Looking into my mouth microbiome

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The gut biome is interesting enough, but bacteria colonize just about every part of the body, so recently I’ve been studying [my uBiome mouth test results](http://blog.richardsprague.com/2014/10/whats-in-my-microbiome.html). The simple [GitHub RuBiome utilities](https://github.com/richardsprague/uBiome) I use for analyzing my gut will work for that too, so here’s a short example of how I did it:

First I [loaded my uBiome data](http://blog.richardsprague.com/2015/01/how-to-analyze-ubiome-sample-in-excel.html) into two variables, one for each sample: June 2014 (junMouth) and the other from October 2014 (OctMouth), after [a visit to my dentist](http://blog.richardsprague.com/2014/10/why-review-dentists.html).

Let’s see which species are new in the later (October) sample:

octToJunChange <- uBiome\_sample\_unique(OctMouth,junMouth)

## count missing.tax\_name  
## 1 3640 bacterium NLAE-zl-P562  
## 2 2725 Streptococcus sanguinis  
## 3 2075 Capnocytophaga gingivalis  
## 4 1969 Peptostreptococcus sp. oral clone FG014  
## 5 1618 Granulicatella adiacens

One of those species, *Streptococcus sanguinis* looks interesting. [Wikipedia](https://en.wikipedia.org/wiki/Streptococcus_sanguinis) says this:

*S. sanguinis* is a normal inhabitant of the healthy human mouth where it is particularly found in dental plaque, where it modifies the environment to make it less hospitable for other strains of Streptococcus that cause cavities, such as Streptococcus mutans.

No cavities? Nice! More good news: this quick check confirms that I don’t have any *S. mutans*:

OctMouth[grepl("Streptococcus",OctMouth$tax\_name),]$tax\_name

## [1] Streptococcus Streptococcus pseudopneumoniae   
## [3] Streptococcus sanguinis Streptococcus constellatus   
## [5] Streptococcus anginosus group Streptococcus sp. oral clone GM006  
## [7] Streptococcus thermophilus Streptococcus oralis   
## [9] Streptococcus gordonii   
## 250 Levels: [Eubacterium] sulci ... Veillonellaceae

Then I look at the species that disappeared (went extinct) between the two samples:

junToOctChange <- uBiome\_sample\_unique(junMouth,OctMouth)

## count missing.tax\_name  
## 1 6034 Capnocytophaga granulosa  
## 2 4153 Peptostreptococcus sp. oral clone FL008  
## 3 3375 Prevotella sp. oral clone ID019  
## 4 2691 Streptococcus rubneri  
## 5 1571 Prevotella buccae

Anything in the genus [*Capnocytophaga*](https://en.wikipedia.org/wiki/Capnocytophaga) is an opportunistic pathogen, so I say good riddance. Usually they’re fine, but if your immune system dips they can turn bad.

[Streptococcus rubneri](http://www.ncbi.nlm.nih.gov/pubmed/23749274) was discovered a couple years ago, so little is known about it.

[Prevotella buccae](https://microbewiki.kenyon.edu/index.php/Prevotella) is more interesting. It seems to be implicated in periodontal disease (yuk!) but that genus is involved too in breaking down proteins and carbohydrates.

Hard to say what’s really going on. Meanwhile, here are the biggest changes (increase) since the first sample:

junToOctCompare <- uBiome\_compare\_samples(junMouth,OctMouth)

## tax\_name count\_change  
## 64 Streptococcus pseudopneumoniae 62007  
## 68 Veillonella sp. oral taxon 780 8065  
## 41 Neisseria oralis 4693  
## 2 Abiotrophia sp. oral clone P4PA\_155 P1 2308  
## 28 Granulicatella elegans 1987

Whoah! That first one, *Streptococcus pseudopneumoniae*, looks nasty! [Wikipedia](https://en.wikipedia.org/wiki/Streptococcus_pseudopneumoniae) says it may cause pneumonia, though a recent medical journal says more hopefully that it [“treads the fine line between commensal and pathogen”](http://www.cmnewsletter.com/article/S0196-4399(14)00027-0/abstract?cc=y)

which is a scientific gobbleygook way of saying nobody has a clue. All the more reason to keep testing, submitting, and getting more data. I just sent two more kits to uBiome, and will let you know more as soon as I get back the results.