID
```

# 二、使用场景实例及其用法

### 示例演示:

示例文件: classify.txt

```
1 | $ cat classify.txt |head -n 5
```

```
ZOTU_19 d:Bacteria(1.0000),p:"Bacteroidetes"
   (1.0000), c:Sphingobacteriia(1.0000), o: "Sphingobacteriales"
   (1.0000), f:Chitinophagaceae(1.0000), g:Parafilimonas(0.9400), s:Parafilimonas_t
   errae(0.8836)
   d:Bacteria,p:"Bacteroidetes",c:Sphingobacteriia,o:"Sphingobacteriales",f:Chit
   inophagaceae,g:Parafilimonas,s:Parafilimonas_terrae
  ZOTU_5 d:Bacteria(1.0000),p:"Bacteroidetes"(1.0000),c:"Bacteroidia"
   (0.7800),o:"Bacteroidales"
   (0.6084), f:Prolixibacteraceae(0.3650), g:Mariniphaga(0.0621), s:Mariniphaga_ana
   erophila(0.0105) +
                              d:Bacteria,p:"Bacteroidetes"
3 ZOTU_9 d:Bacteria(1.0000),p:"Bacteroidetes"
   (1.0000), c:Flavobacteriia(1.0000), o: "Flavobacteriales"
   (1.0000), f:Flavobacteriaceae(1.0000), g:Flavobacterium(1.0000)
   d:Bacteria,p:"Bacteroidetes",c:Flavobacteriia,o:"Flavobacteriales",f:Flavobac
   teriaceae,g:Flavobacterium
4 ZOTU_12 d:Bacteria(1.0000),p:"Bacteroidetes"(1.0000),c:"Bacteroidia"
   (1.0000), o: "Bacteroidales" (1.0000), f: "Porphyromonadaceae"
   (1.0000),g:Petrimonas(1.0000),s:Petrimonas_{sulfuriphila}(1.0000) +
   d:Bacteria,p:"Bacteroidetes",c:"Bacteroidia",o:"Bacteroidales",f:"Porphyromon
   adaceae",g:Petrimonas,s:Petrimonas_sulfuriphila
5 ZOTU_7 d:Bacteria(1.0000),p:"Bacteroidetes"(1.0000),c:"Bacteroidia"
   (1.0000), o: "Bacteroidales" (1.0000), f: "Porphyromonadaceae"
   (1.0000), g:Macellibacteroides(0.5700), s:Macellibacteroides_fermentans(0.3249)
   d:Bacteria,p:"Bacteroidetes",c:"Bacteroidia",o:"Bacteroidales",f:"Porphyromon
   adaceae"
```

#### 运行命令:

过滤 USEARCH SINTAX/NBC 分类结果中为 d:Bacteria 的序列。

```
1 | $ atlas-utils filter -t "d:Archaea" classify.txt | head -n2
```

参数选项1: 设置 -r 参数,输出过滤后的OTU ID。

```
1 $ atlas-utils filter -t d:Archaea -r classify.txt 2> identifiers.txt | head -n 2
```

```
ZOTU_19 d:Bacteria(1.0000),p:"Bacteroidetes"
   (1.0000),c:Sphingobacteriia(1.0000),o:"Sphingobacteriales"
   (1.0000),f:Chitinophagaceae(1.0000),g:Parafilimonas(0.9400),s:Parafilimonas_t
   errae(0.8836)
   d:Bacteria,p:"Bacteroidetes",c:Sphingobacteriia,o:"Sphingobacteriales",f:Chit
   inophagaceae,g:Parafilimonas,s:Parafilimonas_terrae
  ZOTU_5 d:Bacteria(1.0000),p:"Bacteroidetes"(1.0000),c:"Bacteroidia"
   (0.7800),o:"Bacteroidales"
   (0.6084), f:Prolixibacteraceae(0.3650), g:Mariniphaga(0.0621), s:Mariniphaga_ana
   erophila(0.0105)
                      +
                                d:Bacteria,p:"Bacteroidetes"
3 [biostack@biostack example] atlas-utils filter -t d:Archaea -r classify.txt
   2> identifiers.txt | head -n 2
4 ZOTU_19 d:Bacteria(1.0000),p:"Bacteroidetes"
   (1.0000),c:Sphingobacteriia(1.0000),o:"Sphingobacteriales"
   (1.0000),f:Chitinophagaceae(1.0000),g:Parafilimonas(0.9400),s:Parafilimonas_t
   errae(0.8836)
   d:Bacteria,p:"Bacteroidetes",c:Sphingobacteriia,o:"Sphingobacteriales",f:Chit
   inophagaceae,g:Parafilimonas,s:Parafilimonas_terrae
5 ZOTU_5 d:Bacteria(1.0000),p:"Bacteroidetes"(1.0000),c:"Bacteroidia"
   (0.7800),o:"Bacteroidales"
   (0.6084), f: \texttt{Prolixibacteraceae} (0.3650), g: \texttt{Mariniphaga} (0.0621), s: \texttt{Mariniphaga\_ana}
   erophila(0.0105)
                       +
                                d:Bacteria,p:"Bacteroidetes"
```

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