**A comparative study of the bacterial diversity and composition of nursery piglets’ oral fluid, feces, and housing environment**

Buiatte, et al.

**Summary of the netAnalyze function (NetCoMi Package) output for feces, pen floor and oral fluid samples**

**Feces**

**Component Sizes**

Size: 38 1  
#: 1 4

**Global Network Properties**

*Largest Connected Component (LCC):*

* Relative LCC Size: 0.90476
* Clustering Coefficient: 0.29894
* Modularity: 0.29251
* Positive Edge Percentage: 56.17978
* Edge Density: 0.12660
* Natural Connectivity: 0.04073
* Vertex Connectivity: 1.00000
* Edge Connectivity: 1.00000
* Average Dissimilarity\*: 0.95782
* Average Path Length\*\*: 1.90362

*Whole Network:*

* Number of Components: 5.00000
* Clustering Coefficient: 0.29894
* Modularity: 0.27200
* Positive Edge Percentage: 56.17978
* Edge Density: 0.10337
* Natural Connectivity: 0.03575 \*Dissimilarity = 1 - edge weight  
  \**Path length = Units with average dissimilarity*

**Clusters**

* In the whole network
* Algorithm: cluster\_louvain

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Name | 0 | 1 | 2 | 3 | 4 | 5 |
| # | 4 | 7 | 8 | 9 | 10 | 4 |

**Hubs**

In alphabetical/numerical order

Based on empirical quantiles of centralities

* Agathobacter
* Anaerovibrio
* Dialister

**Centrality Measures**

* In decreasing order
* Centrality of disconnected components is zero

*Degree (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Score** |
| *Anaerovibrio* | 0.31707 |
| *Sharpea* | 0.26829 |
| *Prevotella\_9* | 0.21951 |
| *Agathobacter* | 0.21951 |
| *Dialister* | 0.21951 |
| *Escherichia-Shigella* | 0.19512 |
| *Succinivibrio* | 0.19512 |
| *Intestinimonas* | 0.19512 |
| *Rikenellaceae* RC9 gut group | 0.17073 |
| *[Eubacterium] coprostanoligenes group* Family | 0.17073 |

*Betweenness Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Betweenness Centrality (Normalized)** |
| *Prevotella\_9* | 0.19820 |
| *Sharpea* | 0.17417 |
| *Agathobacter* | 0.15616 |
| *Anaerovibrio* | 0.14114 |
| *Blautia* | 0.13514 |
| *Succinivibrio* | 0.11862 |
| *Muribaculaceae* Family | 0.11712 |
| *Coprococcus* | 0.06156 |
| *Intestinimonas* | 0.05856 |
| *Dialister* | 0.05556 |

*Closeness Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Closeness Centrality (Normalized)** |
| *Anaerovibrio* | 0.96280 |
| *Agathobacter* | 0.92569 |
| *Sharpea* | 0.89050 |
| *Acidaminococcus* | 0.85145 |
| *Dialister* | 0.85118 |
| *Escherichia-Shigella* | 0.81279 |
| *Succinivibrio* | 0.81112 |
| *Megasphaera* | 0.80881 |
| *Prevotella\_9* | 0.79607 |
| *Intestinimonas* | 0.78934 |

*Eigenvector Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Eigenvector Centrality (Normalized)** |
| *Anaerovibrio* | 1.00000 |
| *Agathobacter* | 0.93095 |
| *Dialister* | 0.80135 |
| *Acidaminococcus* | 0.79409 |
| *Megasphaera* | 0.73981 |
| *Escherichia-Shigella* | 0.48395 |
| *[Eubacterium] coprostanoligenes* group Family | 0.47010 |
| *Rikenellaceae* RC9 gut group | 0.43101 |
| *Prevotella\_9* | 0.40535 |
| *Succinivibrio* | 0.39839 |

**Pen floor**

**Component Sizes**

Size: 87  
#: 1

**Global Network Properties**

***Whole Network:***

* Number of Components: 1.00000
* Clustering Coefficient: 0.55057
* Modularity: 0.09941
* Positive Edge Percentage: 48.77743
* Edge Density: 0.42609
* Natural Connectivity: 0.11618
* Vertex Connectivity: 19.00000
* Edge Connectivity: 19.00000
* Average Dissimilarity\*: 0.86433
* Average Path Length\*\*: 1.00739  
  \*Dissimilarity = 1 - edge weight  
  \**Path length = Units with average dissimilarity*

**Clusters**

* In the whole network
* Algorithm: cluster\_louvain

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Name** | **1** | **2** | **3** | **4** |
| **#** | 27 | 22 | 14 | 24 |

**Hubs**

In alphabetical/numerical order

Based on empirical quantiles of centralities

* *[Eubacterium] coprostanoligenes group Family*
* *Candidatus Saccharimonas*
* *Clostridium sensu stricto 6*
* *Muribaculaceae Family*
* *Prevotella\_9*

**Centrality Measures**

* In decreasing order
* Computed for the complete network

*Degree (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Degree (Normalized)** |
| *[Eubacterium] coprostanoligenes group* Family | 0.79070 |
| *Clostridium sensu stricto 6* | 0.70930 |
| *Sharpea* | 0.61628 |
| *Agathobacter* | 0.61628 |
| *Prevotella\_9* | 0.60465 |
| *Muribaculaceae* Family | 0.59302 |
| *Coprococcus* | 0.58140 |
| *Terrisporobacter* | 0.55814 |
| *Selenomonadaceae* Family | 0.55814 |
| *Butyricicoccus* | 0.55814 |

*Betweenness Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Betweenness Centrality (Normalized)** |
| *Clostridium sensu stricto 6* | 0.05773 |
| *[Eubacterium] coprostanoligenes group* Family | 0.03365 |
| *Collinsella* | 0.01970 |
| *Faecalibacterium* | 0.01778 |
| *Anaerovibrio* | 0.01696 |
| *Lactobacillus* | 0.01532 |
| *Sharpea* | 0.01532 |
| *Olsenella* | 0.01423 |
| *Weissella* | 0.01368 |
| *Agathobacter* | 0.01341 |

*Closeness Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Closeness Centrality (Normalized)** |
| *Clostridium sensu stricto 6* | 1.49944 |
| *Muribaculaceae* Family | 1.37060 |
| *Prevotella* | 1.34886 |
| *[Eubacterium] coprostanoligenes group* Family | 1.32607 |
| *Prevotella\_9* | 1.26252 |
| *Sharpea* | 1.24624 |
| *Candidatus Saccharimonas* | 1.24233 |
| *Schwartzia* | 1.22684 |
| *Terrisporobacter* | 1.22385 |
| *Prevotellaceae* UCG-004 | 1.22068 |

*Eigenvector Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Eigenvector Centrality (Normalized)** |
| *[Eubacterium] coprostanoligenes group* Family | 1.00000 |
| *Clostridium sensu stricto 6* | 0.94731 |
| *Muribaculaceae* Family | 0.86290 |
| *Prevotella\_9* | 0.80205 |
| *Candidatus Saccharimonas* | 0.75930 |
| *Prevotella* | 0.75305 |
| *Prevotellaceae* UCG-004 | 0.75041 |
| *Aerococcus* | 0.74514 |

**Oral fluid**

**Component Sizes**

Size: 39 1  
#: 1 3

**Global Network Properties**

*Largest Connected Component (LCC):*

* Relative LCC Size: 0.92857
* Clustering Coefficient: 0.43246
* Modularity: 0.35496
* Positive Edge Percentage: 60.90909
* Edge Density: 0.14845
* Natural Connectivity: 0.04317
* Vertex Connectivity: 1.00000
* Edge Connectivity: 1.00000
* Average Dissimilarity\*: 0.94864
* Average Path Length\*\*: 1.57705  
  \*Dissimilarity = 1 - edge weight  
  \**Path length = Units with average dissimilarity*

*Whole Network:*

* Number of Components: 4.00000
* Clustering Coefficient: 0.43246
* Modularity: 0.32397
* Positive Edge Percentage: 60.90909
* Edge Density: 0.12776
* Natural Connectivity: 0.03910

**Clusters**

* In the whole network
* Algorithm: cluster\_louvain

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Name** | **0** | **1** | **2** | **3** | **4** | **5** |
| # | 3 | 9 | 7 | 5 | 10 | 8 |

**Hubs**

In alphabetical/numerical order

Based on empirical quantiles of centralities

* *Olsenella*
* *Sharpea*
* *Streptococcus*

**Centrality Measures**

* In decreasing order
* Centrality of disconnected components is zero

*Degree (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Degree (Normalized)** |
| *Streptococcus* | 0.34146 |
| *Sharpea* | 0.34146 |
| *Dialister* | 0.29268 |
| *Olsenella* | 0.26829 |
| *Moraxella* | 0.24390 |
| *Butyricicoccaceae* Family | 0.24390 |
| *Agathobacter* | 0.21951 |
| *Megasphaera* | 0.19512 |
| *Clostridium* sensu stricto 1 | 0.19512 |
| *Faecalibacterium* | 0.19512 |

*Betweenness Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Betweenness Centrality (Normalized)** |
| *Streptococcus* | 0.14367 |
| *Moraxella* | 0.14367 |
| *Butyricicoccaceae* Family | 0.13371 |
| *Sharpea* | 0.12091 |
| *Agathobacter* | 0.11522 |
| *Anaerovibrio* | 0.10669 |
| *Megasphaera* | 0.10526 |
| *Dialister* | 0.10242 |
| *Catenibacterium* | 0.07397 |
| *Veillonella* | 0.07255 |

*Closeness Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Closeness Centrality (Normalized)** |
| *Sharpea* | 1.04432 |
| *Streptococcus* | 1.02129 |
| *Olsenella* | 0.97870 |
| *Dialister* | 0.94262 |
| *Butyricicoccaceae* Family | 0.92928 |
| *Agathobacter* | 0.92695 |
| *Moraxella* | 0.89717 |
| *Anaerovibrio* | 0.88866 |
| *Fournierella* | 0.87079 |
| *Megasphaera* | 0.86339 |

*Eigenvector Centrality (Normalized):*

|  |  |
| --- | --- |
| **Genus** | **Eigenvector Centrality (Normalized)** |
| *Sharpea* | 1.00000 |
| *Olsenella* | 0.96264 |
| *Streptococcus* | 0.92285 |
| *Fournierella* | 0.69748 |
| *Coriobacteriaceae* UCG-002 | 0.60608 |
| *Incertae Sedis* | 0.55376 |
| *Catenisphaera* | 0.52986 |
| *Terrisporobacter* | 0.48983 |
| *Dialister* | 0.46282 |
| *Agathobacter* | 0.41658 |

This dataset can also be assessed by running the corresponding script of each network analysis in R. Scripts are available in the Github page provided in this article.