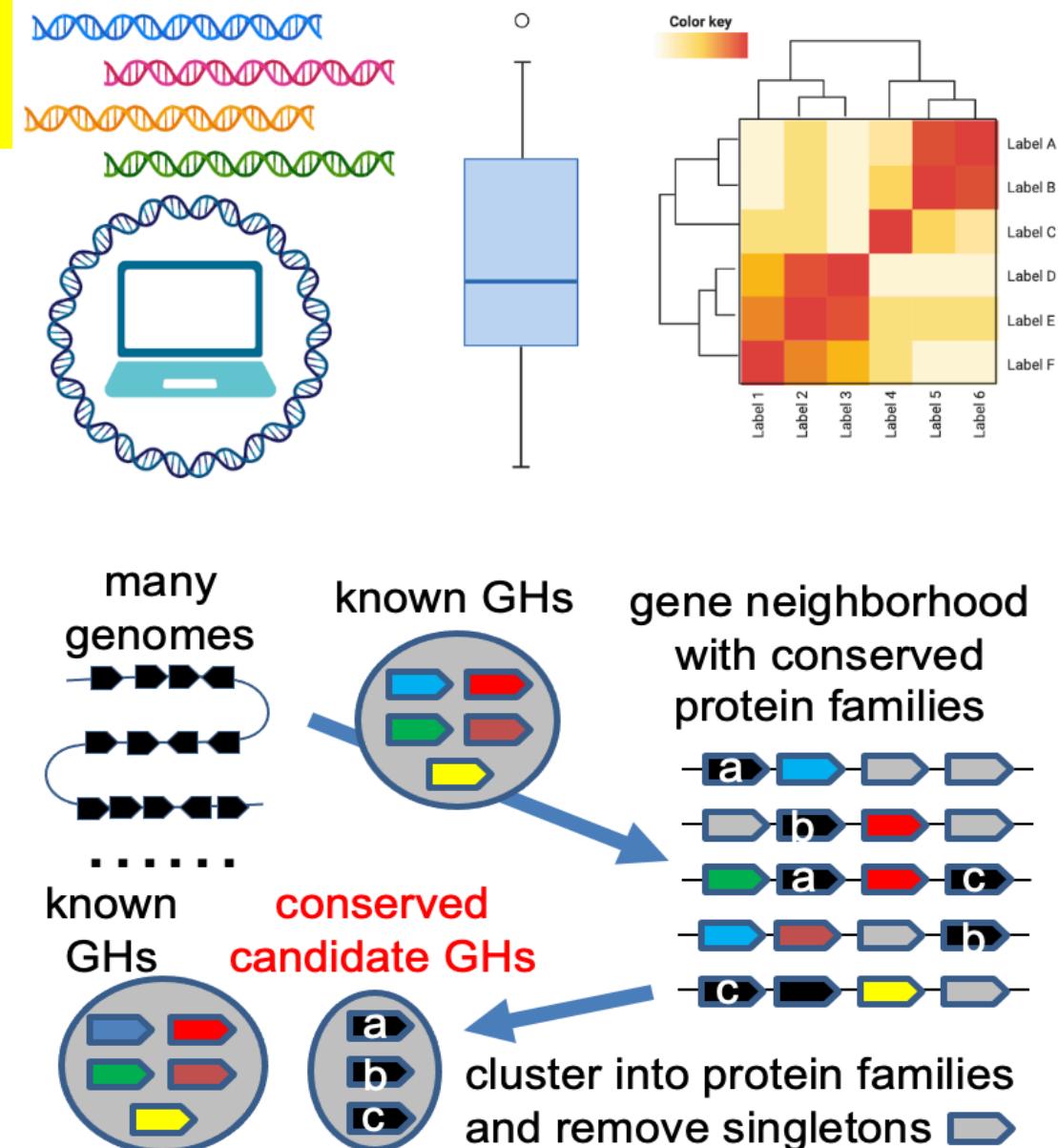


Choose a day and RSVP: <https://www.when2meet.com/?15855740-coIPZ>

Computational Biology Summer Workshop

- **Free** to anyone with life/agricultural science background
- Organized by **Dr. Yanbin Yin**, Associate Prof of Nebraska Food for Health Center & Food Science & Tech Dept
- Taught by **experienced bioinformatics postdocs and students** of NFHC
- Practical **Bash, Python and R skills** to analyze sequencing data and produce publishable graphs
- **Hands-on project** of (meta)genome mining for carbohydrate active enzymes as a case study
- **Date:** A half day (4h) of the 3rd week (20-23) of June will be chosen according to a **time survey** (see the top)
- **Location:** In person at **Food Innovation Center 220**



Schedule (June 20 and 23, FIC 111)

Time	Presenter	Topic
12:00-12:30pm	Yanbin	Introduction to the workshop & project
12:30-1:00pm	Tang	UHGG Bacteroides MAGs & stat visualization
1:00-1:45pm	Yuchen	CAZyme & CGC annotation & stat visualization
1:45-2:30pm	Yuchen	Anvio pan-genome analysis & phylogeny visualization
2:30-2:45pm		Break
2:45-3:30pm	Bowen	Pfam annotation & protein seq clustering of nSGs & visualization
		Glycan substrate prediction & CGC clustering & network visualization
3:30-4:15pm	Tang	
4:15-5:00pm	Jinfang	ML prediction for new GH/PL from conserved nSGs

acknowledgements

Jerry

Arthur

Ved



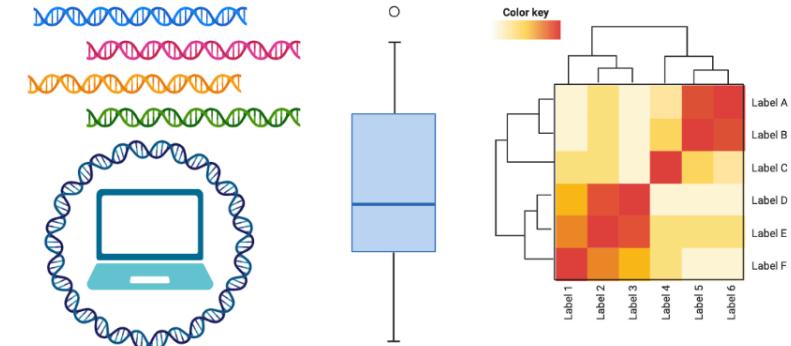
Yuchen

Tang

Bowen

Jinfang

what you need to know



- use holland computing cluster so **bring a laptop and have an HCC account**
- hands-on activities with a **real-world genome mining project**
- **focus on data visualization** during workshop demonstration
- some data computing takes long time, but all **intermediate files and codes are provided**
- use **HCC OnDemand** -> R studio + Shell terminal

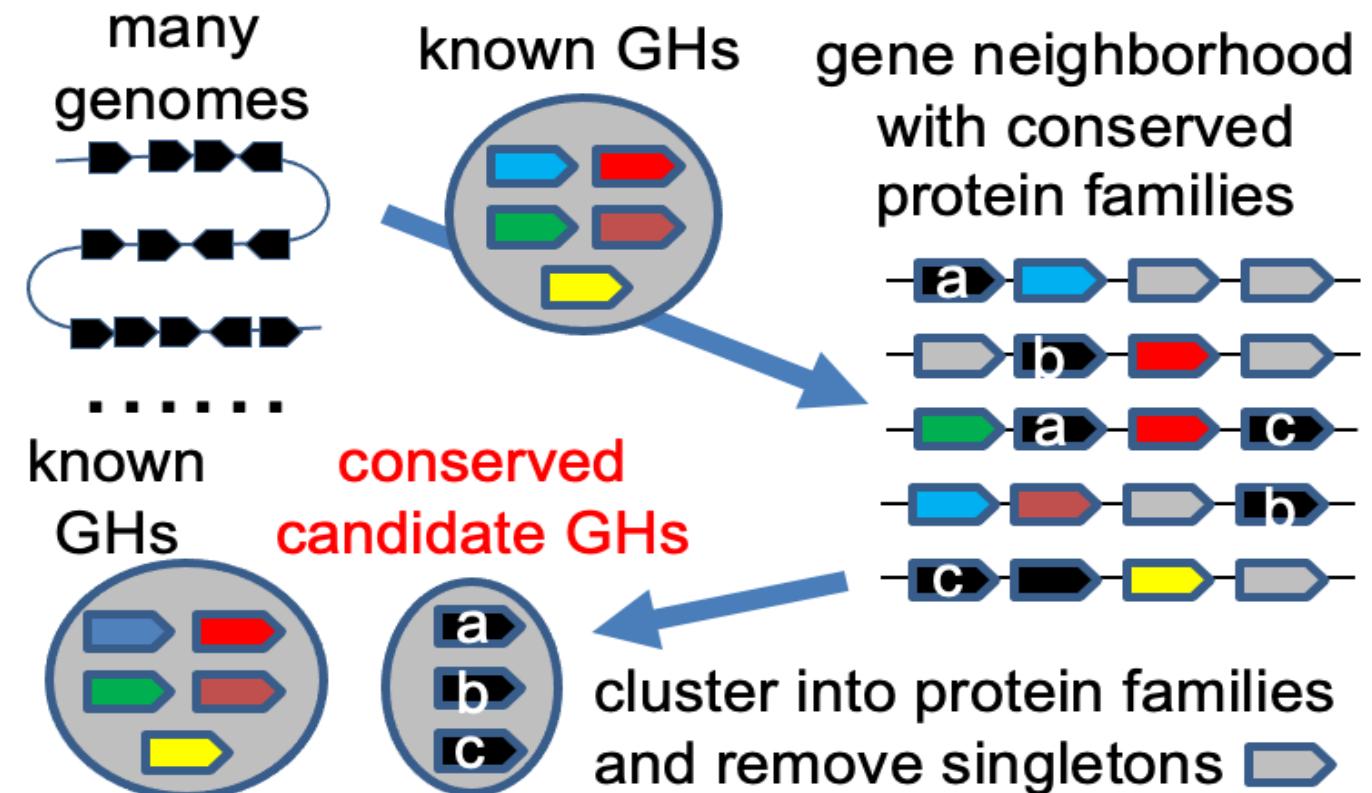
lower your expectations



- don't expect you will understand/learn everything we say
- it is okay if you can't follow every step (all the codes and files are provided)
- the instructors won't have time to explain all the codes (it's a win as long as you can get the right graphs/files)
- questions are welcomed, but we will try to stay on time

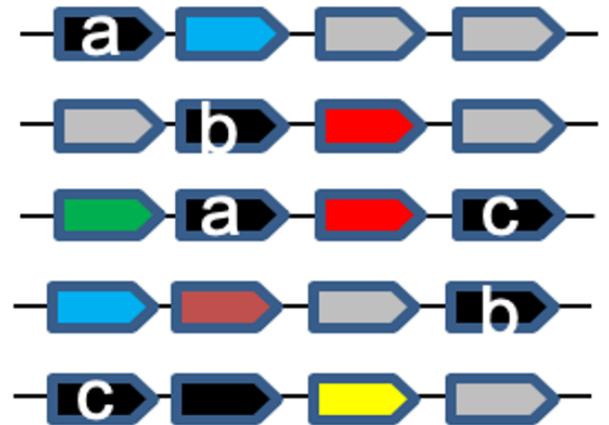
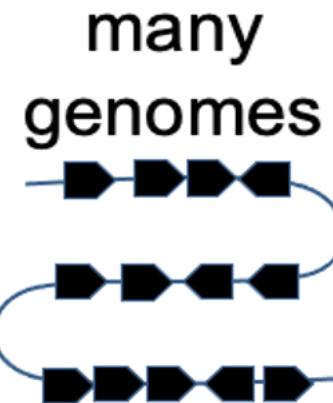
about the project

- a new project from a recent proposal
- it will or should work
- input -> genomes,
output -> new GH predictions
- our focus is data analysis and visualization



steps

- input -> 45 *Bacteroides* genomes from human gut
- find CAZymes and CGCs (CAZyme gene clusters)
- find null or non-signature genes in CGCs
- cluster nSGs into families
- predict the likelihood of conserved nSG families to be new CAZymes



(meta)genome mining

Targeted search of genomes for specific pathways or genes with important economic values using advanced computational data mining approaches

Review Article | [Published: 03 June 2021](#)

Mining genomes to illuminate the specialized chemistry of life

[Marnix H. Medema](#), [Tristan de Rond](#) & [Bradley S. Moore](#) 

[Nature Reviews Genetics](#) **22**, 553–571 (2021) | [Cite this article](#)

7427 Accesses | **26** Citations | **110** Altmetric | [Metrics](#)

Systematic discovery of antiphage defense systems in the microbial pangenome

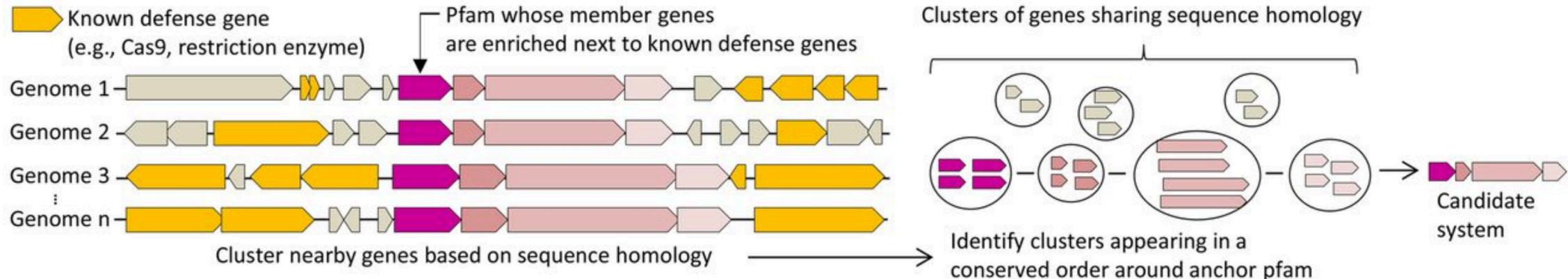
Shany Doron^{*}, Sarah Melamed^{*}, Gal Ofir, Azita Leavitt, Anna Lopatina, Mai Keren, Gil Amitai, Rotem Sorek[†]

^{*} See all authors and affiliations

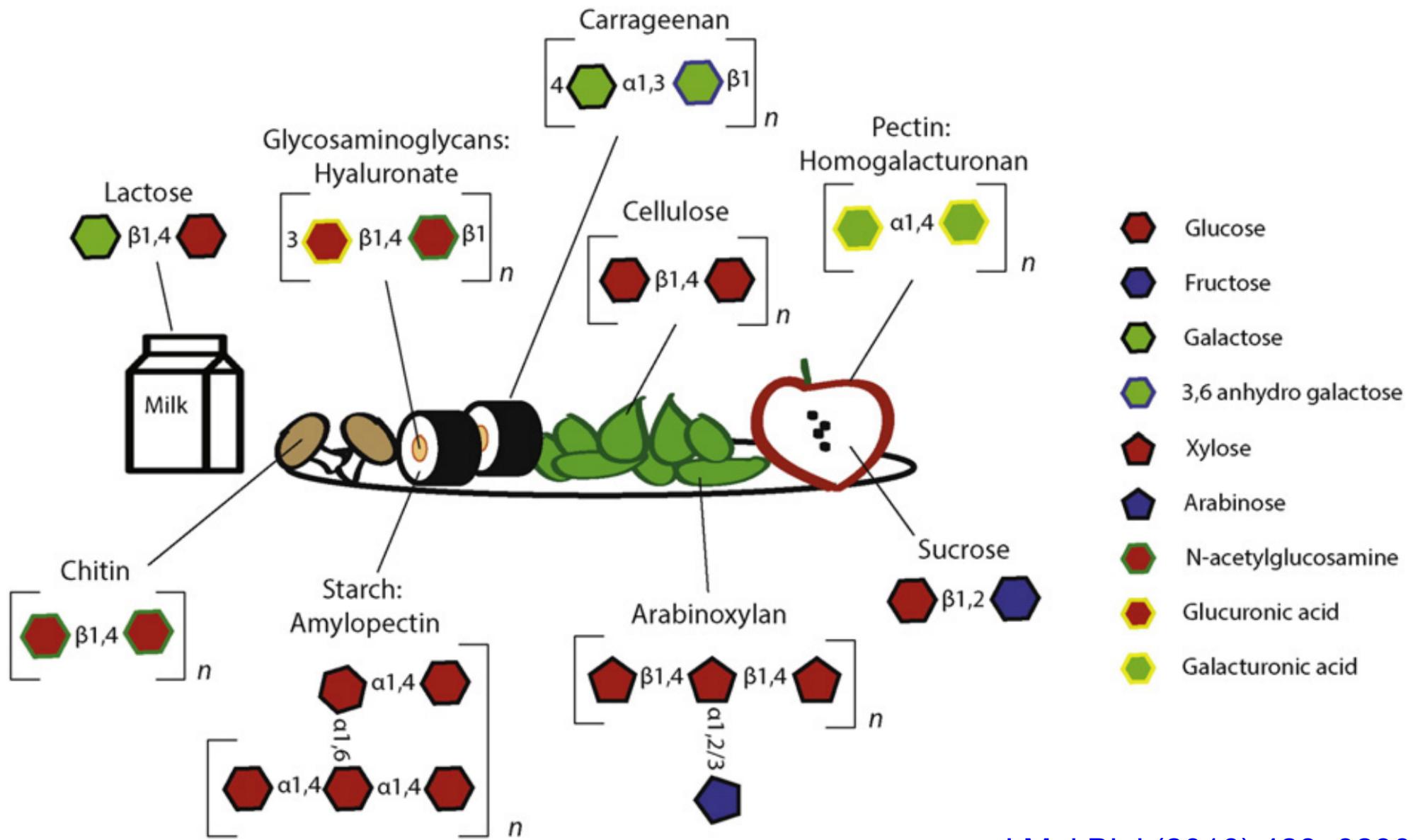
Science 02 Mar 2018;
Vol. 359, Issue 6379, eaar4120
DOI: 10.1126/science.aar4120

Defense island: gene clusters that encode antiphage defense genes

A



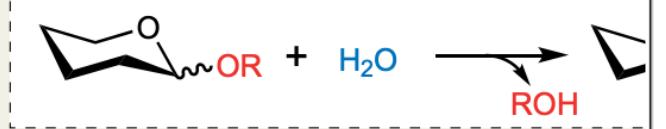
a high diversity of dietary carbohydrates



diverse glycosidic linkages exist in the dietary carbs

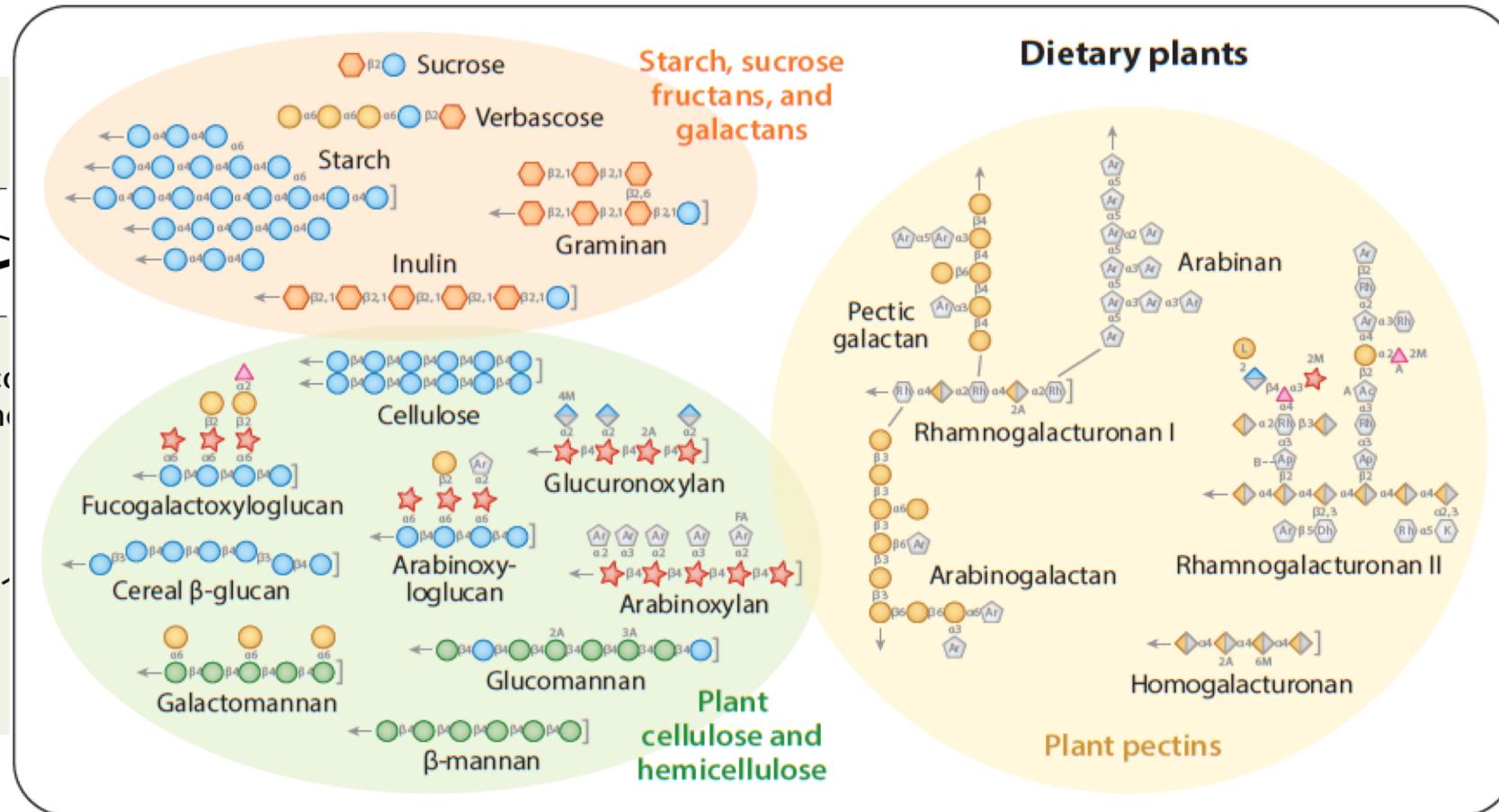
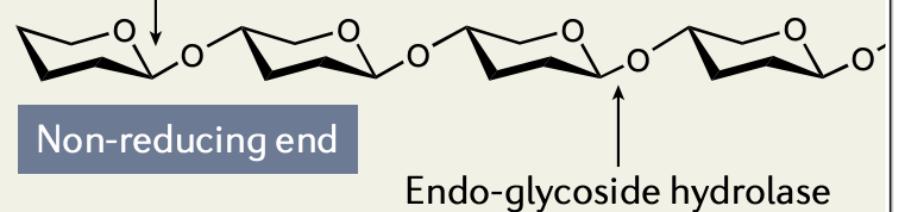
Nature Reviews Microbiology (2022)

Glycoside hydrolases



R = Monosaccharide, oligosaccharide or polysaccharide or aglycone

Exo-glycoside hydrolase

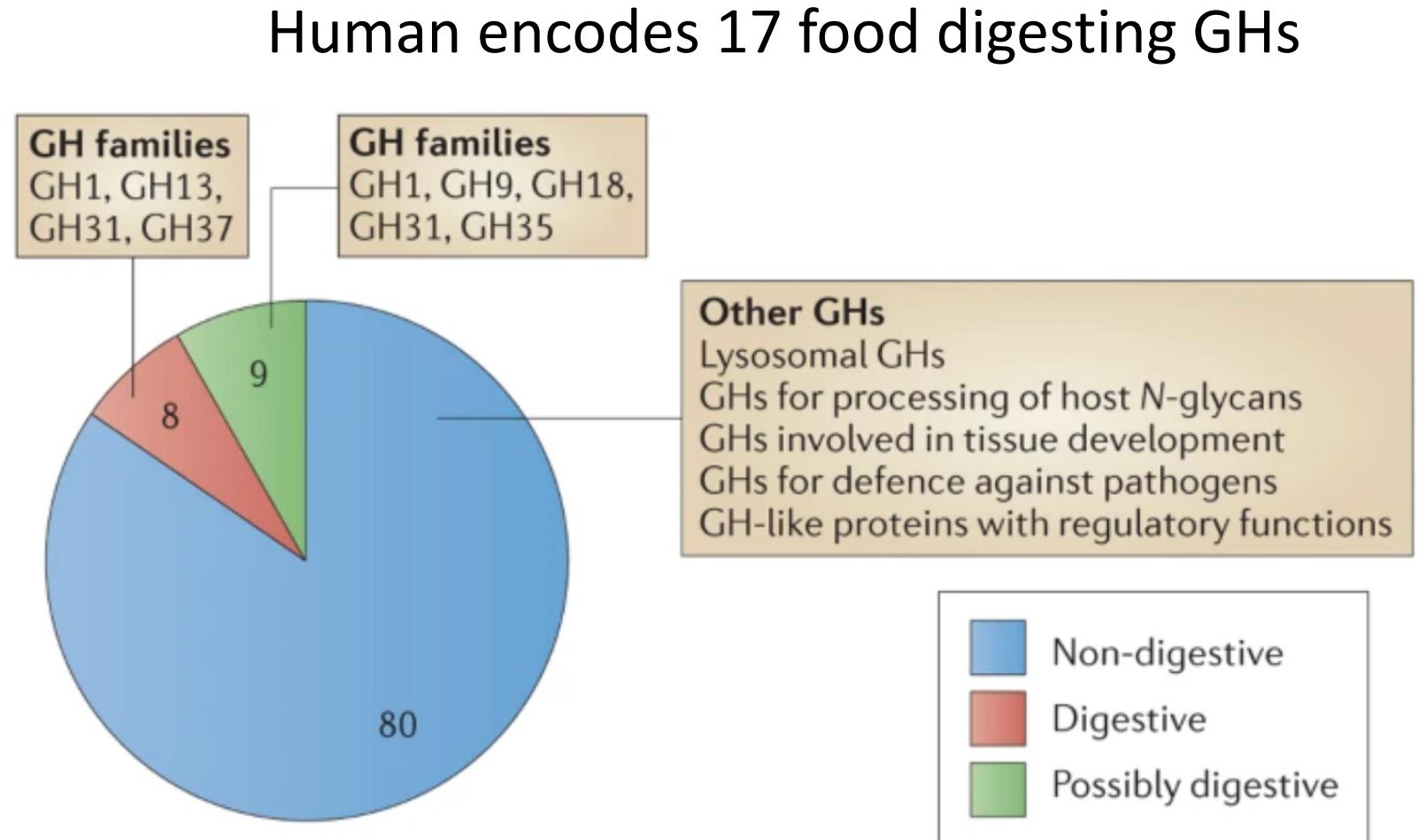


Annu. Rev. Microbiol (2017) 71:349–69

diverse glycosidic linkages need various CAZymes to break

<http://www.cazy.org/>

- GlycosylTransferases (GTs): 115
- Glycoside Hydrolases (GHs): 172
- Polysaccharide Lyases (PLs): 42
- Carbohydrate Esterases (CEs): 19
- Auxiliary Activities (AAs): 17
- Carbohydrate-Binding Modules (CBMs): 89



Cantarel B. et al. 2009, *Nucleic Acids Res*
Lombard V. et al. 2014, *Nucleic Acids Res*

NATURE REVIEWS | MICROBIOLOGY, doi:10.1038/nrmicro3050, Kaoutari, 2013

gut bacteria dedicate > 6% of their genes to CAZymes

Bacterium	Total CAZymes	GH	GT	PL	CE	Total CBMs
<i>Bacteroides thetaiotaomicron</i> VPI-5482	386	263	87	16	20	31
<i>B. xyloisolvans</i> XB1A*	349	224	81	22	22	26
<i>B. vulgatus</i> ATCC-8482	279	177	78	7	17	18
<i>B. fragilis</i> 638R	223	138	78	1	6	26
<i>Roseburia intestinalis</i> XB6B4*	175	115	46	0	14	11
<i>Butyrivibrio fibrisolvans</i> 16/4*	115	75	37	0	3	31
<i>Ruminococcus chamanellensis</i> 18P13*	87	54	12	9	12	34
<i>Bifidobacterium adolescentis</i> ATCC15703	94	54	37	0	3	6

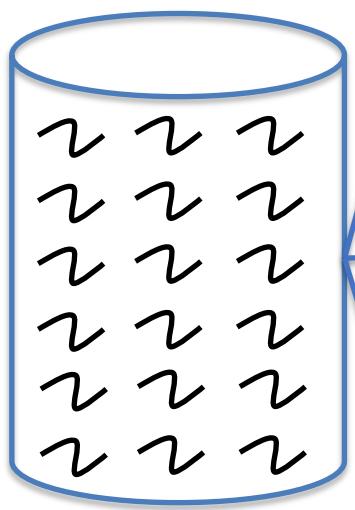
Gut Microbes 3:4, 289-306; 2012

1000 (species) x 100 (genes) = 100,000 CAZymes

dbCAN2 combines three tools for CAZyme genome mining



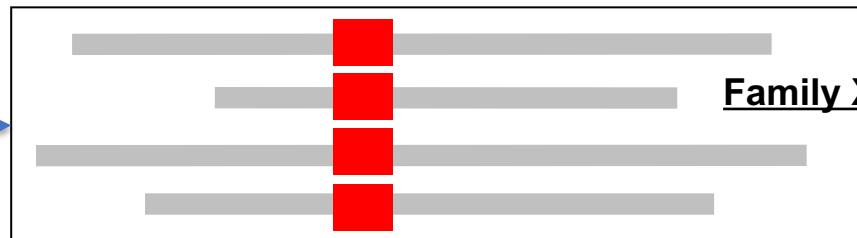
New genome



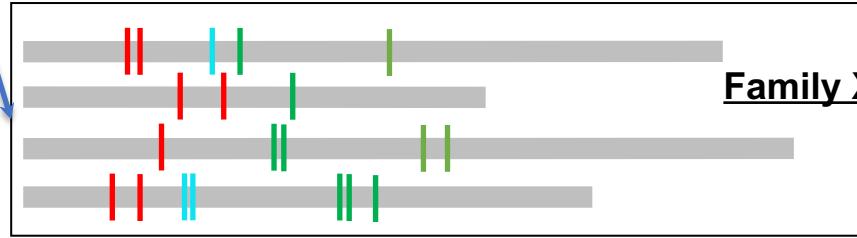
BLAST vs. CAZy (before 2012)



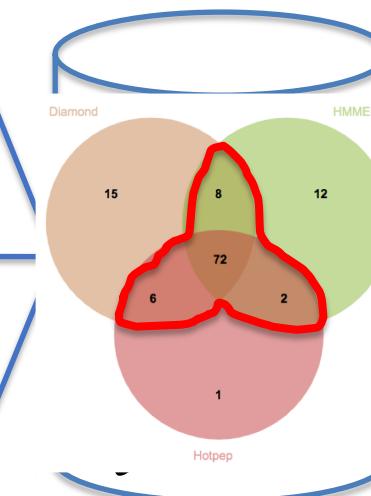
HMMER vs. dbCAN (after 2012)



eCAMI (after 2017)



CAZymes



Tanner

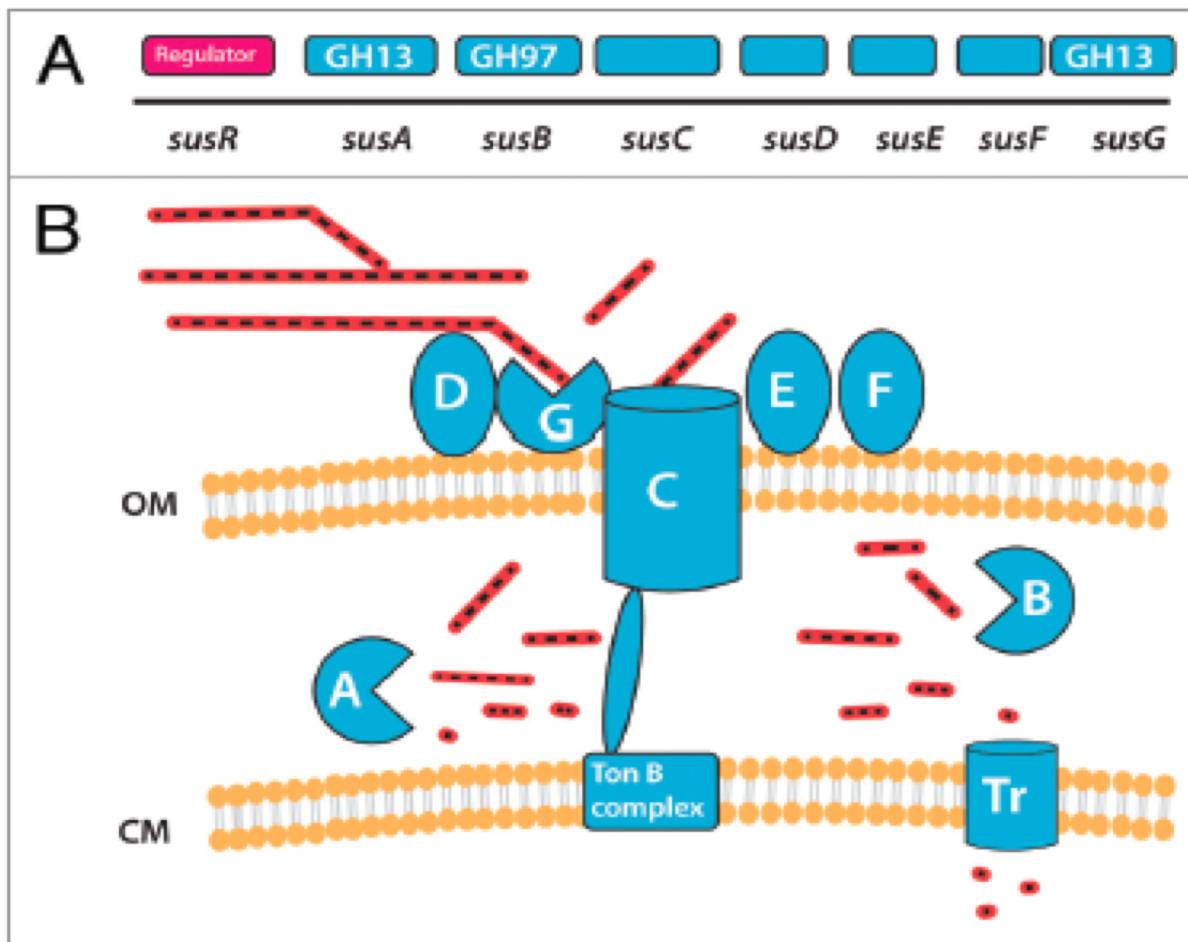


Le

*dbCAN: Yin et al, Nucleic acids research 2012
eCAMI: Xu J et al., Bioinformatics, 2020*

PUL: polysaccharide utilization loci

Sus in *Bacteroides thetaiotaomicron*



Gut Microbes 3:4, 289-306; 2012

Species	Number of PULs ^a	Habitat
<i>Bacteroides thetaiotaomicron</i>	90	Gut
<i>Bacteroides ovatus</i>	118	Gut
<i>Bacteroides fragilis</i>	60	Gut
<i>Bacteroides xylanisolvans</i>	100	Gut
<i>Proteiniphilum acetatigenes</i>	77	Wastewater sludge
<i>Chitinophaga pinensis</i>	106	Soil
<i>Chitinophaga niabensis</i>	153	Soil
<i>Cytophaga hutchinsonii</i>	2	Soil
<i>Flavobacterium johnsoniae</i>	40	Soil/freshwater
<i>Prevotella melaninogenica</i>	25	Upper respiratory tract
<i>Prevotella salivae</i>	32	Mouth
<i>Prevotella ruminicola</i>	24	Rumen
<i>Zobellia galactanivorans</i>	61	Marine

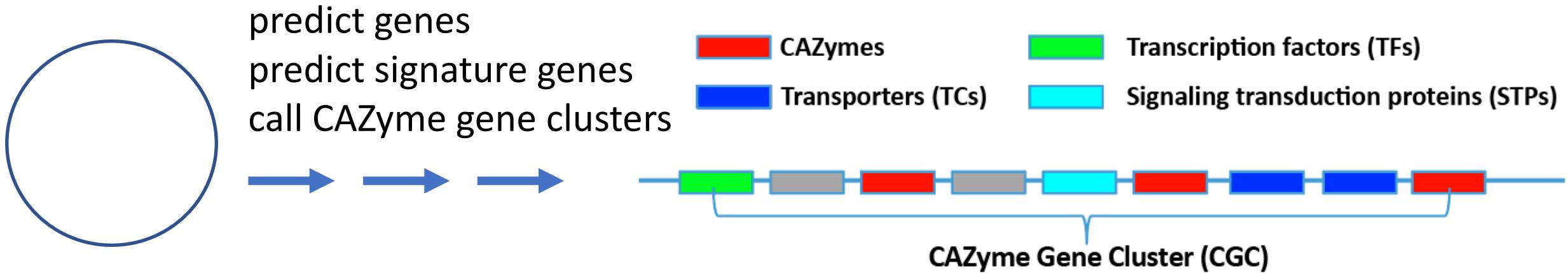
Environmental Microbiology Reports (2021)

CGC-Finder: predict CAZyme gene clusters from (meta)genomes

Huang et al., Nucleic Acids Res 2018



Le



The distance threshold:

how many **non-signature genes** are inserted between two adjacent signature genes

Summary



a very high diversity of carbs in our diet (other environment too)

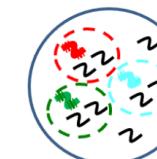
dbCAN -> automated CAZyme genome mining

dbCAN-PUL -> literature derived PULs with known carb substrates

complex carb degrading genes form gene clusters in genomes

CGC-Finder can mine for these CGCs (without substrates)

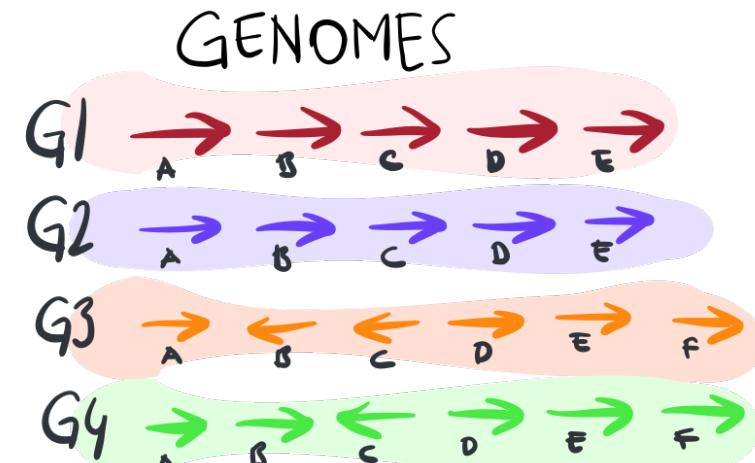
dbCAN-seq



dbCAN-sub
Subfamily → EC → substrates



pan-genomics



GENES FASTA

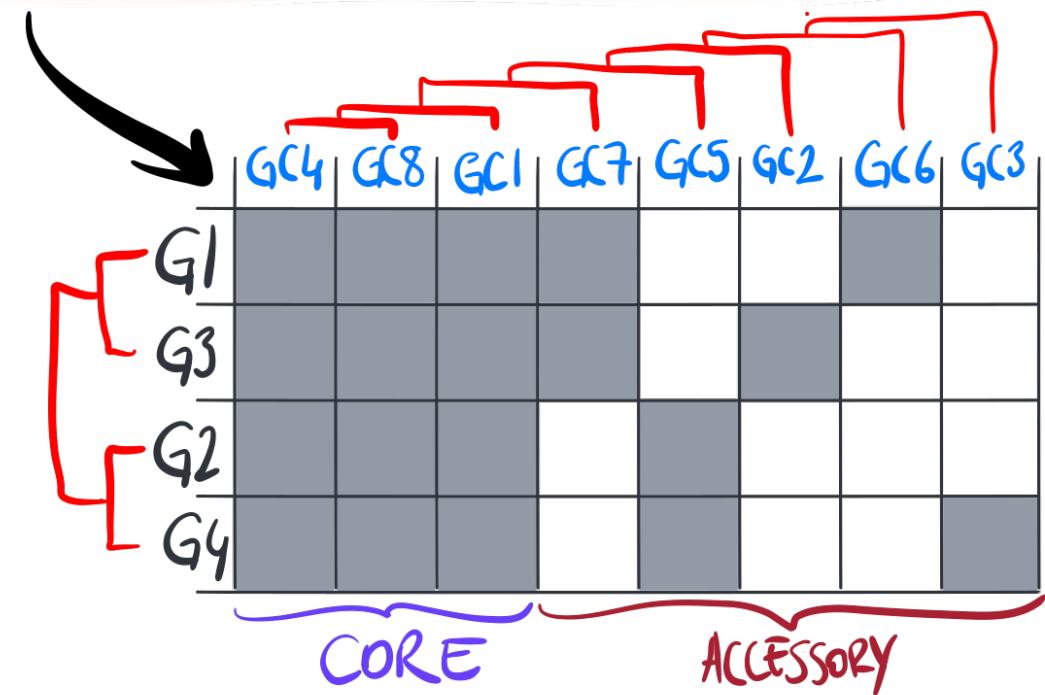
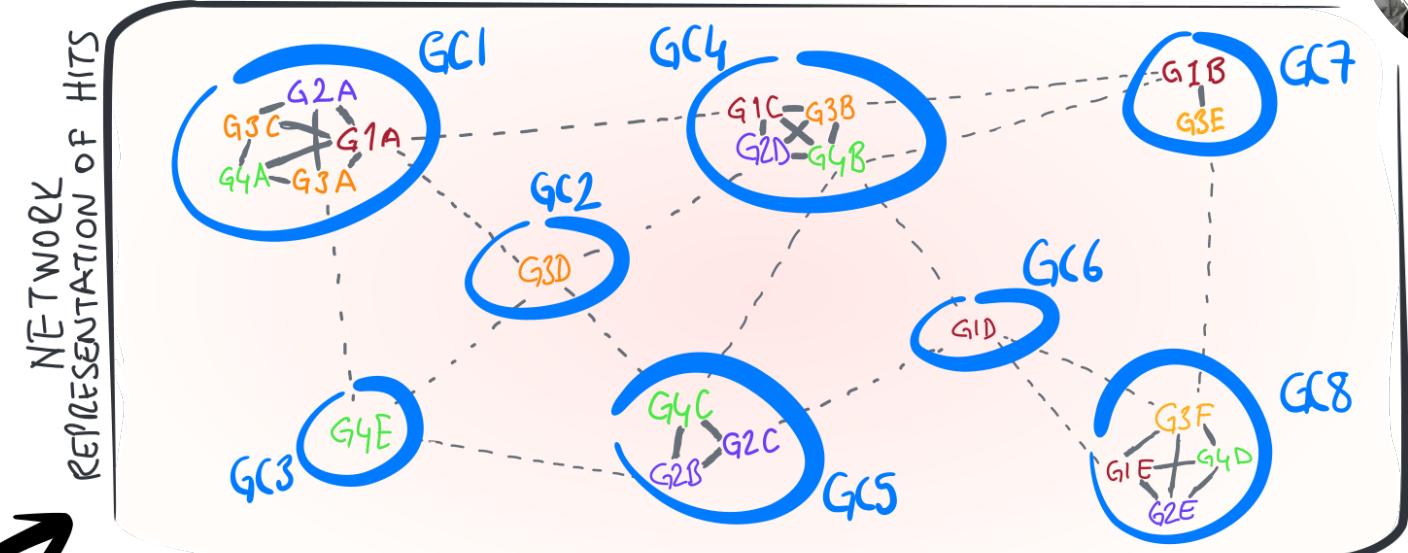
```
> G1A MSKYLLEIGTEELP...
> G1B MRRIVLFLTRKGFA...
> G1C MDFVFGKKVRKGE...
(... 4 more...)
> G2C MSKYLTEIGPEELI...
> G2D MPFVFGKLVRLE...
(... 11 more...)
> G4E MSKYLTEIGPEELI...
> G4F MRLIVLTLTRKLFA...
```

BLAST SEARCH

BLAST DB

BLAST HITS

G1A → G1A	100%
G1A → G1B	0%
G1A → G1C	4%
(...)	
G1A → G2A	97%
(...)	
G1A → G3A	94%
G1A → G3B	0%
G1A → G3C	92%
(...)	
G3A → G3A	100%
G3A → G3B	0%
G3A → G3C	96%
(...)	
G4F → G4F	100%



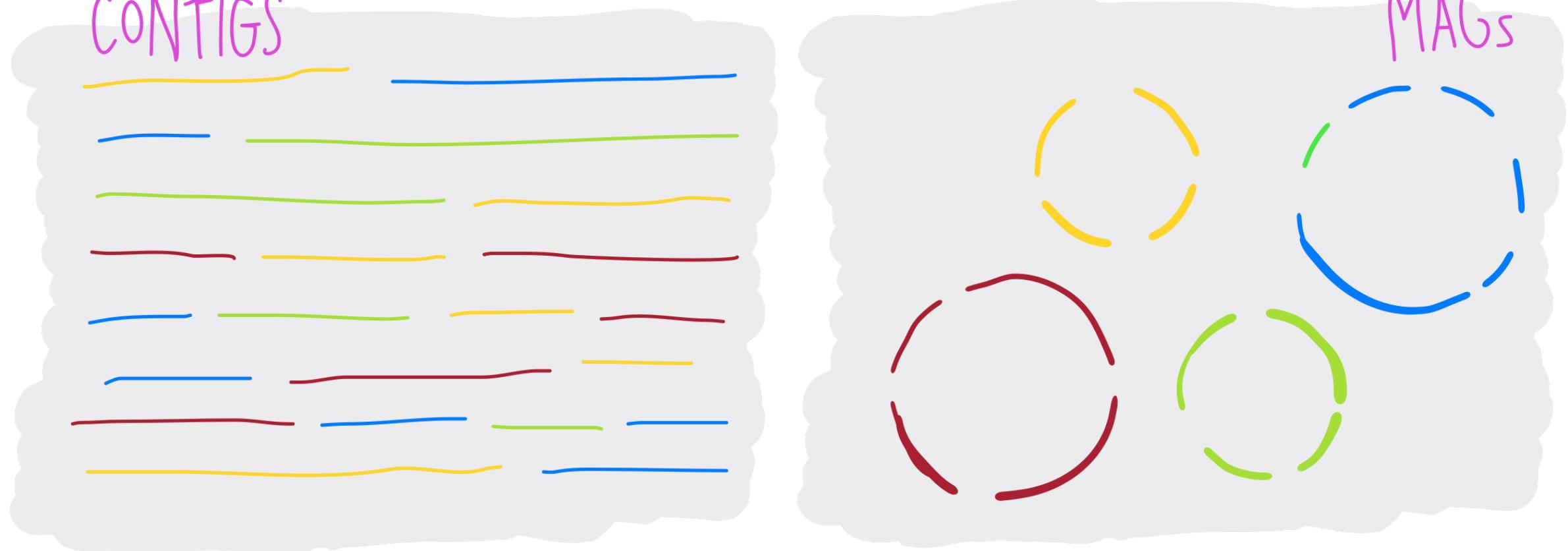
MAGs

SEQUENCE COMPOSITION

CONTIGS

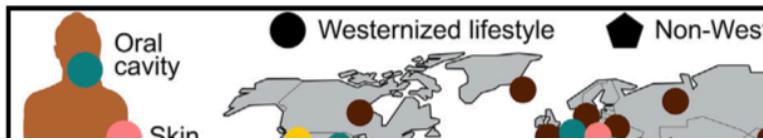
MAGs

DIFFERENTIAL COVERAGE



Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle

Graphical Abstract



Article | Open Access | Published: 11 February 2019

A new genomic blueprint of the human gut microbiota

Alexandre Almeida [✉](#), Alex L. Mitchell, Miguel Boland, Samuel C. Forster, Gregory B. Gloor, Aleksandra Tarkowska, Trevor D. Lawley & Robert D. Finn [✉](#)

Nature 568, 499–504 (2019) | [Cite this article](#)

126k Accesses | 445 Citations | 700 Altmetric | [Metrics](#)

Article | Open Access | Published: 13 March 2019

New insights from uncultivated genomes of the global human gut microbiome

JGI

Stephen Nayfach [✉](#), Zhou Jason Shi, Rekha Seshadri, Katherine S. Pollard & Nikos C. Kyrpides [✉](#)

Nature 568, 505–510 (2019) | [Cite this article](#)

60k Accesses | 223 Citations | 208 Altmetric | [Metrics](#)

EBI

HBC, CGR

Forster, S. C. et al. A human gut bacterial genome and culture collection for improved metagenomic analyses. *Nat. Biotechnol.* 37, 186–192 (2019).

Zou, Y. et al. 1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. *Nat. Biotechnol.* 37, 179–185 (2019).

Schedule (June 20 and 23, FIC 111)

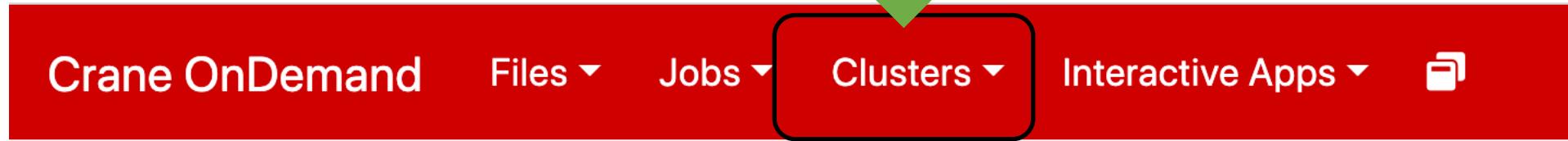
Time	Presenter	Topic
12:00-12:30pm	Yanbin	Introduction to the workshop & project
12:30-1:00pm	Tang	UHGG Bacteroides MAGs & stat visualization
1:00-1:45pm	Yuchen	CAZyme & CGC annotation & stat visualization
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2:30-2:45pm		Break
2:45-3:30pm	Bowen	Pfam annotation & protein seq clustering of nSGs & visualization
		Glycan substrate prediction & CGC clustering & network visualization
3:30-4:15pm	Tang	
4:15-5:00pm	Jinfang	ML prediction for new GH/PL from conserved nSGs

How to Use Crane OnDemand for the Workshop ?

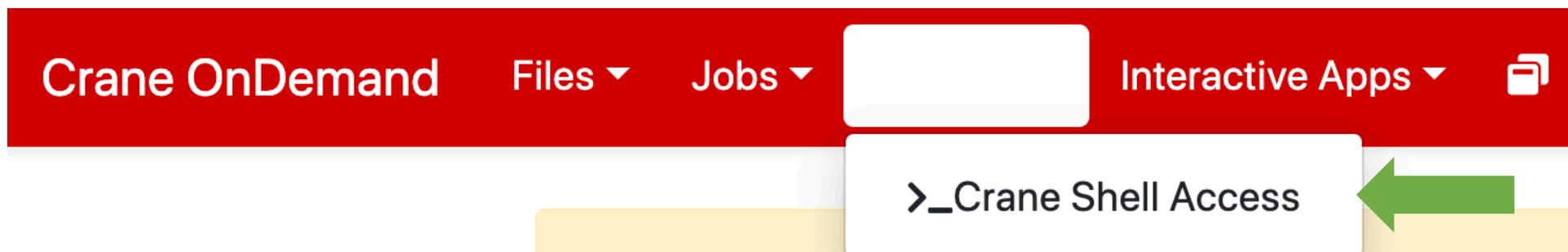


❖Crane OnDemand

1. Click or copy the link to your browser: <https://crane-ood.unl.edu/pun/sys/dashboard>
2. Login using your HCC account.
3. Click “**Clusters**” at the top bar.



4. Select and click the “**_Crane Shell Access**”



❖ Copy folder and open tutorial HTML

Step 1: Change directory from HOME to WORK: `cd $WORK`

```
[tangli@login.crane ~]$ cd $WORK
```

Step 2: Copy all materials to your working directory:

```
cp -r /work/yinlab/tangli/workshop_2022 . &
```

```
cp -r /work/yinlab/tangli/workshop_2022_backup . &
```

Step 3: Click or copy this link to your browser to open GitHub page:

https://github.com/tli14/Workshop_2022_YinLab.

Step 4: Open tutorial HTML file in GitHub page.

☞ Tutorial HTML:

Click this ➔

- [UHGG Genomes](#): UHGG Bacteroides isolate genomes/MAGs & statistics visualization.

Step 5: Follow the tutorial HTML. Copy and paste each cmd to your “Crane shell” and run it.

UHGG Genomes

1. Select Bacteroides genomes from UHGG

```
In [1]: # Change your directory to UHGG_genomes folder  
cd $WORK/workshop_2022/UHGG_genomes
```

```
In [2]: # Check your working directory  
pwd  
  
/work/yinlab/tangli/workshop_2022/UHGG_genomes
```

```
In [3]: # Select all genomes from Bacteroides genus.  
cat genomes-all_metadata.tsv | grep "s__Bacteroides" > Bacteroides_metadata.tsv
```

```
In [4]: # Covert dos to unix format.  
dos2unix Bacteroides_metadata.tsv  
  
dos2unix: converting file Bacteroides_metadata.tsv to Unix format...
```

```
In [5]: # Select representative genome ids.  
cat genomes-all_metadata.tsv | grep "s__Bacteroides" | cut -f 14 | sort | uniq > spe_list.txt
```

```
In [6]: # Select representative genomes from file.  
python extract_info.py Bacteroides_metadata.tsv spe_list.txt
```

□ Part 1

UHGG Genomes

Unified Human Gastrointestinal Genome (UHGG)

- A total of **289,232** prokaryotic genomes from the human gut microbiome were clustered into **4,744** species representatives.

MGnify Overview Submit data Text search Sequence search Browse data API About Help Login

Biome	Accession	Length	Num. of genomes	Completeness	Contamination	Type	Taxonomy	Last Updated
	MGYG000000001	3219617	4	98.59	0.7	Isolate	GCA-900066495 sp902362365	12/7/2021
	MGYG000000002	4433109	359	99.37	0	Isolate	Blautia_A faecis	12/7/2021
	MGYG000000003	3229518	1181	100	0	Isolate	Alistipes shahii	12/7/2021
	MGYG000000004	3698896	25	98.66	0.22	Isolate	Anaerotruncus colihominis	12/7/2021
	MGYG000000005	3930428	2	99.3	0	Isolate	Terrisporobacter glycolicus_A	12/7/2021

Unified Human Gastrointestinal Genome (UHGG)

- The “[genomes-all_metadata.tsv](#)” was downloaded from this web link:
http://ftp.ebi.ac.uk/pub/databases/metagenomics/mgnify_genomes/human-gut/v2.0
- **Bacteroides:** one of the most important genus in human gut microbiome; CAZyme and PULs are well-studied for this genus.

❖ 45 Bacteroides genomes from UHGG

1. Select representative species genomes in Bacteroides genus (n=45).
2. Download genomes.
3. Collect metadata information: genome id, species name, genome types, genome length, protein count, contig N50, completeness, country and continent.
4. Visualize metadata information for 45 genomes.

Use Crane OnDemand Rstudio server:

1. Click “**Interactive Apps**” at the top bar.
2. Click “**Rstudio Server**” to start the Rstudio.

Desktops



GUIs



3D Slicer: Crane

COMSOL Multiphysics: Crane



DSI-Studio: Crane



FreeSurfer: Crane



MATLAB: Crane



Mathematica: Crane



RELION: Crane

Servers



Code Server: Crane



Jupyter Lab



RStudio Server



TensorBoard: Crane

Use Crane OnDemand Rstudio server:

3. Increase running time to **4 hrs.**

4. Click “**Launch**” at the bottom of the page.



Launch

RStudio Server version:

vv0.18.0_39_g00fab8c

This app will launch RStudio Server an IDE for R on the Crane cluster.

R version

4.1 (RStudio 1.4)

This defines the version of R you want to load.

R variant

Basic

This defines the variant of R you want to load. Details on the non-Bioconductor variants are found [here](#). The Bioconductor image is described [here](#).

Number of cores

1

Number of cores requested per a node (min 1, max 16)

Running time in hours

4

Maximum runtime in hours of RStudio server (min 1, max 8)



Host: c3706.crane.hcc.unl.edu

 Delete

Created at: 2022-06-16 11:36:46 CDT

Time Remaining: 23 minutes

Session ID: ea8c9741-301d-4848-8e88-b31e99087717

Importing modules with R

Import module function

```
source(file.path(Sys.getenv("LMOD_PKG"), "init/R"))
```

Load system module

```
module("load", "blast")
```

Load custom module

```
module("use", "~local/share/lmodfiles")
module("load", "MyModuleA")
```

 ® Login to RStudio Server

6

6. Click to login.

To login, use the following credentials:

Username: tangli

Password:  Click to copy

5

5. Click to copy the password.

Sign in to RStudio

Username:

tangli

Password:

.....

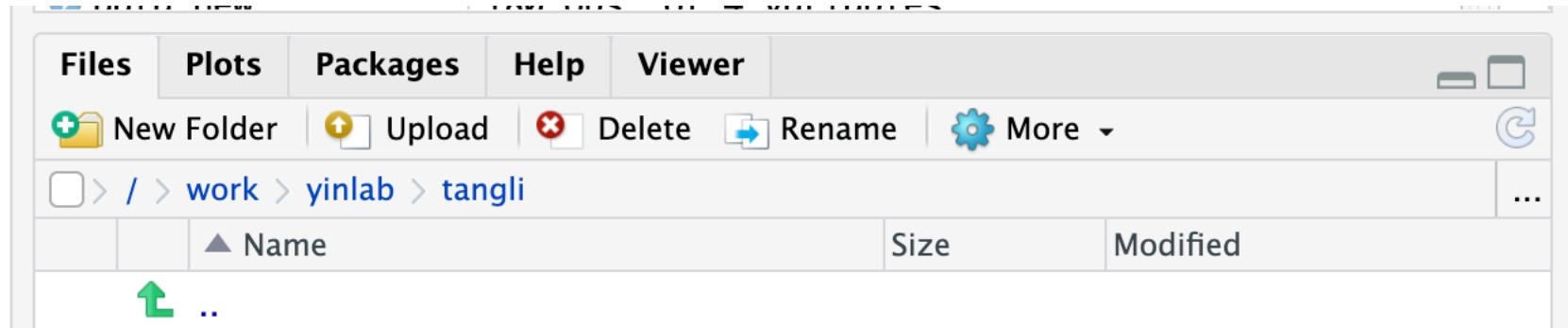
Stay signed in when browser closes

You will automatically be signed out after 60 minutes of inactivity.

Sign In

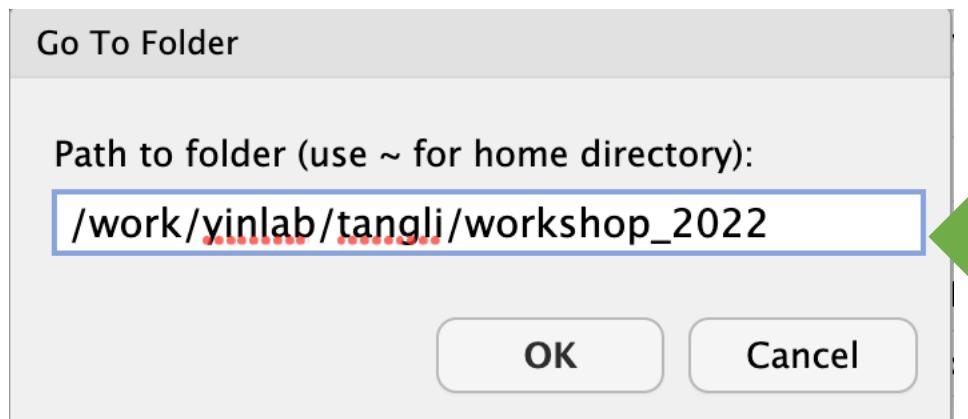
7

7. Login using username and copied password.



8

8. Click “...” to change the directory

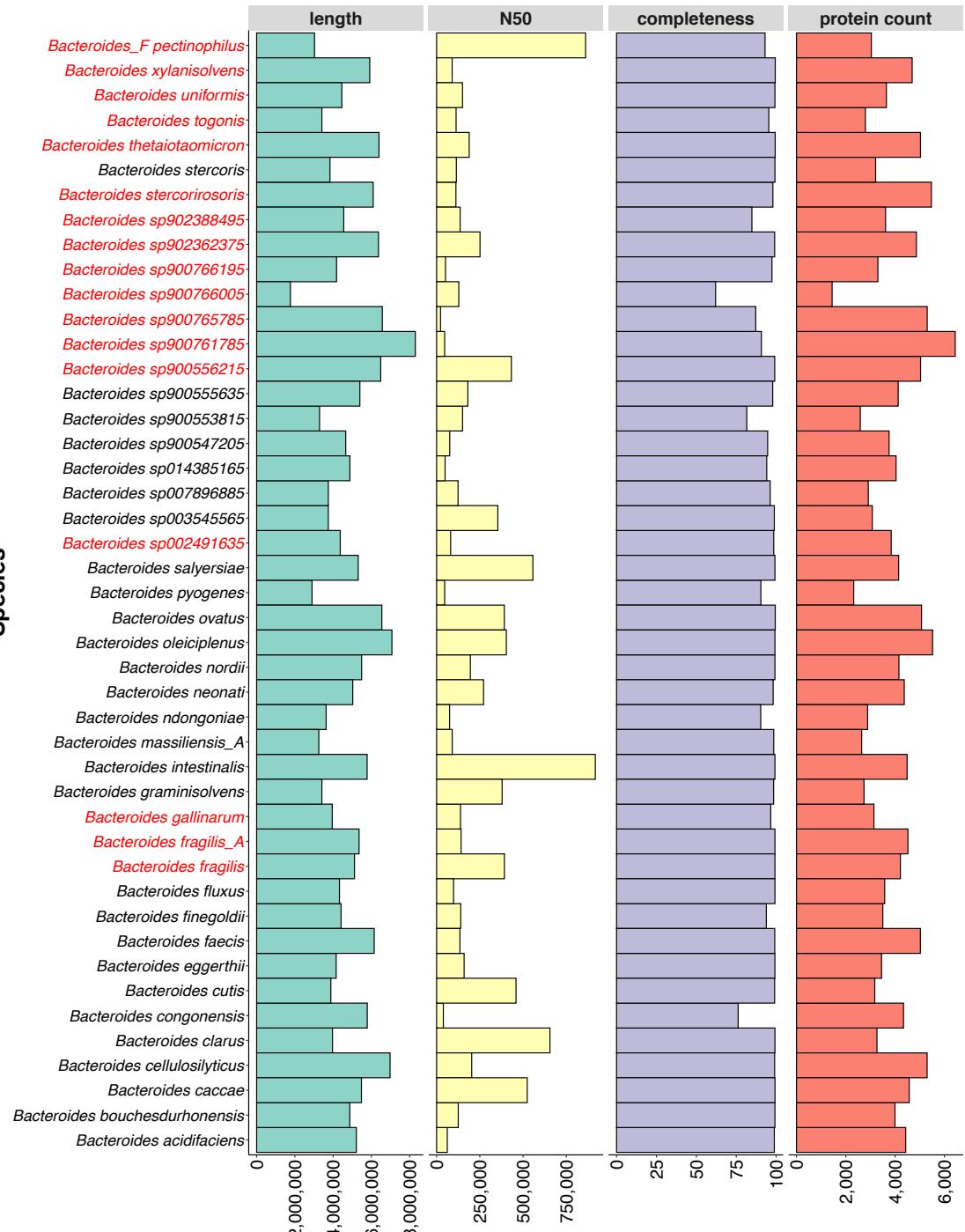


9

9. Enter your working directory path:
/work/your_group/your_name/works
hop_2022

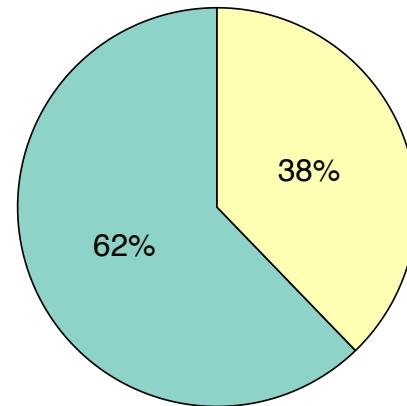
❖ The Overall Statistics of 45 genomes

- Genomes: 17 MAGs (red) and 28 isolates (back).
- Average Length: ~4.87 Mb.
- Completeness: 99.46% - 62.07% (only 5 genomes < 90%)
- Protein count: 6,436 - 1,444.

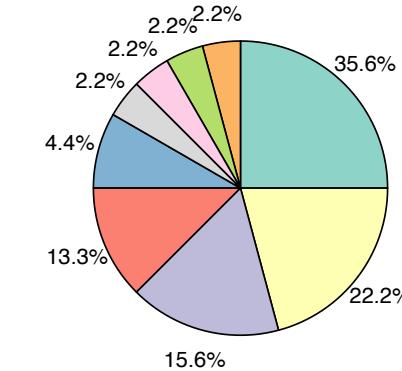


❖ The Overall Statistics of 45 genomes

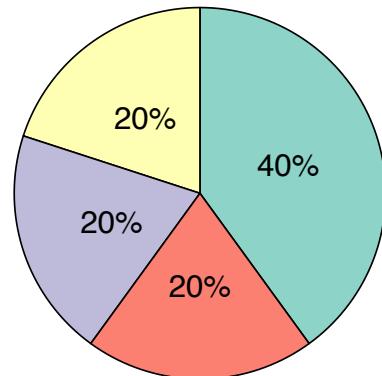
- More isolate genomes than MAGs.
- Most are from China, United States and United Kingdom.
- Mainly from Asia.



Genome Type
■ Isolate
■ MAG



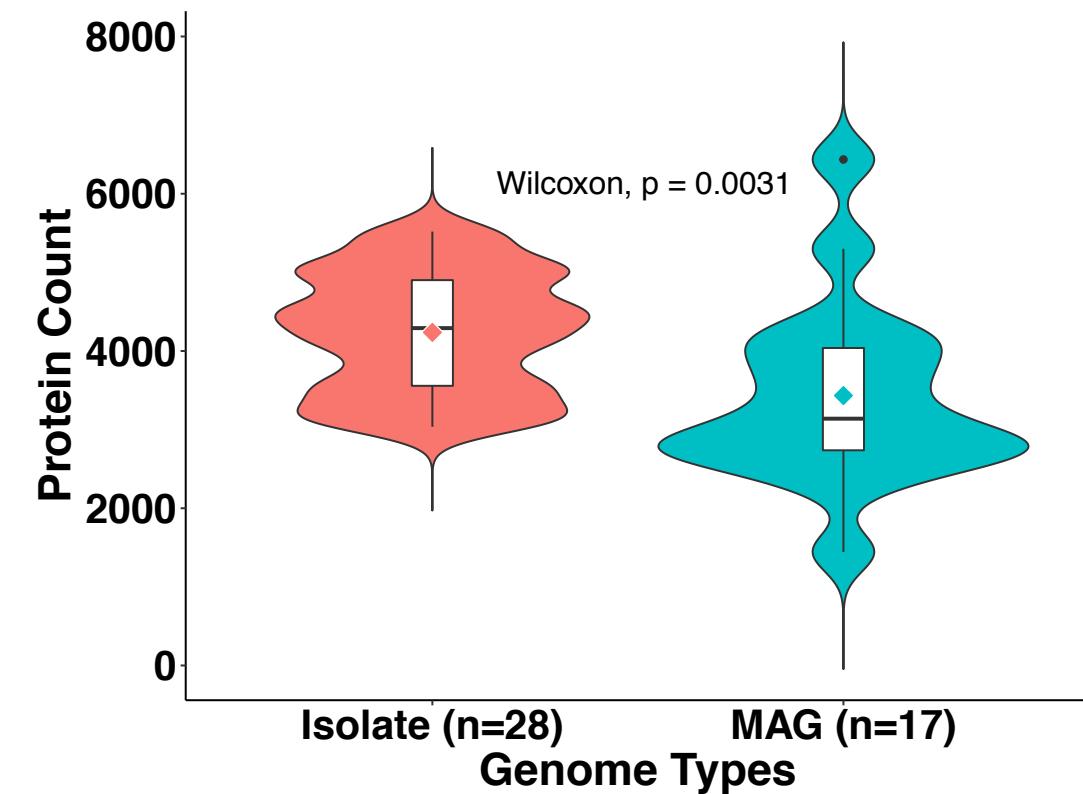
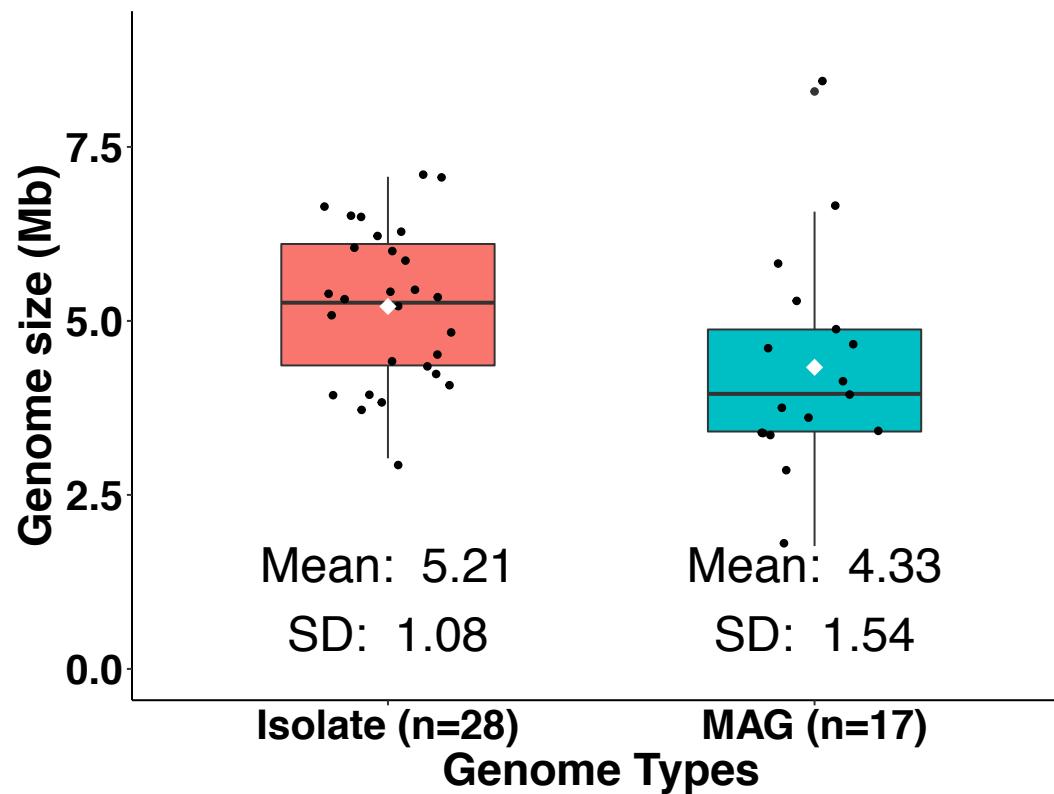
Country
■ China
■ not provided
■ United States
■ United Kingdom
■ Canada
■ Estonia
■ Germany
■ Ireland
■ Kazakhstan



Continent
■ Asia
■ Europe
■ North America
■ not provided

❖ Group comparison for 45 genomes.

- Isolate genomes have larger average genome size and more proteins than MAGs.



□ Part 2

CAZyme and CGC analyses

❖ Run dbCAN3 for CAZyme and CGC annotation

Github: https://github.com/linnabrown/run_dbcan

Online server: <https://bcb.unl.edu/dbCAN2/>

- Install and run on terminal or submit sequence to online server

- dbCAN3 output files

```
cgc.gff
cgc.out
cgc_standard.out
diamond.out
eCAMI.out
hmmer.out
overview.txt
stp.out
tf-1.out
tf-2.out
tp.out
uniInput
```

- cgc_standard.out

CGC#	Gene	Type	Contig	ID	Protein ID	Gene	Start	Gene Stop	Direction	Protein Family
CGC1		CAZyme	MGYG000001313_17		MGYG000001313_00026	8246	10834	-	GH3	
CGC1		TC	MGYG000001313_17		MGYG000001313_00027	11063	12571	-	2.A.50.2.1	
CGC2		TC	MGYG000001313_17		MGYG000001313_00354	371036	371953	-	2.A.4.7.9	
CGC2		null	MGYG000001313_17		MGYG000001313_00355	372128	374287	+	null	
CGC2		null	MGYG000001313_17		MGYG000001313_00356	374329	374808	+	null	
CGC2		CAZyme	MGYG000001313_17		MGYG000001313_00357	374866	377136	-	PL6 PL6_1	
CGC2		null	MGYG000001313_17		MGYG000001313_00358	377167	378744	-	null	
CGC2		TC	MGYG000001313_17		MGYG000001313_00359	378753	380198	-	8.A.46.1.2	
CGC2		TC	MGYG000001313_17		MGYG000001313_00360	380217	383324	-	1.B.14.6.1	
CGC2		null	MGYG000001313_17		MGYG000001313_00361	383604	383711	-	null	
CGC2		CAZyme	MGYG000001313_17		MGYG000001313_00362	383793	385955	+	PL17 PL17_2	
CGC2		null	MGYG000001313_17		MGYG000001313_00363	385987	386331	+	null	
CGC2		TC	MGYG000001313_17		MGYG000001313_00364	386337	387803	+	2.A.1.14.25	
CGC3		TC	MGYG000001313_17		MGYG000001313_00377	400867	401637	+	3.A.1.15.15	
CGC3		null	MGYG000001313_17		MGYG000001313_00378	401795	405139	+	null	
CGC3		CAZyme	MGYG000001313_17		MGYG000001313_00379	405162	405776	+	CE4	
CGC4		CAZyme	MGYG000001313_17		MGYG000001313_00393	416047	417153	-	GH105	

❖ CAZyme and CGC analyses

- Count the number of CAZymes and CGCs in each genome

```
genome_id,taxa,num_genes,num_CAZyme,num_cgc,num_genes_in_cgc,num_cazyme_in_cgc,num_TC_in_cgc,num_TF_in_cgc,  
MGYG000000013,Bacteroides sp902362375,4861,459,110,883,348,247,23,25,240,0.094425,0.18165  
MGYG000000029,Bacteroides finegoldii,3500,309,76,590,231,161,13,13,172,0.0882857,0.168571  
MGYG000000054,Bacteroides acidifaciens,4428,276,67,425,156,129,8,10,122,0.0623306,0.0959801  
MGYG000000057,Bacteroides sp002491635,3839,212,58,375,141,112,9,3,110,0.0552227,0.0976817  
MGYG000000098,Bacteroides bouchesdurhonensis,3994,233,59,334,118,116,5,9,86,0.0583375,0.0836254  
MGYG000000105,Bacteroides clarus,3263,225,59,454,157,139,18,6,134,0.0689549,0.139136  
MGYG000000196,Bacteroides thetaiotaomicron,5027,404,96,728,257,208,25,19,219,0.080366,0.144818
```

(taxa_number_count_and_percentage.csv)

- CAZyme family analyses

```
genome_id,taxa,gene_id,CAZyme_family,CAZyme_class  
MGYG000000013,Bacteroides sp902362375,MGYG000000013_00026,GH29,GH  
MGYG000000013,Bacteroides sp902362375,MGYG000000013_00028,GH16,GH  
MGYG000000013,Bacteroides sp902362375,MGYG000000013_00030,GH76,GH  
MGYG000000013,Bacteroides sp902362375,MGYG000000013_00037,GH92,GH  
MGYG000000013,Bacteroides sp902362375,MGYG000000013_00039,GH76,GH  
MGYG000000013,Bacteroides sp902362375,MGYG000000013_00040,GH130,GH
```

(taxa_cazyme_family.csv)

- Visualization by R, go to RStudio!

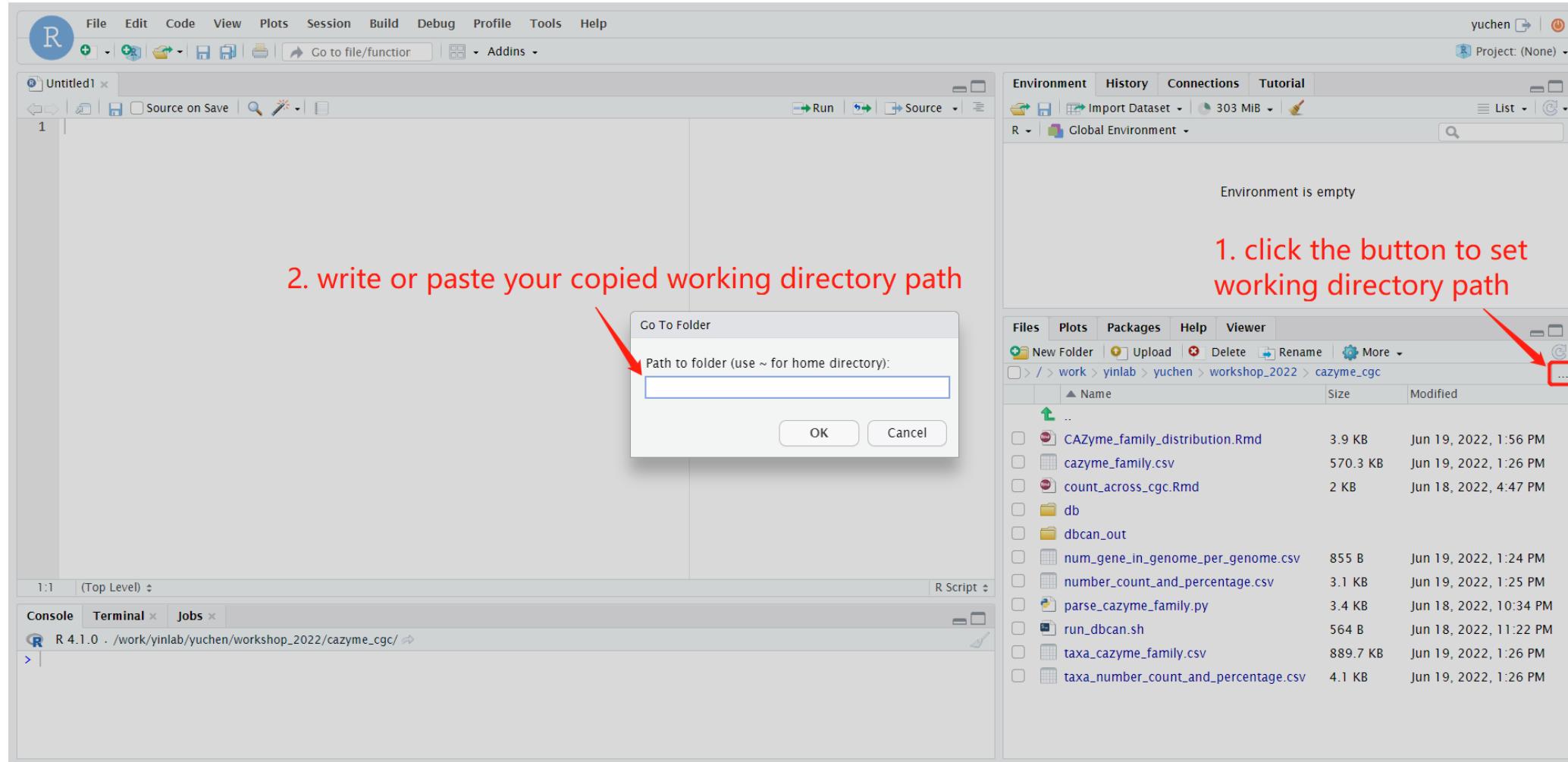
R Markdown file for making plots:

count_across_cgc.Rmd

CAZyme_family_distribution.Rmd

❖ Visualization in RStudio

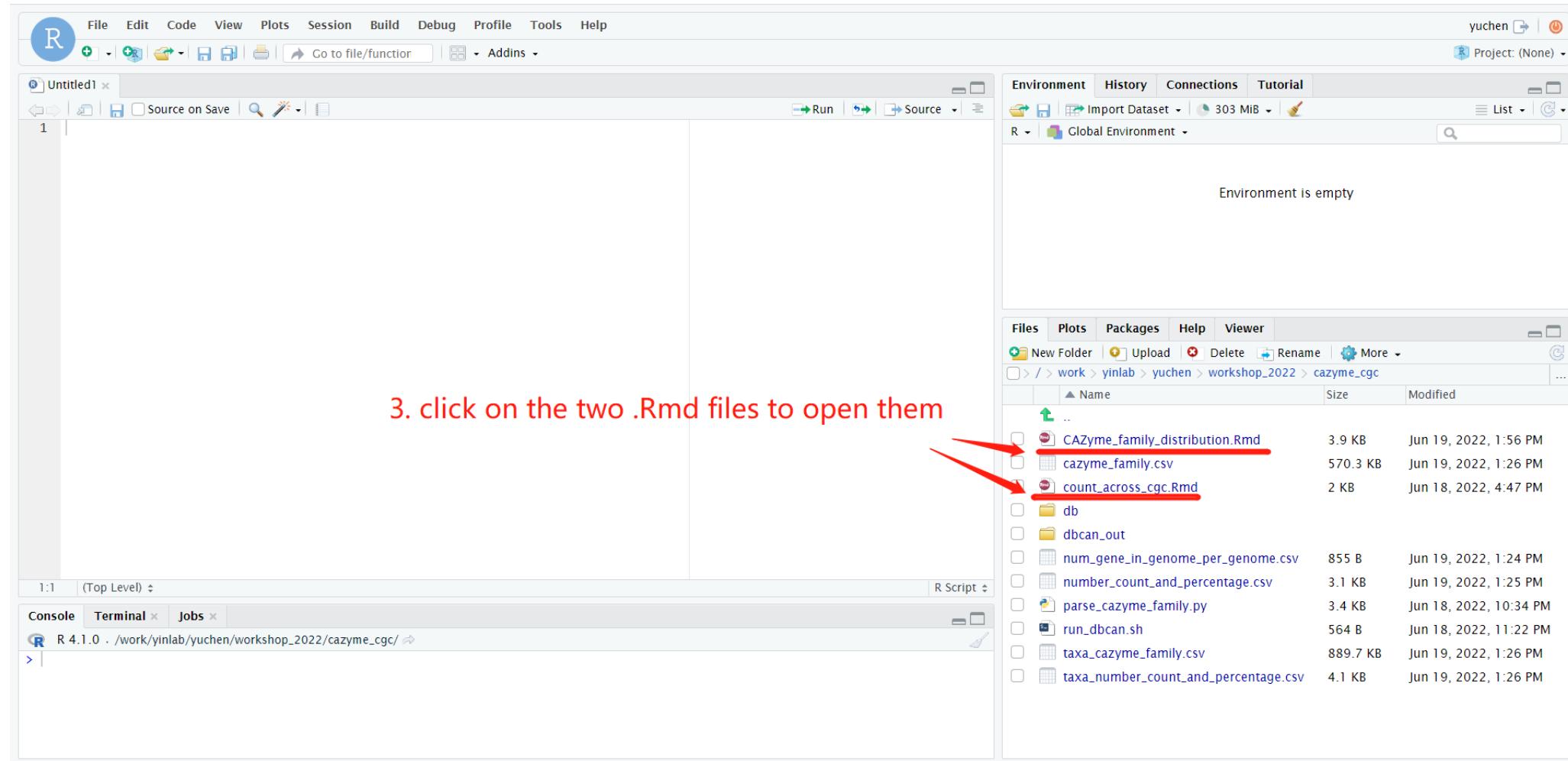
- Set working directory to `cazyme_cgc/`



❖ Visualization in RStudio

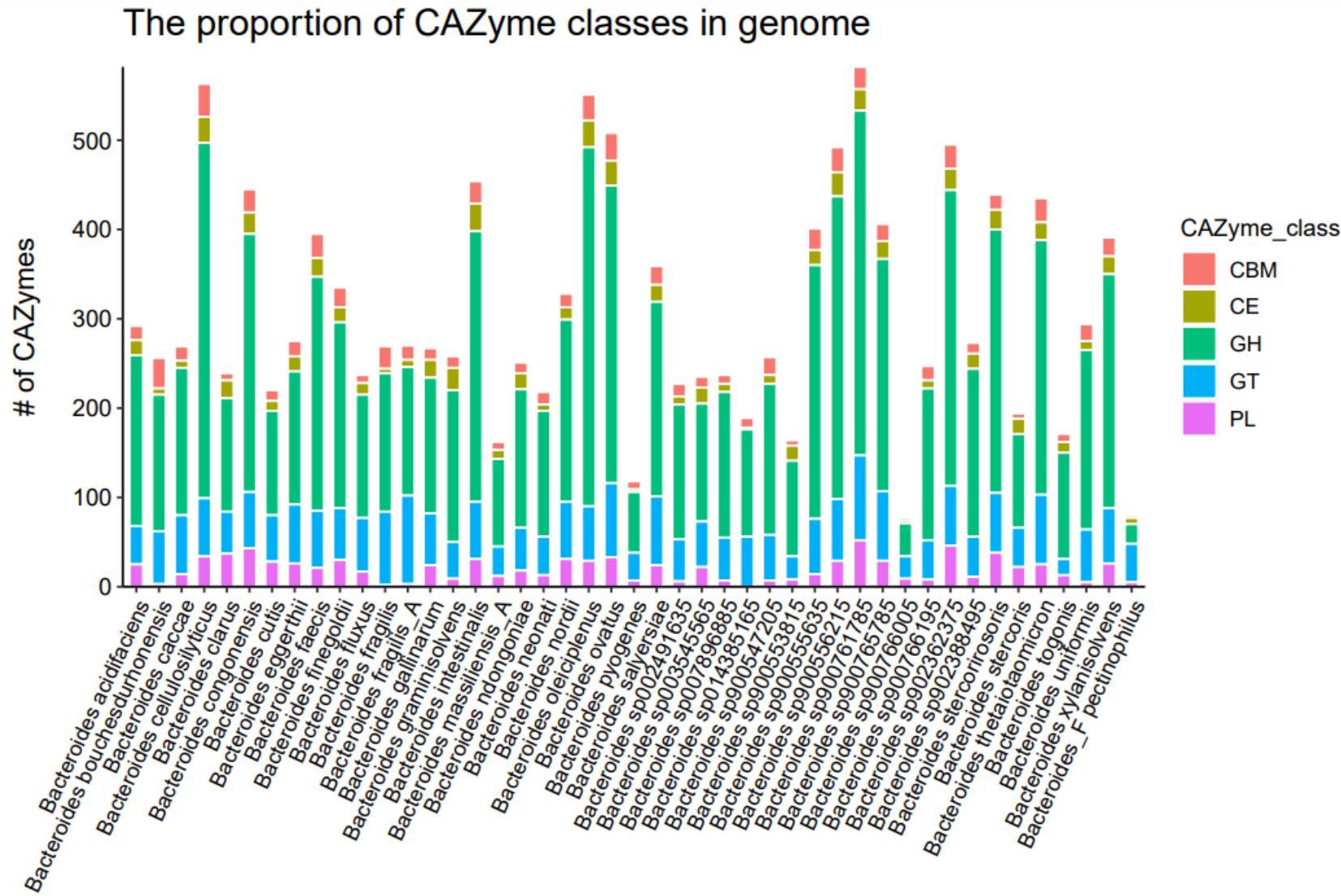
- Set working directory to `cazyme_cgc/`

R Markdown file for making plots:
`count_across_cgc.Rmd`
`CAZyme_family_distribution.Rmd`



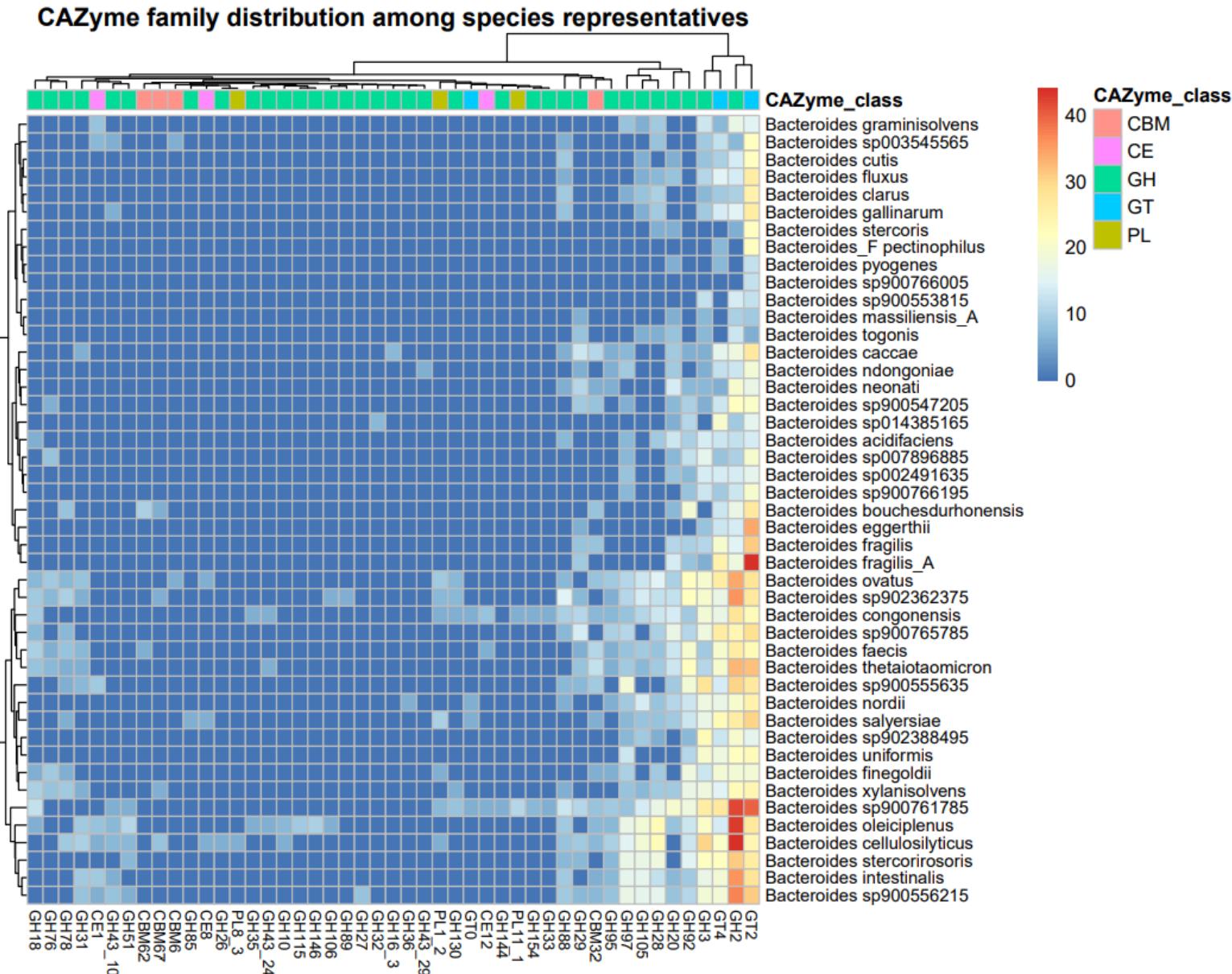
- Plots of CAZyme and CGC analyses

- The proportion of CAZyme classes in genome (cazy_class_stackbar.pdf)
 - The total number of CAZymes varies across genomes.
 - GH account for the largest proportion in most of genomes



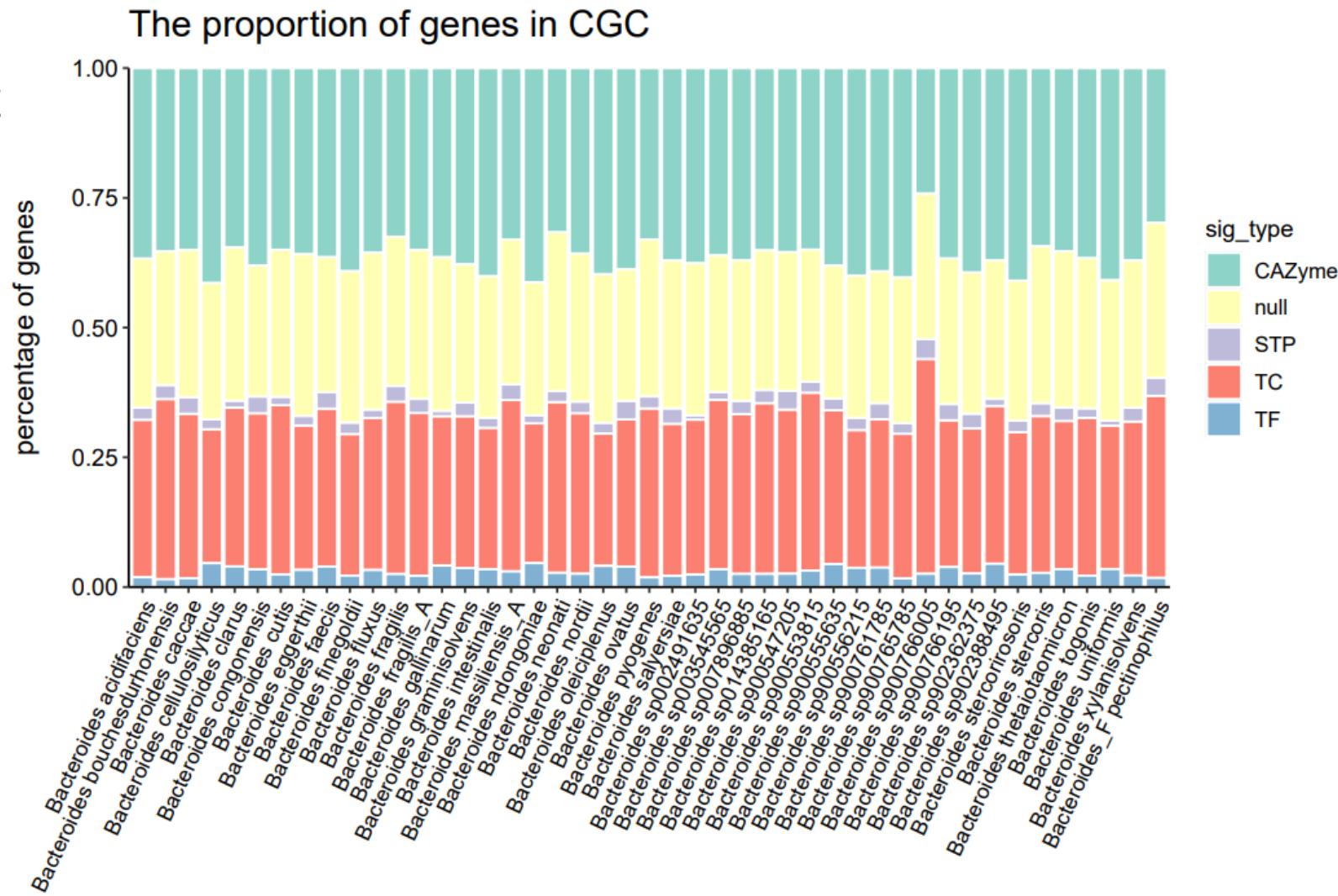
- Plots of CAZyme and CGC analyses

- CAZyme family distribution among spp representatives (cazy_distr_hm.pdf)
 - The number of CAZyme families in one genome > 5
 - Some CAZyme e.g. GT2, GH3 are very common and abundant



❖ Plots of CAZyme and CGC analyses

- The proportion of genes in CGC (prop_sig_cgc_stackbar.pdf)
 - Null genes account for a relatively large proportion within CGC in each genome



□ Part 3

Pan-genomics by anvi'o
Phylogeny analysis based on SCG alignment by anvi'o

❖ Pangenomics by anvi'o

- Make anvio contig database and import dbCAN annotation

function_import_table/

```
MGYG000000013_import.CAZymeinCGC.tsv  
MGYG000000013_import.CAZyme.tsv  
MGYG000000013_import.cgc.tsv  
MGYG000000029_import.CAZymeinCGC.tsv  
MGYG000000029_import.CAZyme.tsv  
MGYG000000029_import.cgc.tsv
```

45_Bacteroides_spp_rep_seq/

```
MGYG000000013_ext_gene_call.txt  
MGYG000000013.fna  
MGYG000000013.fna.fixed.fa  
MGYG000000013.fna.fixed.fa.db  
MGYG000000013.fna.fixed.fa.report.txt
```

- Make Pan-genome by anvi'o

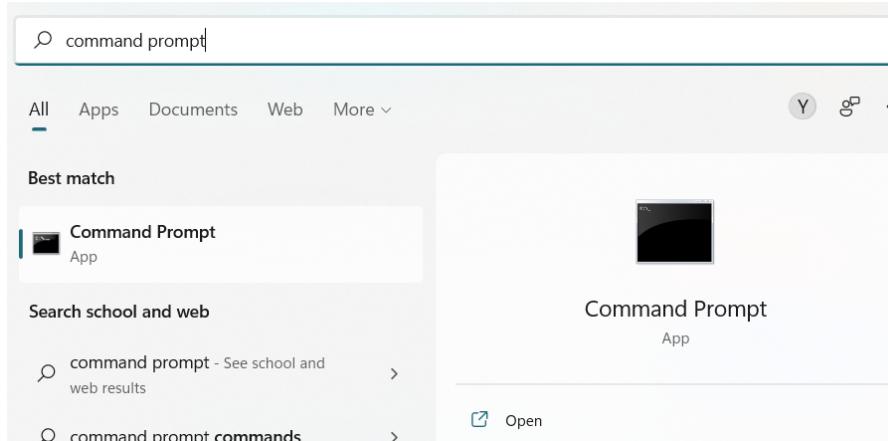
Pan_OUT/

```
combined-aas.fa  
combined-aas.fa.unique  
combined-aas.fa.unique.diamond  
combined-aas.fa.unique.names  
diamond-search-results.txt  
diamond-search-results.txt.unique  
log.txt  
mcl-clusters.txt  
mcl-input.txt  
UHGG_Bacteroides_Pangenome-PAN.db
```

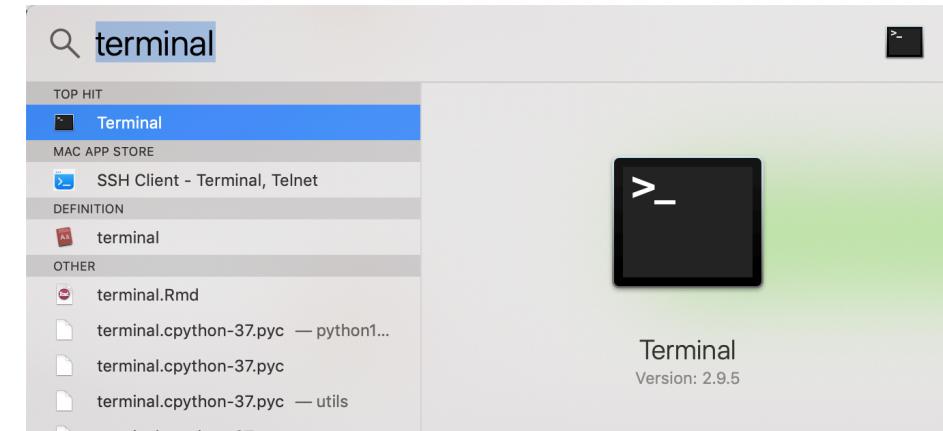
- Visualize anvi'o pan-genome on the interactive page
[open local computer terminal]

- Visualize Anvi'o Pan-genome on the interactive page
- Find your **local computer terminal** and open it

Windows: “Command Prompt”



Mac: “Terminal”



- Type in following command lines **on your local computer terminal**

```
ssh -L 8080:localhost:8080 yourusername@crane.unl.edu
```

```
cd $WORK/workshop_2022/pan_genomics/
```

```
ml anvio/7
```

```
anvi-display-pan -g storage-GENOMES.db -p Pan_OUT/UHGG_Bacteroides_Pangenome-PAN.db --server-only -P 8080
```

- Visualize Anvi'o Pan-genome on the interactive page
- If succeed, your terminal should look like the picture.
- The server port 8080 may be occupied by others sometimes, just try 8079, 8078,
- Then open your web browser, go to the web address:
<http://localhost:8080>

```
yuchen@login.crane:/work/yinlab/yuchen/workshop_June_2022/anvio_pangenome
Have questions? See the documentation!
https://hcc.unl.edu/docs/

For SLURM docs, see https://hcc.unl.edu/docs/submitting\_jobs/

HCC currently has no storage that is suitable for HIPAA, PHI, PID, classified or other data sets for which access is legally restricted. Users are not permitted to store such data on HCC machines.

Blocks [ /home [ G:yinlab>[ 9.9% (49.5GiB/500GiB) ] [ /work [ [ 22.2% (11.1TiB/50TiB) ] [ /common [ ] U:yuchen>[ 11.9% (2.4GiB/20GiB) ] [ 5.6% (2.8TiB/50TiB) ] [ 24.3% ( 7.3TiB/30TiB) ] [ 1.4PiB ) ] [ 43.6% (839.3TiB/1.9PiB) ] key: (Blocks) storage space
key: (U)ser, (G)roup, (E)ntire system
above output generated by 'hcc-du' command, type 'hcc-du -h' for more options

Purge policy on /work, see https://hcc.unl.edu/docs/handling\_data/data\_storage/#purge-policy
[yuchen@login.crane ~]$ cd $WORK/workshop_June_2022/anvio_pangenome/
[yuchen@login.crane anvio_pangenome]$ ml anvio/7
[yuchen@login.crane anvio_pangenome]$ anvi-display-pan -g storage-GENOMES.db -p Pan_OUT/UHGG_Bacteroides_Pangenome-PAN.db --server-only -P 8080
Interactive mode .....: pan
Genomes storage .....: Initialized (storage hash: hash3754dd42)
Num genomes in storage .....: 45
Num genomes will be used .....: 45
Pan DB .....: Initialized: Pan_OUT/UHGG_Bacteroides_Pangenome-PAN.db (v. 14)
Gene cluster homogeneity estimates .....: Functional: [YES]; Geometric: [YES]; Combined: [YES]

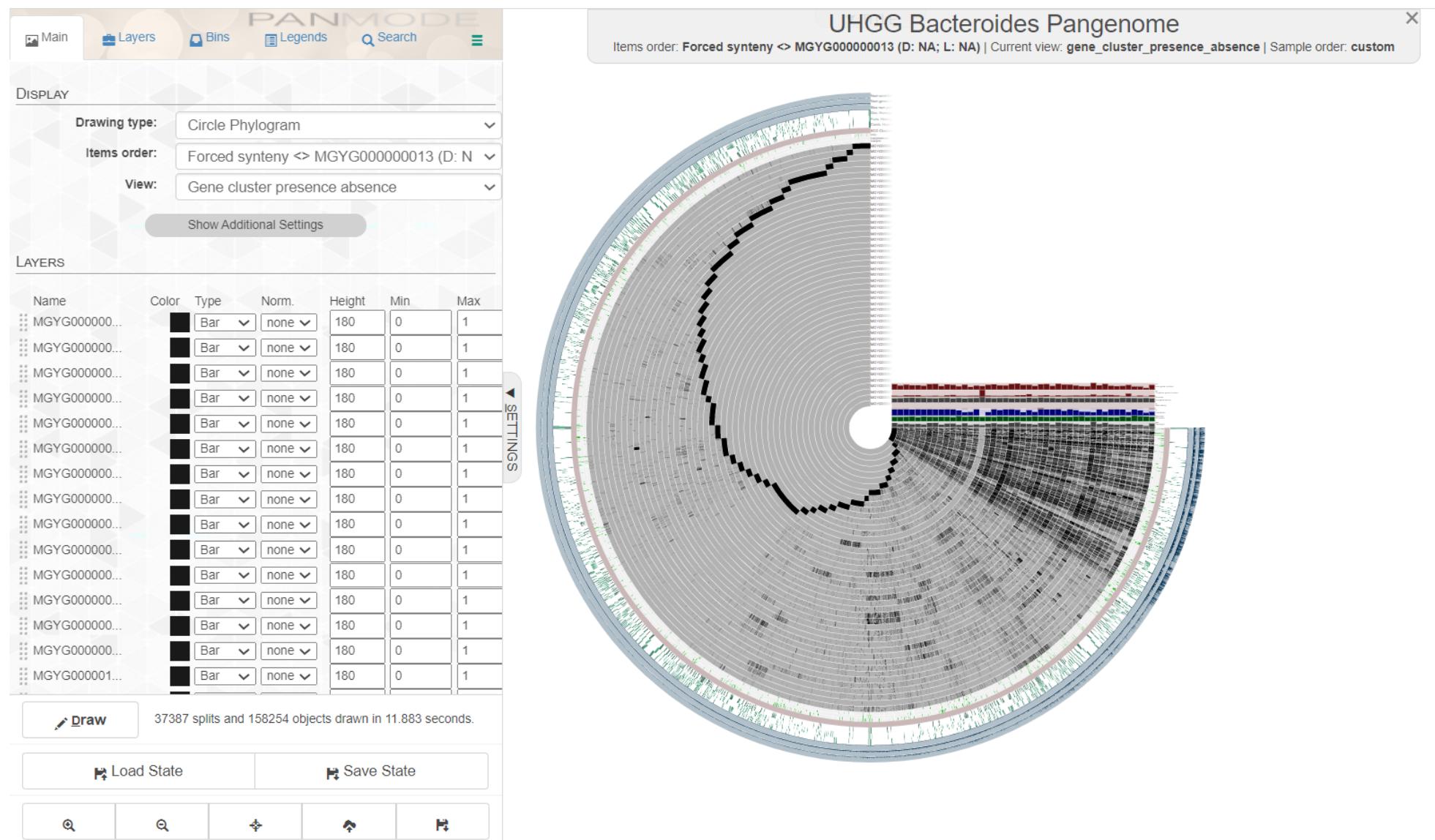
* Gene clusters are initialized for all 37387 gene clusters in the database.

WARNING
=====
This pan genome (which you gracefully named as 'UHGG_Bacteroides_Pangenome') does not seem to have any hierarchical clustering of gene clusters it contains. Maybe you skipped the clustering step, maybe anvi'o skipped it on your behalf because you had too many gene clusters or something. Anvi'o will do its best to recover from this situation. But you will very likely not be able to see a hierarchical dendrogram in the resulting display even if everything goes alright.. In some cases using a parameter like '--min-occurrence 2', which would reduce the number of gene clusters by removing singletons that appear in only one genome can help solve this issue and make your pan genome great again.

Server address .....: http://0.0.0.0:8080

* When you are ready, press CTRL+C once to terminate the server and go back to the command line.
```

- Visualize Anvi'o Pan-genome on the interactive page <http://localhost:8080>



❖ Phylogeny analysis based on SCG alignment by anvi'o

- Open iTOL web page (<https://itol.embl.de/upload.cgi>)
- Upload newick content for tree visualization

1. Go to the "Upload" page

Trees uploaded anonymously are deleted after 1 day. If you want to keep them private and protected, or have multiple trees to visualize, we recommend creating an iTOL account. If you already have an account, please [login first](#).

Datasets and other annotation files should be dragged and dropped directly onto the interactive tree display. Please check the [help pages](#) for detailed instructions and dataset template files. Example tree and annotation files [are available for download](#).

Upload a new tree

Tree name:
optional

Paste your tree into the box below, or select a file using the **Tree file** selector. You can also simply drag and drop the tree file onto the page (only a regular plain text file, not QIIME QZA files).

Tree text: 2. Paste your copied newick file content here

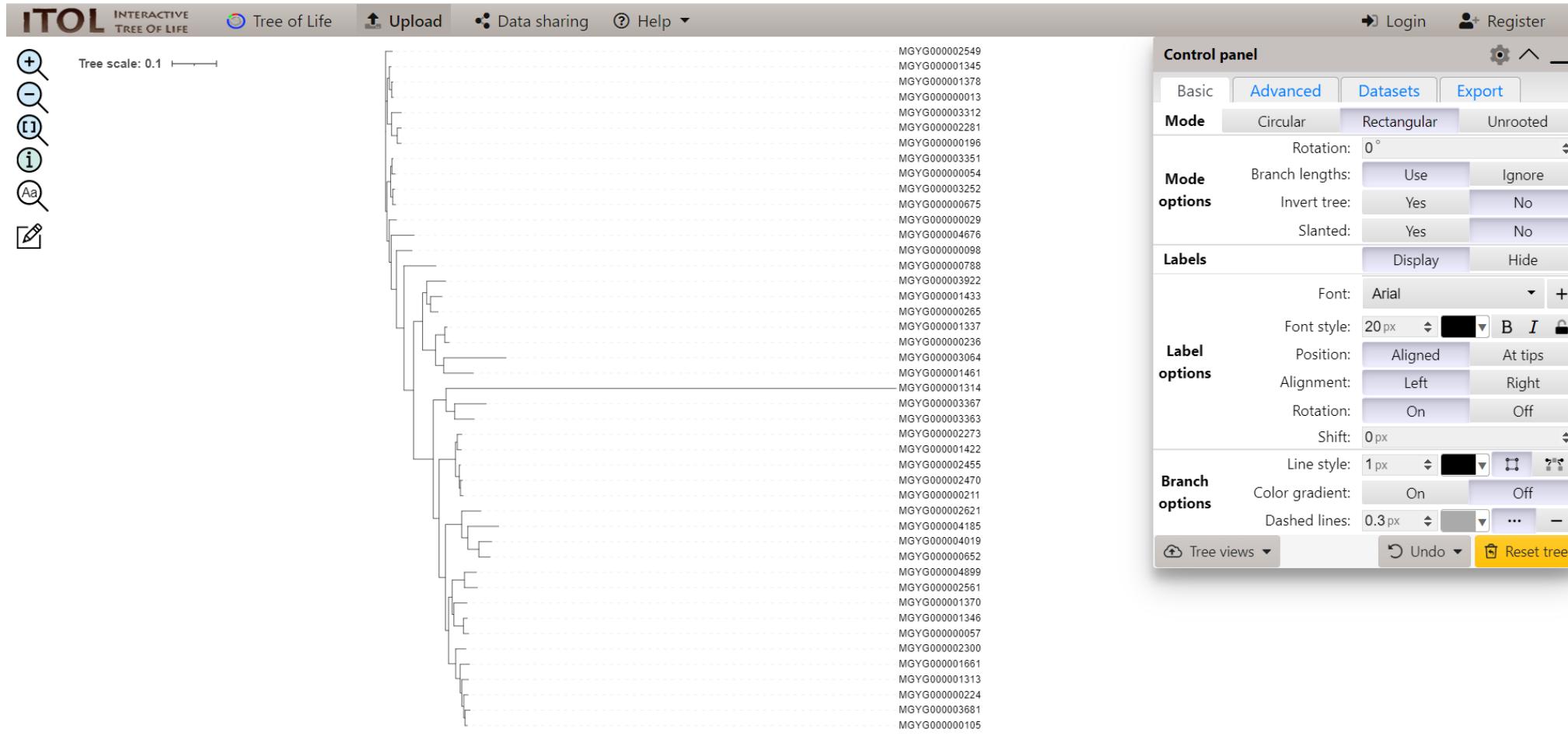
Tree file:
 No file chosen

3. Click "Upload"

Citation: Letunic and Bork (2021) *Nucleic Acids Res* doi: [10.1093/nar/gkab301](https://doi.org/10.1093/nar/gkab301) | Privacy Policy

design & development: [biobyte solutions](#)

❖ Phylogeny analysis based on SCG alignment by anvi'o



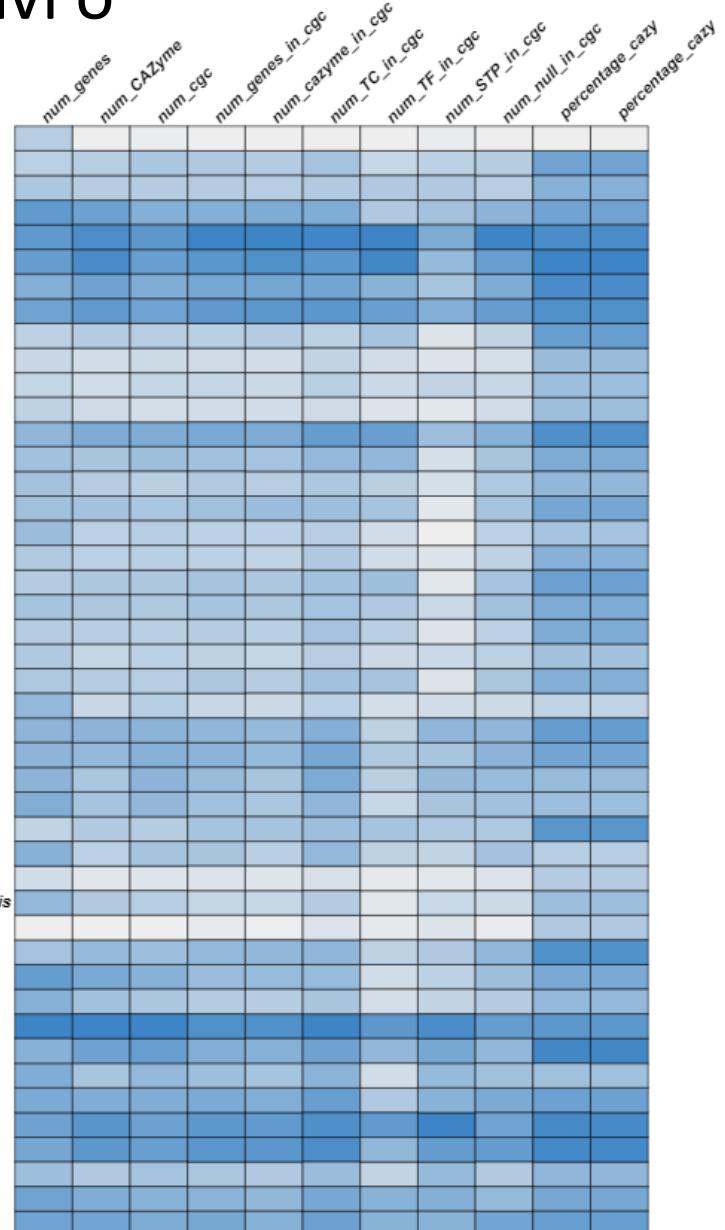
❖ Phylogeny analysis based on SCG alignment by anvi'o

The screenshot shows the iTOL web interface. At the top, there is a navigation bar with links for "Tree of Life", "Upload", "Data sharing", "Help", "Login", and "Register". On the left, there is a vertical toolbar with icons for zooming in and out, selecting nodes, and other functions. The main area displays a phylogenetic tree with many branches. To the right of the tree is a "Control panel" window. The "Basic" tab is selected in the panel. A red box highlights the "Upload annotation files" button, which has an upward arrow icon. Below the tree, there is a list of identifiers: MGYG000002549, MGYG000001345, MGYG000001378, MGYG00000013, MGYG000003312, MGYG000002281, MGYG000000196, MGYG000003351, MGYG000000054, MGYG000003252, MGYG000000675, MGYG000000029, MGYG000004676, MGYG000000098, MGYG000000788, MGYG000003922, MGYG000001433, MGYG000000265, MGYG000001337, MGYG000000236, MGYG000003064, MGYG000001461, MGYG000001314, MGYG000003367, MGYG000003363, MGYG000002273, MGYG000001422, MGYG000002455, MGYG000002470, MGYG000000211, MGYG000002621, MGYG000004185, MGYG000004019, MGYG000000652, MGYG000004899, MGYG000002561, MGYG000001370, MGYG000001346, MGYG000000057, MGYG000002300, MGYG000001661, MGYG000001313, MGYG000000224, MGYG000003681, and MGYG000000105.

Click the upload button or drag the iTOL annotation files to the page

- ❖ Phylogeny analysis based on SCG alignment by anvi'o

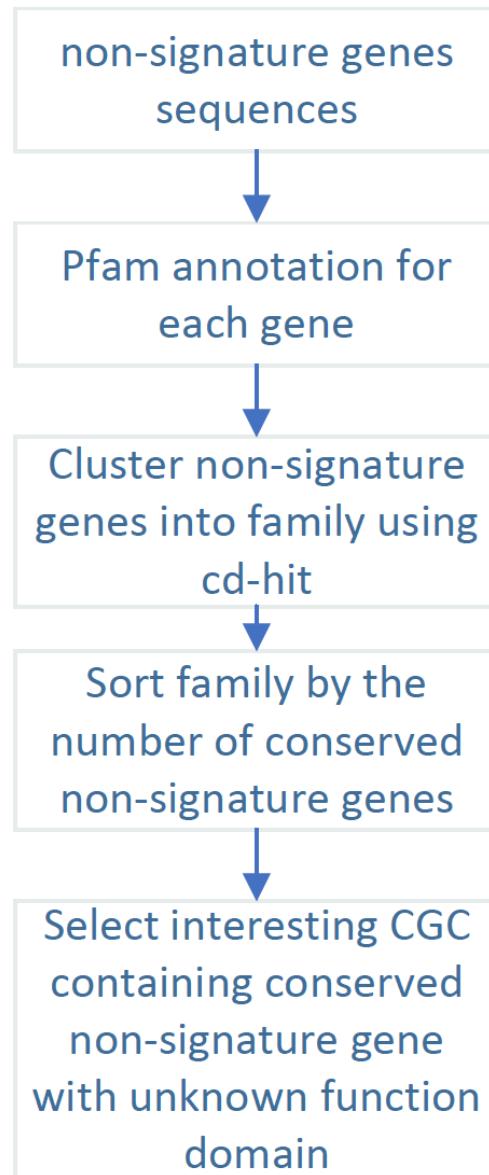
- The annotation files are on the github:
https://github.com/tli14/Workshop_2022_YinLab
 - You can also customize your own tree!
The iTOL help page:
<https://itol.embl.de/help.cgi>



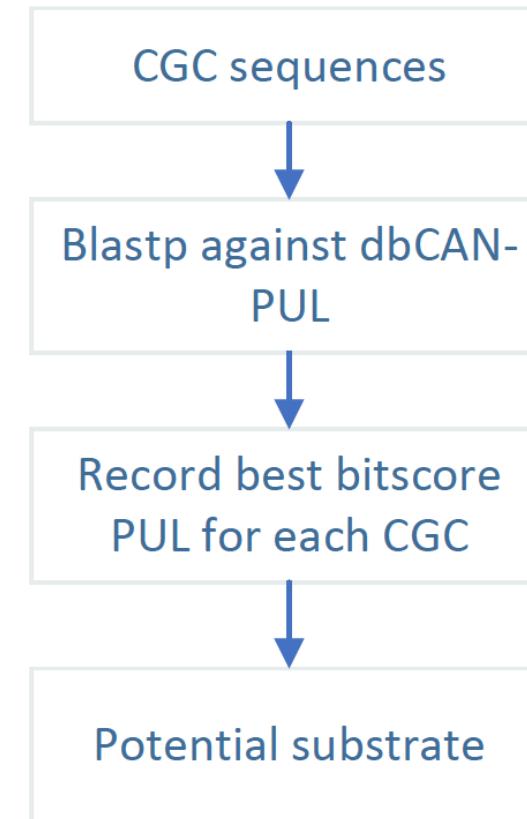
□ Part 4

Pfam annotation of non-signature genes

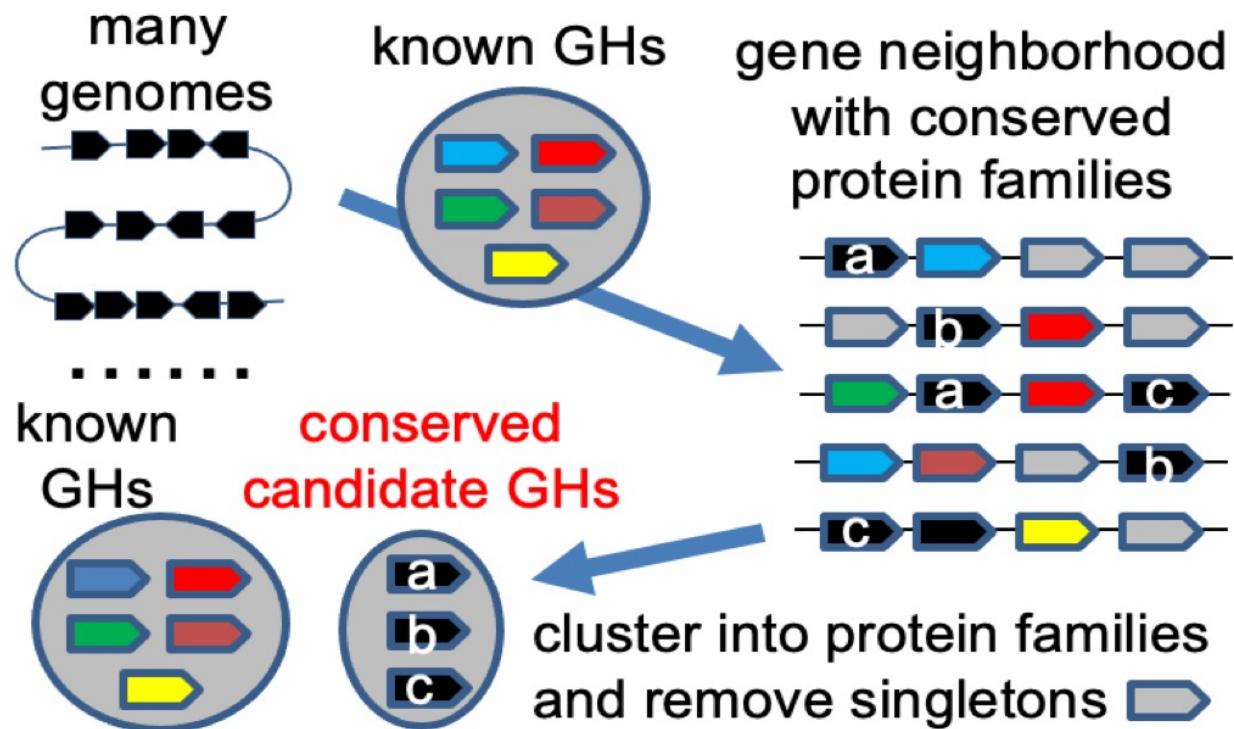
Pipeline of conserved non-signature genes



Pipeline of substrate prediction



Pipeline of conserved non-signature genes



Script Name: Prepare_null_gene.sh

Script Function: Extract all non-signature gene sequences from dbCAN result.

- Input 1: all the fasta sequence (**uniInput**)
- Input 2: cgc predicted by dbCAN (**cgc_standard.out**)
- Output: non-signature gene protein sequences (**non-signature.pep**)

Script Name: pfam_parallel_job.sh

Script Function: Domain annotation of non-signature genes to get possible function

- Input 1: **non-signature** protein sequences
- Input 2: Pfam database.
- Output: domain annotation

Script Name: cd-hit.sh

```
cd-hit -i .pep -o non-signature_40.pep -c 0.4 -M 0 -T 32 -n 2
```

Part1 Function:

- Input: non-signature protein sequences
- Output: clustered non-signature protein at 40% identity

-c 0.4 : global identity = 0.4

-M 0: Memory usage not limited

-T 32: CPU 32

-n 2: word size for global identity

Part2 Function:

Annotate the non-signature gene clusters with pfam.

Pipeline of Substrate Prediction

Script Name: Prepare_CGC_seq.sh

Script Function: Extract all CGC sequences from dbCAN result.

- Input 1: **unilnput** all the fasta sequence
- Input 2: **cgc_standard.out**, CGCs predicted by dbCAN
- Output: all CGC sequences

Script Name: blastp.sh

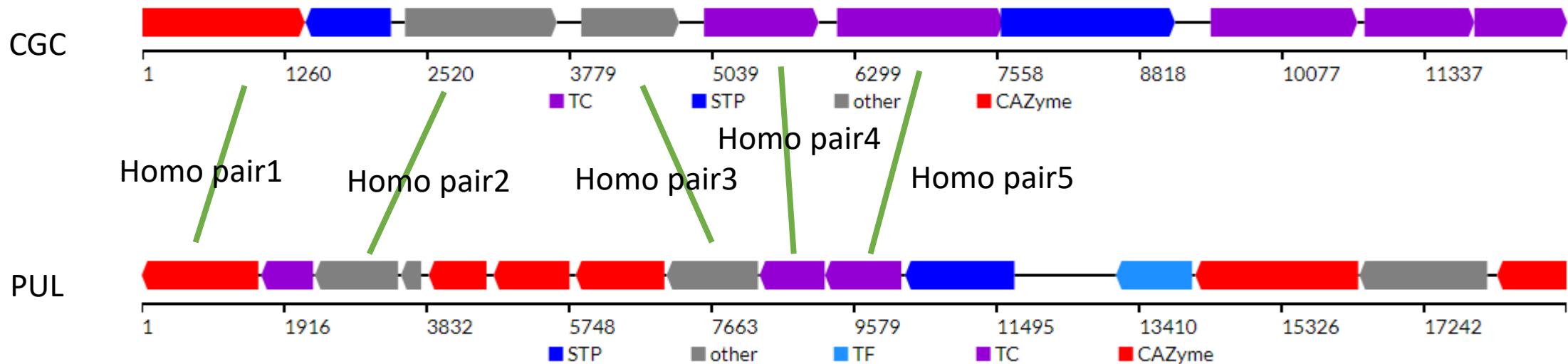
Script Function: CGC database search against with PUL database to find homologous

- Input 1: CGC sequences
- Input 2: dbCAN-PUL database, download from dbCAN-PUL server
- Output: homologous hits

Script Name: substrate.sh

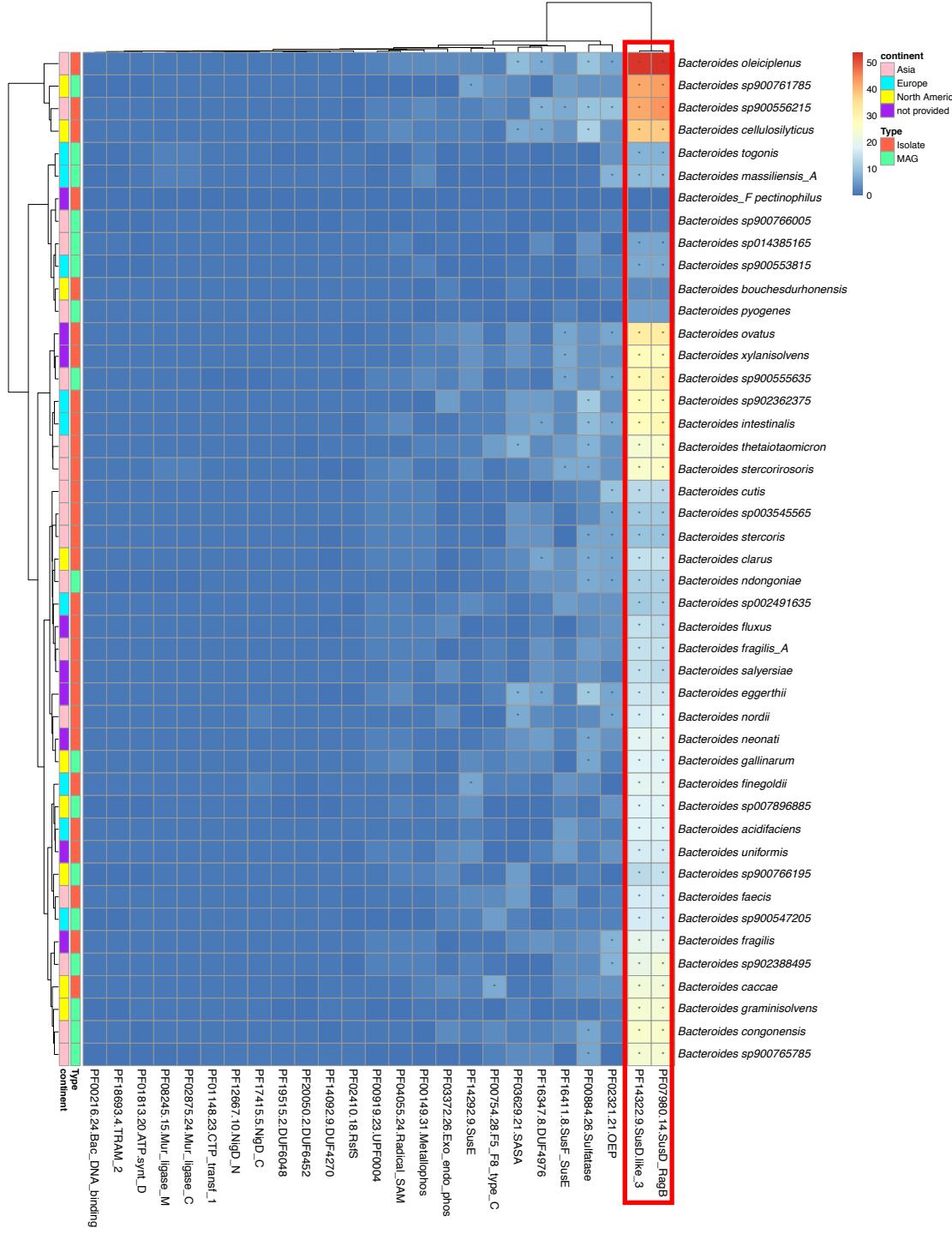
Script Function: Deal with blastp result to infer potential substrate

- Input 1: blastp outputs (Bacteroides.CGC.PUL.blastp)
- Input 2: CGC predictions (cgc_standard.out)
- Input 3: **dbCAN-PUL.xlsx**
- Output: CGC with substrate



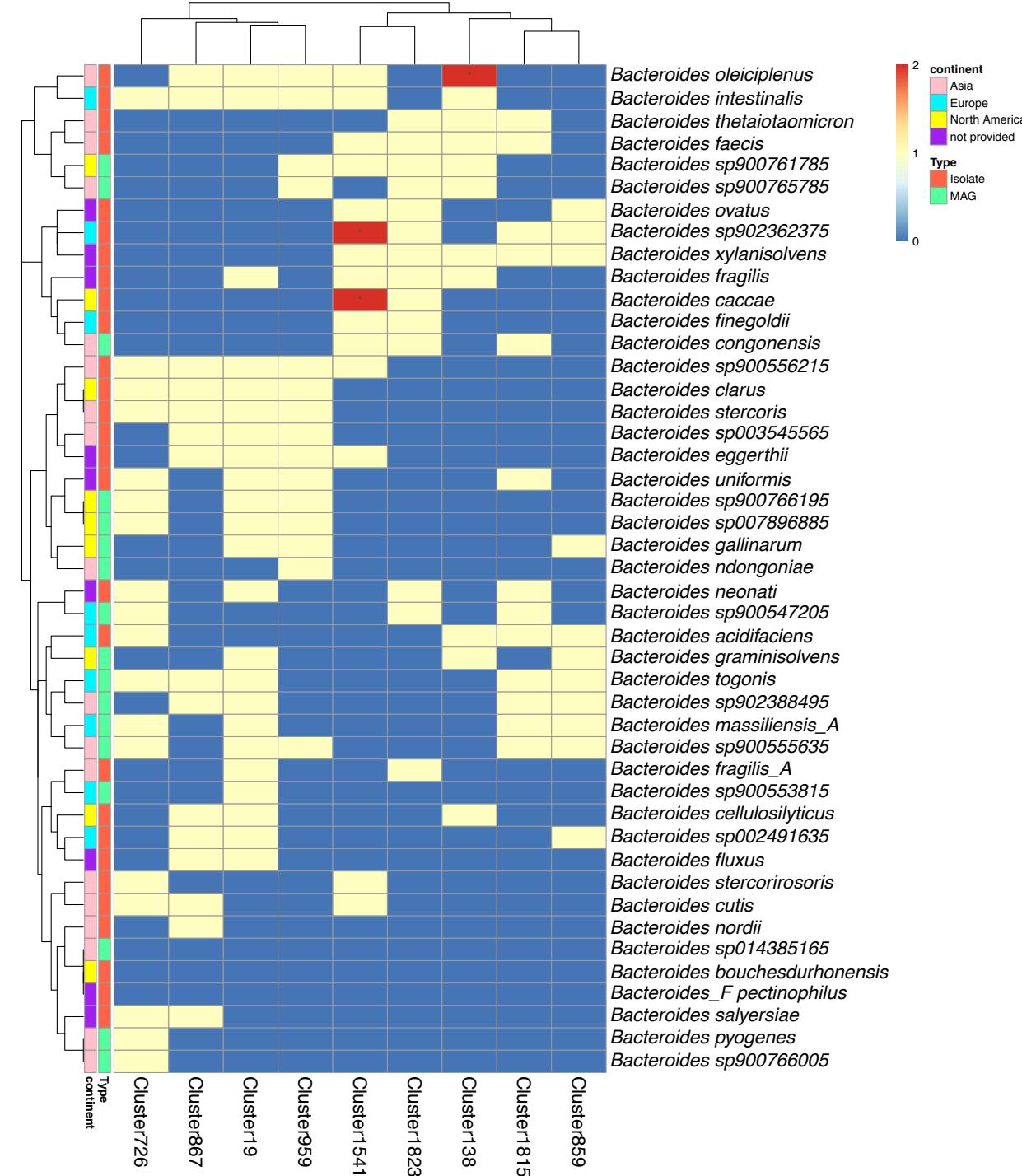
❖ Pfam annotation for non-signature genes (nSGs)

- Two Pfam families (PF07980.14 and PF14322) can be found in 44/45 genomes → only absent in *Bacteroides_F pectinophilus*.
- A total of 25 Pfam families can be found in > 30 genomes.



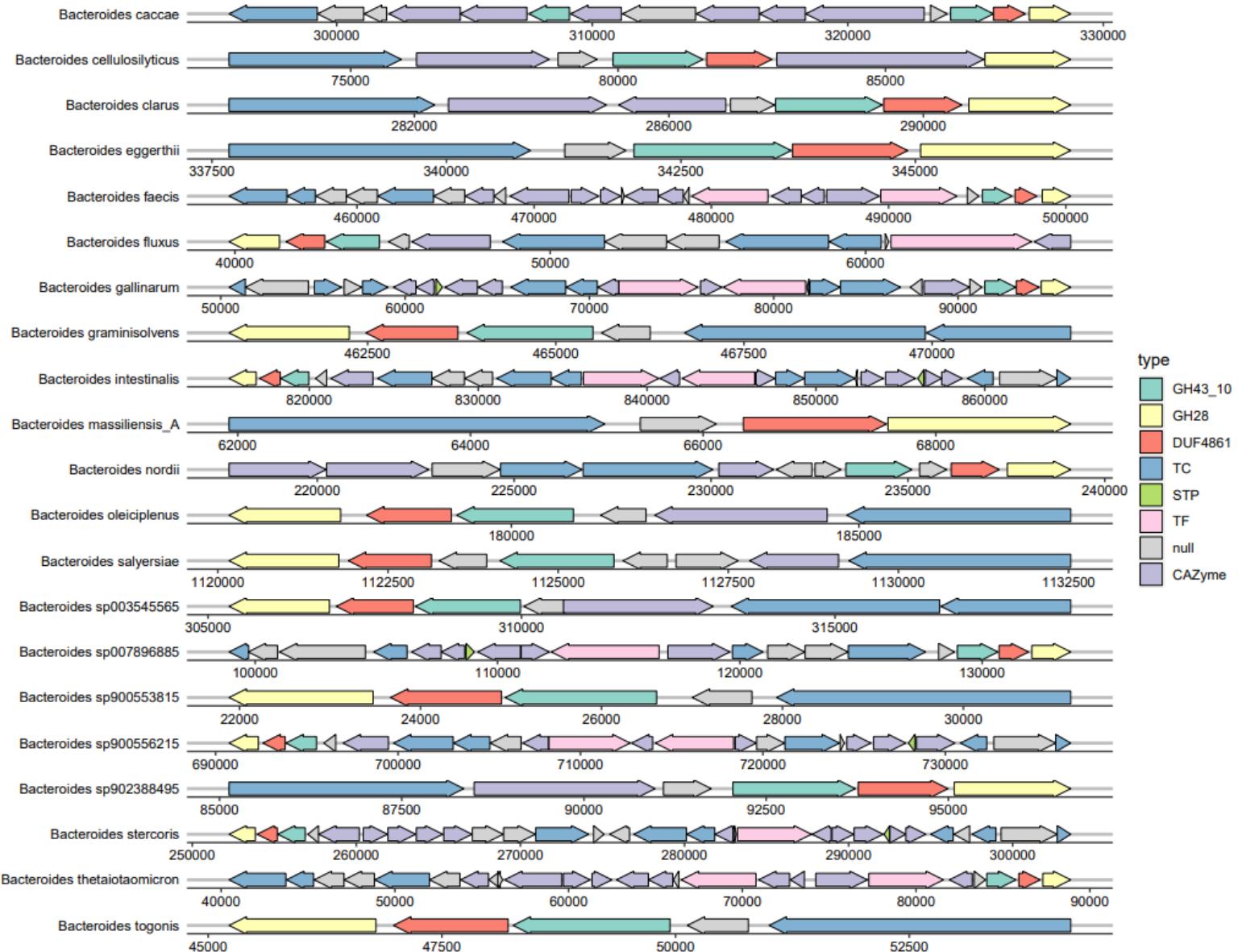
❖ Pfam unannotated protein clusters for nSGs

- The nSGs were clustered into protein clusters.
 - Some protein clusters without Pfam annotation were found in > 10 genomes, which might be conserved nSGs in Bacteroides genus.



❖ CGC synteny plot with conserved nSG family highlighted

- The proportion of genes in CGC (cgc_synteny.pdf)
- Null gene DUF4861 without pfam function annotated is conserved in 21 of 45 genomes
- CGC containing DUF4861 is also conserved across genomes, with GH43_10 and GH28
- Haven't ordered by phylogeny



□ Part 5

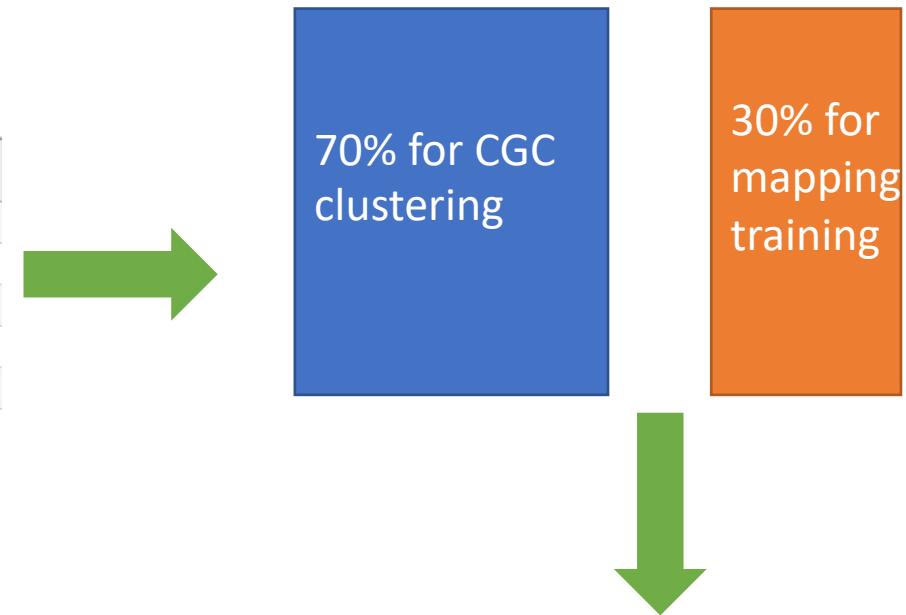
CGC clustering

❖ CGCs clustering

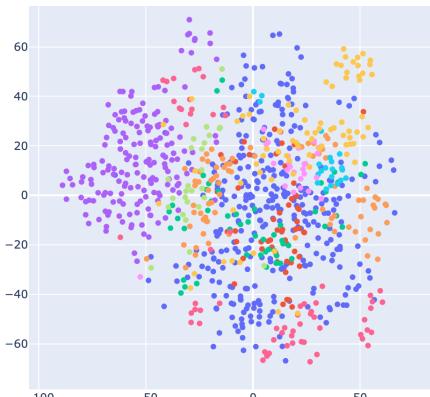
1. Prepare Input Table

Genome_ID	CGC_ID	sig_gene_seq	low_level_substr	Species
MGYG000000013	MGYG000000013_1ICGC1	1.B.14,GH29,GH16,GH76	galactomannan	Bacteroides sp902362375
MGYG000000013	MGYG000000013_1ICGC2	1.B.14,HTH_AraC,GH92,GH76,GH1...	alpha-mannan	Bacteroides sp902362375
MGYG000000013	MGYG000000013_1ICGC3	GH18,8.A.46,1.B.14	host glycan	Bacteroides sp902362375
MGYG000000013	MGYG000000013_1ICGC4	GH13,GH97,1.B.14	starch	Bacteroides sp902362375
MGYG000000013	MGYG000000013_1ICGC6	2.A.21,GT2,2.A.1,SIS,GH115,GH95,...	arabinoxylan	Bacteroides sp902362375

2. Train and Test Subsets



5. Visualization



4. CGC clustering

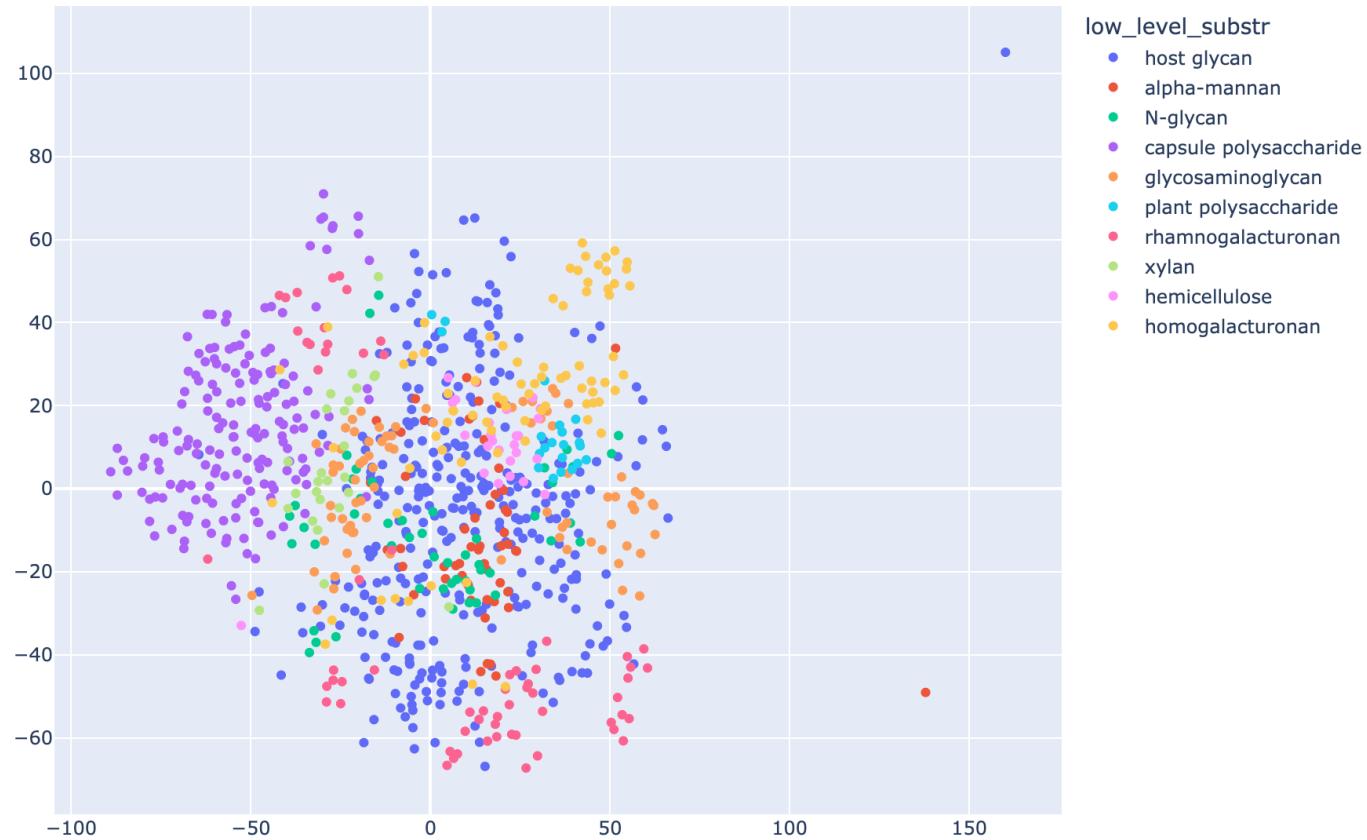
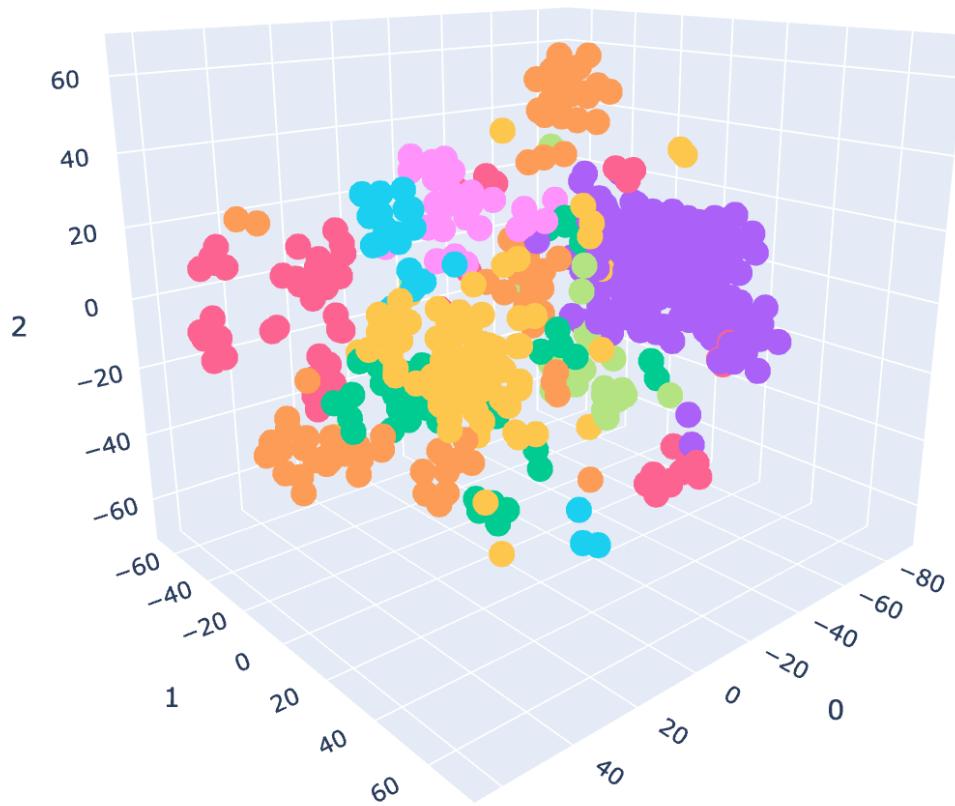
cluster_id	number of samples
4	80
39	81
7	1
24	141
42	5

3. Convert words to vectors

```
0: '1.A.1',
1: '1.A.11',
2: '1.A.13',
3: '1.A.22',
4: '1.A.23',
5: '1.A.26',
```

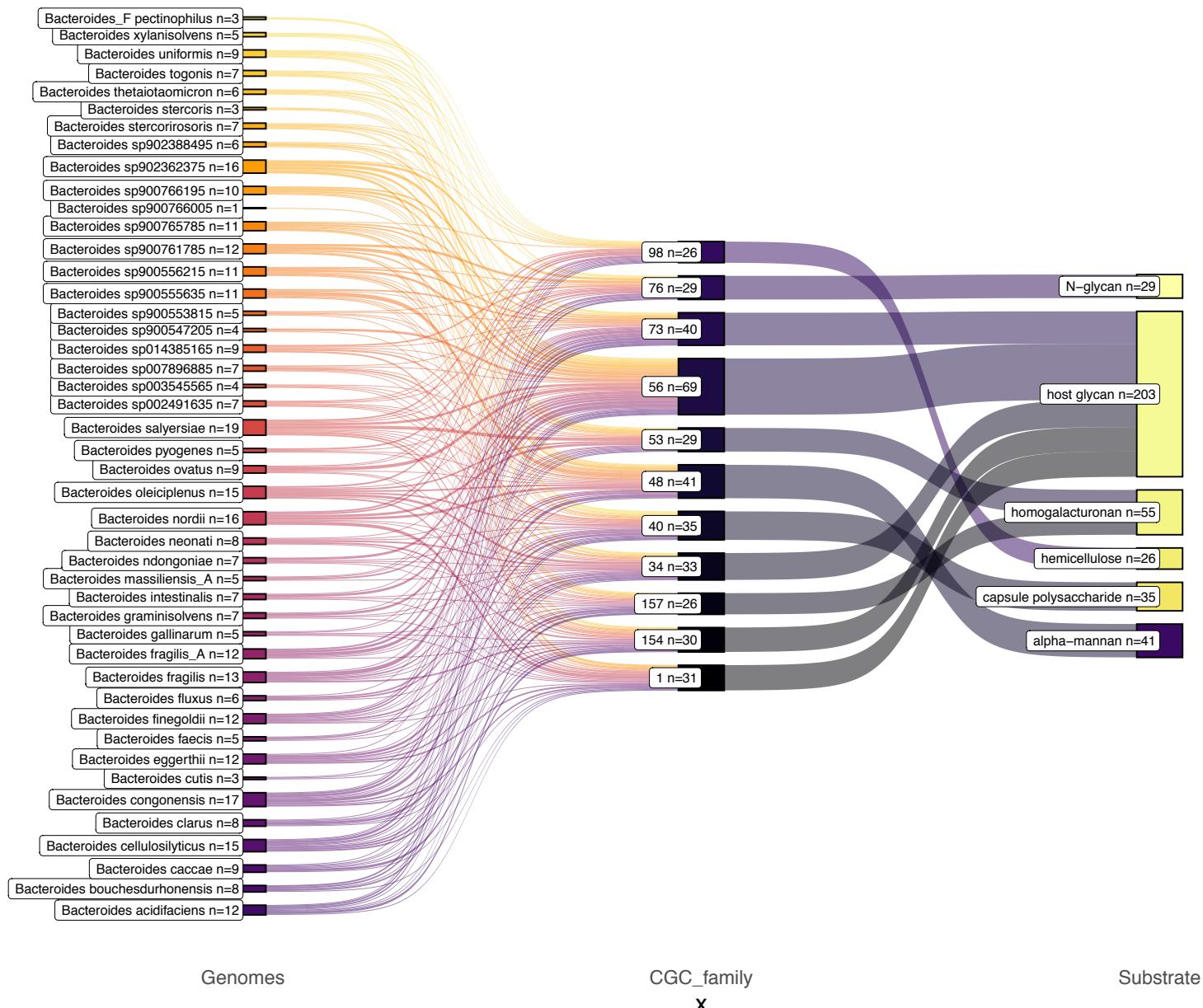
❖ CGCs clustering results

- T-distributed Stochastic Neighbor Embedding (**TSNE**) plot: visualize high-dimensional data.
- The top 10 CGC families and their substrates were found.



❖ CGCs clustering results

- **Sankey plot:** allows to show study flows.
- 11 CGC families contain at least 25 CGC sequences.
- Host glycan is the most abundant substrate for these CGC families.





Thank You!

