taxon-utils之计算给定分类的谱系：lineage

一、taxon-utils lineage介绍

功能描述：

`taxon-utils lineage` 计算给定分类的谱系.

命令行接口：

```
$ taxon-utils  lineage

Usage: taxon-utils lineage [options] <taxon.map> <tab|taxonIds>

Options:
  -c INT   column for taxon translate, default: [2]
  -n       print lineage for specified node, using ',' for multi taxonId.
```

可选参数：

```
  -c    整型       指定转化的列，默认为第二列；
  -n               输出指定节点的世系
```

二、使用场景实例及其用法

示例演示：

示例文件在: `data` 目录

示例文件： `classify.txt.gz`, `taxon.map.gz`

```
$ zcat classify.txt.gz | head -n  6
```

```
C       A01050:204:HF7FGDSXY:4:1101:12943:1016  25457   150|149 0:22 25457:4 0:7 25458:5 0:78 |:| 3:4 3343:5 8109:2 25457:5 25460:1 25457:6 25693:5 0:48 25458:2 0:1 3343:2 14694:7 3343:10 3:5 0:12
C       A01050:204:HF7FGDSXY:4:1101:12337:1031  18331   150|149 0:60 31294:5 0:25 18331:3 0:23 |:| 0:93 18331:3 0:19
C       A01050:204:HF7FGDSXY:4:1101:16866:1047  8364    150|150 0:17 20367:2 35825:1 0:8 3:4 20616:5 3:1 4523:5 3:3 0:9 3:5 0:19 27173:2 0:12 27173:2 0:21 |:| 0:2 2878:3 24660:5 28576:3 30576:2 3:13 0:9 2483:17 27170:3 2483:2 27170:5 3:6 8364:3 3:7 8364:3 27172:2 8364:5 27172:6 171:5 0:15
C       A01050:204:HF7FGDSXY:4:1101:22742:1047  23158   150|150 0:82 23158:4 0:30 |:| 0:116
C       A01050:204:HF7FGDSXY:4:1101:28664:1063  559     150|150 0:22 559:3 0:7 171:5 0:79 |:| 0:116
C       A01050:204:HF7FGDSXY:4:1101:20473:1094  25986   150|150 0:45 25986:3 0:68 |:| 0:116
```

注意事项：`classify`文件为`Kraken2`分类的结果，第一列为标识符：`C`：可以分类的序列，`U`：不能分类的序列，第三列为分类的`Taxonomy ID`，可以为`NCBI`分类号或者使用`GTDB`的自定义分类号，正常我们只需要第二列和第三列。

```
$ zcat taxon.map.gz | head -n 6
```

```
1       1       no rank root    root
2       1       superkingdom    Archaea root
3       1       superkingdom    Bacteria        root
4       3       phylum  4572-55 Bacteria
5       3       phylum  AABM5-125-24    Bacteria
6       3       phylum  AB1-6   Bacteria
```

运行命令：

```
$ zcat classify.txt.gz | grep -P "^C" | cut -f2,3 | head -n 6
```

```
A01050:204:HF7FGDSXY:4:1101:12943:1016  25457
k:Bacteria,p:Eremiobacterota,c:Eremiobacteria,o:UBP12,f:UBA5184,g:Palsa-1478,s:Palsa-1478 sp003140215   3,56,265,1390,3343,8109,25457
A01050:204:HF7FGDSXY:4:1101:12337:1031  18331
k:Bacteria,p:Gemmatimonadota,c:Gemmatimonadetes,o:Gemmatimonadales,f:Gemmatimonadaceae,g:Fen-1231,s:Fen-1231 sp003171215
3,78,283,806,2237,5826,18331
A01050:204:HF7FGDSXY:4:1101:16866:1047  8364
k:Bacteria,p:Actinobacteriota,c:Actinobacteria,o:Actinomycetales,f:Micrococcaceae,g:Pseudarthrobacter   3,9,171,559,2483,8364
A01050:204:HF7FGDSXY:4:1101:22742:1047  23158
k:Bacteria,p:Proteobacteria,c:Alphaproteobacteria,o:Rhizobiales,f:Beijerinckiaceae,g:Methylobacterium,s:Methylobacterium sp003173775
3,110,175,1021,1696,7507,23158
A01050:204:HF7FGDSXY:4:1101:28664:1063  559
k:Bacteria,p:Actinobacteriota,c:Actinobacteria,o:Actinomycetales
3,9,171,559
A01050:204:HF7FGDSXY:4:1101:20473:1094  25986
k:Bacteria,p:Actinobacteriota,c:Actinobacteria,o:Actinomycetales,f:Dermatophilaceae,g:Pedococcus,s:Pedococcus sp001426245
3,9,171,559,1919,8203,25986
```

将第二例翻译成物种世系格式：

```
$ zcat classify.txt.gz | grep -P "^C" | cut -f2,3 | head -n 6 | taxon-utils lineage   -c 2  taxon.map.gz -

A01050:204:HF7FGDSXY:4:1101:12943:1016  25457   root,Bacteria,Eremiobacterota,Eremiobacteria,UBP12,UBA5184,Palsa-1478,Palsa-1478 sp003140215    1,3,56,265,1390,3343,8109,25457
A01050:204:HF7FGDSXY:4:1101:12337:1031  18331   root,Bacteria,Gemmatimonadota,Gemmatimonadetes,Gemmatimonadales,Gemmatimonadaceae,Fen-1231,Fen-1231 sp003171215 1,3,78,283,806,2237,5826,18331
A01050:204:HF7FGDSXY:4:1101:16866:1047  8364    root,Bacteria,Actinobacteriota,Actinobacteria,Actinomycetales,Micrococcaceae,Pseudarthrobacter  1,3,9,171,559,2483,8364
A01050:204:HF7FGDSXY:4:1101:22742:1047  23158   root,Bacteria,Proteobacteria,Alphaproteobacteria,Rhizobiales,Beijerinckiaceae,Methylobacterium,Methylobacterium sp003173775   1,3,110,175,1021,1696,7507,23158
A01050:204:HF7FGDSXY:4:1101:28664:1063  559     root,Bacteria,Actinobacteriota,Actinobacteria,Actinomycetales   1,3,9,171,559
A01050:204:HF7FGDSXY:4:1101:20473:1094  25986   root,Bacteria,Actinobacteriota,Actinobacteria,Actinomycetales,Dermatophilaceae,Pedococcus,Pedococcus sp001426245        1,3,9,171,559,1919,8203,25986
```

多输出两列，一列为主要分类水平: 第一列为完整的世系分类， 一列为对应的数值编号， 比如: `root,Bacteria,Actinobacteriota,Actinobacteria,Actinomycetales,Dermatophilaceae,Pedococcus,Pedococcus sp001426245`, 分类之间使用 `,` 分割， 相对于 `translate` 具有完整的分类路径。

命令行参数 1: `-n` 指定需要翻译的数字编号， 比如： `25986`。

```
$ taxon-utils  lineage  -n  taxon.map.gz  25986
```

```
root,Bacteria,Actinobacteriota,Actinobacteria,Actinomycetales,Dermatophilaceae,Pedococcus,Pedococcus sp001426245        1,3,9,171,559,1919,8203,25986
```


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