Presentation Slides

Guidelines and Examples

January 3, 2017

Saarland University
Chair for Clinical Bioinformatics

Introduction

Purpose of these slides

✓ Slide layout, color scheme and font

✓ Figures, tables, formulas

✓ Other tips and references

✗ Exact description of how slides should look like

☞ There is **no** single perfect solution for any presentation

Layout, Color Scheme and Font

Some guidelines for the layout

- **Basic** elements
  - Section/slide title – for "global" orientation
  - Slide counter – helps in navigation during Q&A
- **Optional** elements
  - Presentation title and date
  - Institution name/logo
  - ...
- All these elements should not take too much **space**
  - I.e. main part ($\geq 80\%$) is reserved for the slide content
  - N.B. the slide real-estate is limited; use it efficiently

Some guidelines for the color scheme

- ☞ Appropriate **contrast** between text and background
  - Dark background/light font or Light background/dark font
  - May depend on the presentation room or beamer – **test early**, if possible
  - If not sure use light background and dark font
- ☞ No "aggressive" color combinations, e.g. red and green
- ☞ **Few** main colors, no "rainbow" color scheme
  - Optional: same color scheme for layout and graphics
- ☞ **Plain background** is in most cases the best choice

Some guidelines for the font

- ☞ Neutral and easy to read, **not** "*something like that*"
- ☞ Sufficiently large, e.g. 18pt for main text
- ☞ Avoid using only capital letters
- ☞ Use a different style for titles/keywords, e.g. in **bold**

Figures, Tables, Formulas

Figures

- ☞ Captions/numbering (optional)
- ☞ Appropriate figure **resolution**
  - All relevant details should be recognizable
  - Figures should **not** be pixelated
- ☞ **Consistent** size/placement (alignment)
  - If multiple figures on same slide
- ☞ **Omit** irrelevant details
  - E.g. screenshots – select only relevant area
- ☞ **Highlight** important details
- ☞ Add image **source**
  - Below the figure or on a separate reference slide

Figures: How it COULD be done

✓

Figure 1: *Figure caption*

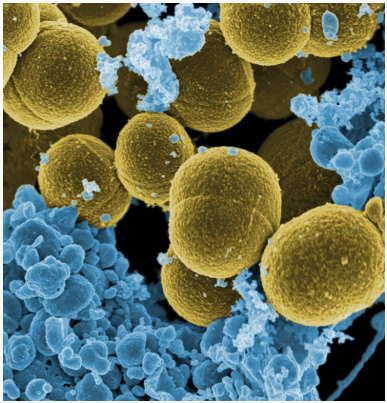
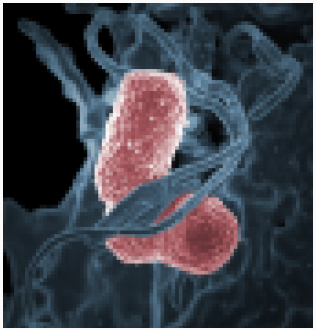


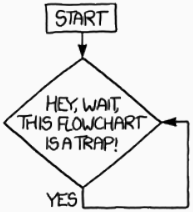
Figure 2: *Another figure caption*

Figures: How it should NOT be done



Figures: When to use?

How something looks like



Workflow

Illustration of a method, e.g. NGS

Results/data as graphs

Tables

- ☞ Captions/numbering (optional)
- ☞ **Structure** the table
  - E.g. header, row blocks, column blocks
- ☞ **Highlight** important data by font family or color
- ☞ **Omit irrelevant** information
  - **Condense** the information; do **not** simply copy & paste
  - More space for important data
- ☞ **Consistent** alignment within the cells

Tables: How it COULD be done

X	Y	Z
block 1	...	...
block 1	...	...
block 1	...	...
block 2	...	...
block 2	Highlight	...
block 2	...	...

Table 1: Example table

Tables: How it should NOT be done

X	Y	Z	An unimportant column	A	B	C
...	...	...	...	...	...	...
...	...	...	...	...	...	...
...	...	...	...	...	...	...
...	...	...	...	...	...	...
...	...	...	...	...	...	...
...	...	...	...	...	...	...
...	...	...	...	...	...	...
...	...	...	...	...	...	...
...	...	...	...	...	...	...

Formulas

- ☞ Use specific **font** for variables
  - Do **not** use the same font as for regular text
- ☞ It is advisable to use formula editor/environment
- ☞ **Explain** the variables in the formula

Formulas: How it COULD be done

This is an example equation for variable X:

$$X = a \times b + Y - \alpha$$

where Y is the input variable and a, b and α are constants

Formulas: How it should NOT be done

This is an example equation for variable X:

$$X = a * b + Y - alpha$$

Structure

Title slide

- ☞ Presentation **title**, e.g. title of the publication
  - If presenting a paper add author names
  - If author list is too long, abbreviate it, e.g. last names of first three authors *et al.*
- ☞ Your **name**
- ☞ Presentation **purpose**, e.g. seminar
- ☞ Presentation **date**
- ☞ Optional: institution/group, logo

Outline/Overview

- ☞ Main **points** of the presentation
- ☞ **Avoid** general and uninformative keywords, i.e. no "Introduction", "Methods" etc.
- ☞ Instead, **concisely** motivate the main problem, how it is addressed, and what are the main improvements/conclusions

Methods

- ☞ Essential theoretical background
- ☞ E.g. workflow, structure, formulas etc.
- ☞ If necessary, provide reasonable simplifications for the purpose of the presentation but know the intricate details for the Q&A

Results

- ☞ Used data: How was it generated? Processed?
- ☞ Analysis steps
- ☞ Relevant results (figures, tables)
- ☞ **Emphasize** and highlight key results

Summary

- ☞ Summary of the approach
- ☞ Summary of the results
- ☞ Conclusions
- ☞ Advantages/drawbacks
- ☞ Future work

Other

☞ References:
- All used papers, books, articles, image sources etc.
- `google.com` or `wikipedia.org` are **not sufficient**, yet may be used as **starting points** of your literature research

☞ Optional: "Thank you" slide

☞ Appendix: Additional information and/or results, information requiring dedicated/explicit explanation etc.

Other suggestions

Preparation

- If the paper includes **supplemental material** – get it, it may contain additional explanations and important information
- Look through the **references** used in the paper – some things not explained in the paper may be found in there
- Preparing a presentation includes almost always additional **literature research** (apart from the mentioned references)

Appearance

- ☞ Export slides to **PDF** if sharing them with someone
  - Same appearance on different operating systems
  - For non-standard fonts, make sure to **embed** them in the PDF
- ☞ Avoid **crowded** slides:
  - **Reduce content**: As little as possible and as much as necessary
  - **Split** into multiple slides, if necessary
- ☞ Choose **appropriate** way of representing information
  - E.g., visualize **complex** things by a **figure** instead of text/formula (if appropriate)
- ☞ Use **simple examples** for your explanations
  - You may have non-experts in the audience
- ☞ **Highlight** important details in text, figures, tables, formulas

Text

- ☞ **No sentences** or **long phrases** (exceptions: quotes)
- ☞ **Paraphrase**, i.e. no copy-paste from paper
- ☞ Check appropriate use of whitespace – it distracts otherwise
  - **One** whitespace **after** a punctuation mark, e.g., comma or period
  - **No** whitespace **before** a punctuation mark

Talk

- **Practice** your talk in front of someone, it will help you to
  - Estimate the length (a bit shorter preferred over much longer)
  - Get additional feedback, possibly from non-experts
- **Talk to the audience**, do not look at the slides all the time
  - If necessary, use flashcards or other notes that you can put in front of you
  - N.B. do **not** simply read from your notes either
- Try to **avoid** making distracting gestures, sounds (e.g. "Um")
- **Explain** all needed details when showing
  - Formulas $\rightarrow$ What is computed? Variables?
  - Figures $\rightarrow$ What is plotted/drawn? Legend? Axes?
  - Tables $\rightarrow$ Column/row content?

  before interpreting
- **Be prepared** to explain all terms/methods/statements on your slides

References

Useful Tools, Links, and Literature

- Ten Secrets to Giving a Good Scientific Talk
- Elsevier: How to give a dynamic scientific presentation
- Butterick's Practical Typography - Presentations
- LaTeX
  - A high-quality typesetting system for writing scientific articles, theses, presentations
  - Freely available, there are many tutorials
  - Many features, e.g. mathematical environment, bibliography, automatic numbering for figures, tables and equations
- Gimp
  - Freely available
  - Can be used to create high-resolution screenshots from PDFs

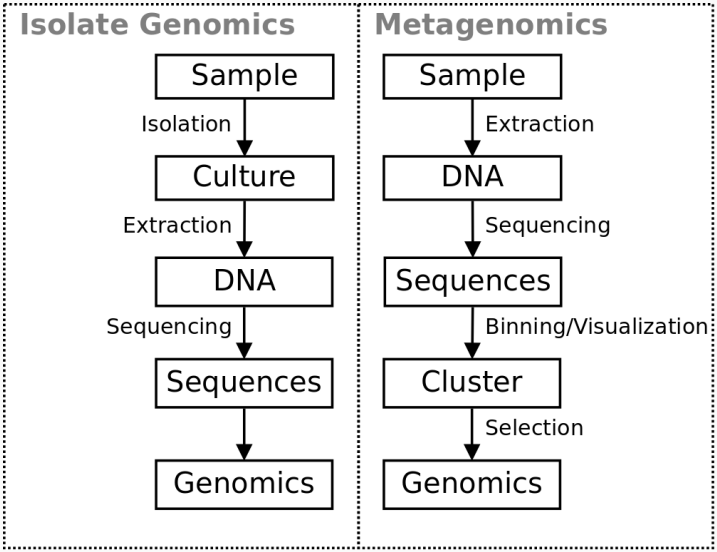
Presentation Example

Masterseminar

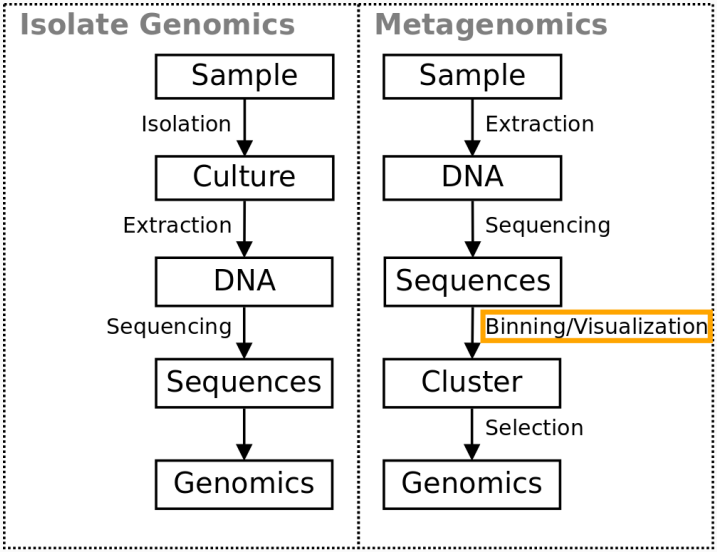
Visualization of metagenomic data utilizing coverage information

Dominik Wermke

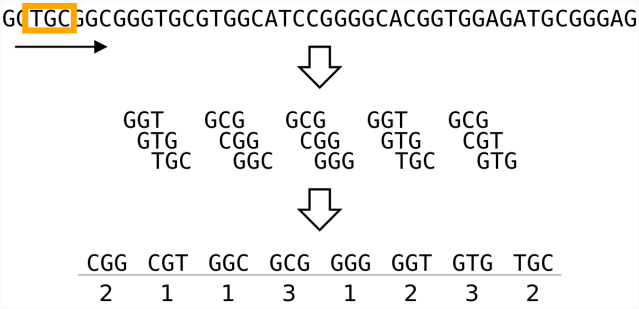
Metagenomics



Metagenomics

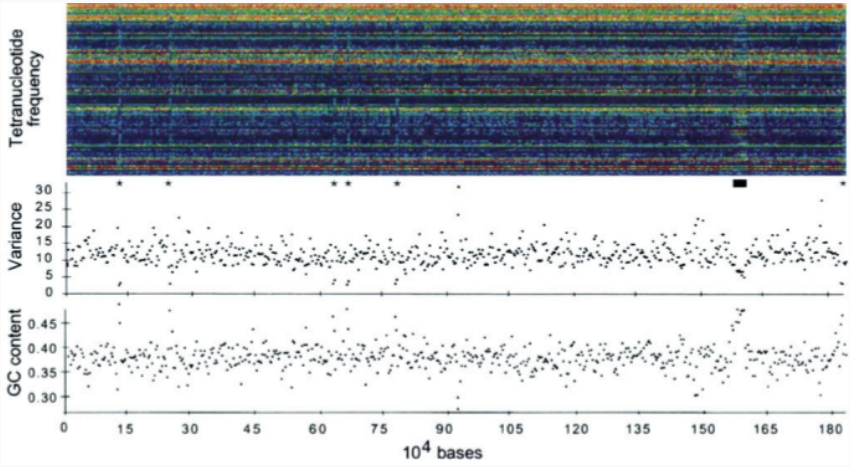


K-mers



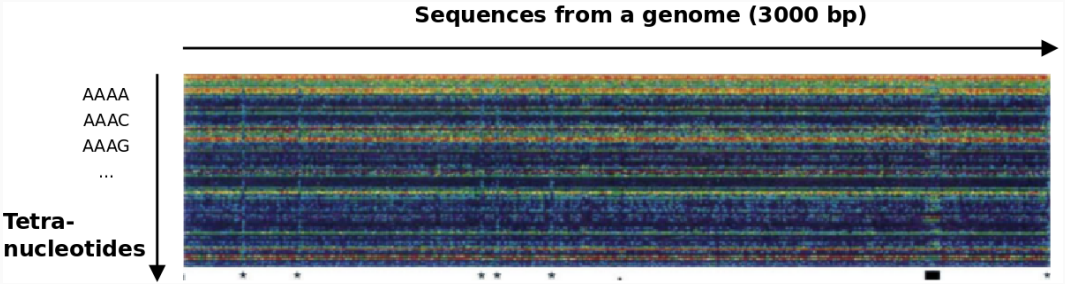
k	2	3	4	5
dimension	16	64	256	1024

K-mers


Tetranucleotide frequency
Variance
30
25
20
15
10
5
0
GC content
0.45
0.40
0.35
0.30
0
15
30
45
60
75
90
105
120
135
150
165
180
10^4 bases

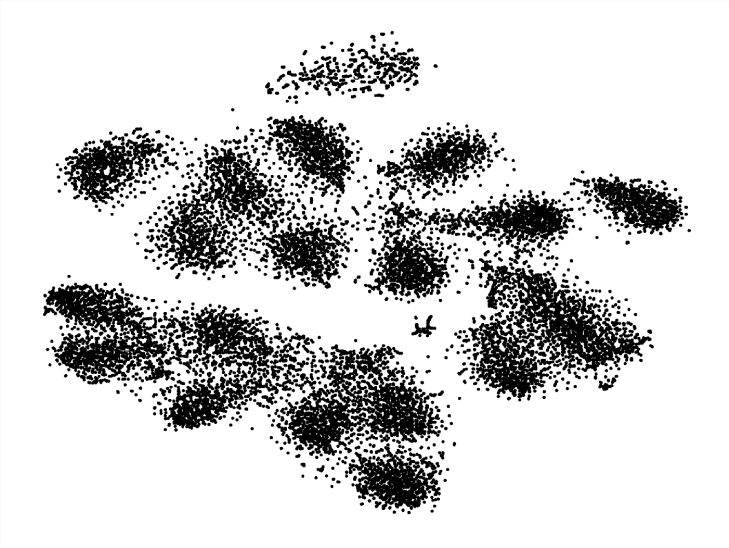
[1]

K-mers

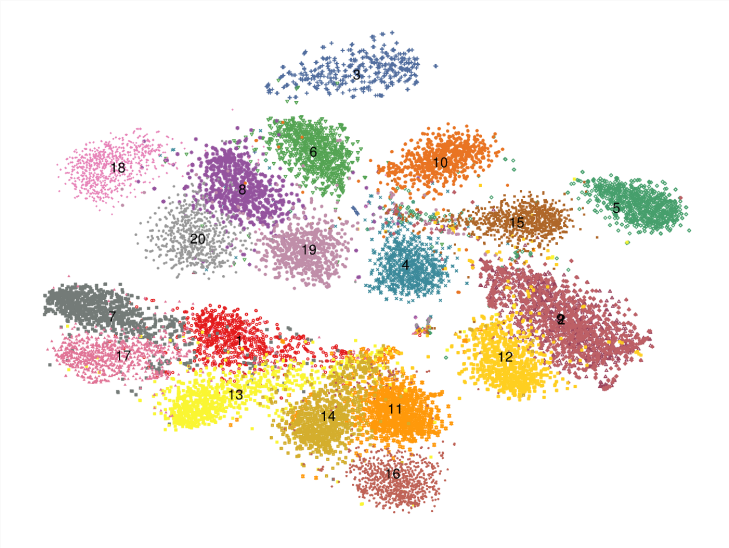

Sequences from a genome (3000 bp)
AAAA
AAAC
AAAG
...
Tetra-
nucleotides

[1]

Visualization



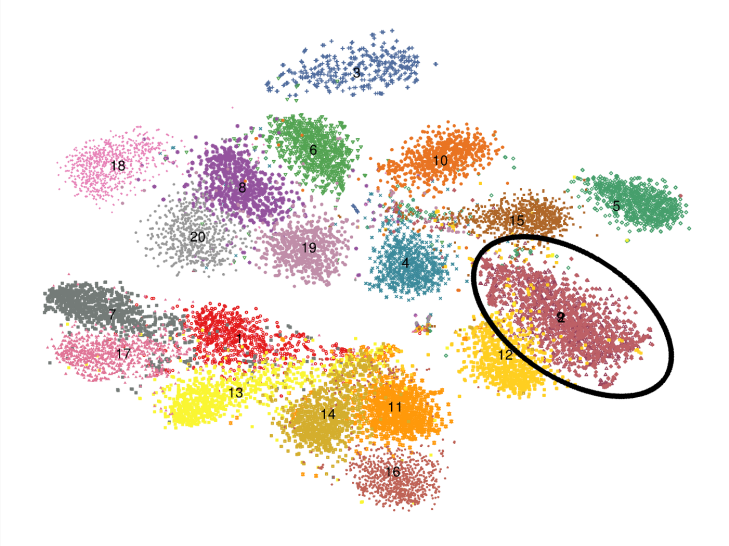
Visualization



Classes:

- (1) Leifsonia xyli
- (2) Escherichia coli UTI89
- (3) Candidatus Carsonella ruddii
- (4) Haemophilus influenzae
- (5) Bacillus amyloliquefaciens
- (6) Brachyspira hyodysenteriae
- (7) Geodermatophilus obscurus
- (8) Rickettsia prowazekii
- (9) Escherichia coli str. 'clone D i14'
- (10) Uncultured Termite group 1 bacterium
- (11) Maricaulis maris
- (12) Marinobacter psychrophilus
- (13) Methylobacterium nodulans
- (14) Aminobacter aminovorans
- (15) Bacillus clausii
- (16) Bordetella hinzii
- (17) Brachybacterium faecium
- (18) Campylobacter subantarcticus
- (19) Candidatus Amoebophilus asiaticus
- (20) Baumannia cicadellinicola

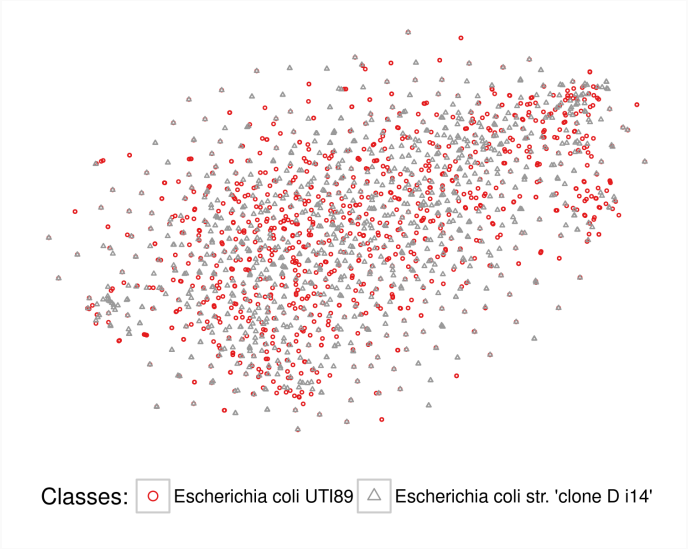
Visualization



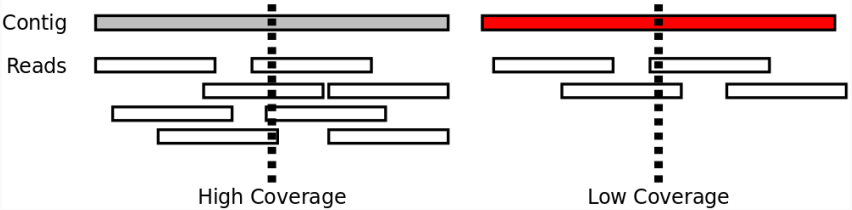
Classes:

- (1) Leifsonia xyli
- (2) Escherichia coli UTI89
- (3) Candidatus Carsonella ruddii
- (4) Haemophilus influenzae
- (5) Bacillus amyloliquefaciens
- (6) Brachyspira hyodysenteriae
- (7) Geodermatophilus obscurus
- (8) Rickettsia prowazekii
- (9) Escherichia coli str. 'clone D i14'
- (10) Uncultured Termite group 1 bacterium
- (11) Maricaulis maris
- (12) Marinobacter psychrophilus
- (13) Methylobacterium nodulans
- (14) Aminobacter aminovorans
- (15) Bacillus clausii
- (16) Bordetella hinzii
- (17) Brachybacterium faecium
- (18) Campylobacter subantarcticus
- (19) Candidatus Amoebophilus asiaticus
- (20) Baumannia cicadellinicola

Visualization

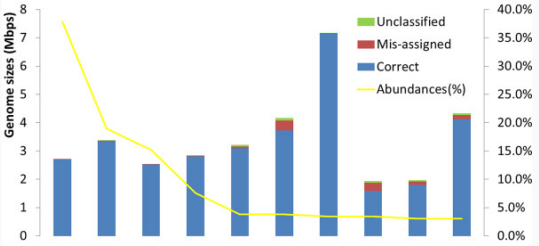


Coverage



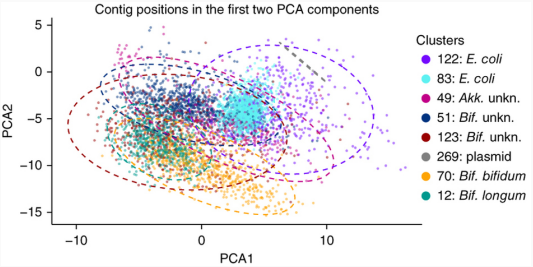
Coverage

MaxBin:



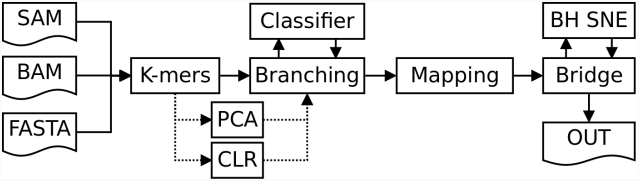
[2]

CONCOCT:

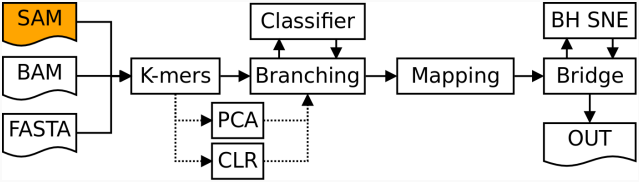


[3]

Implementation

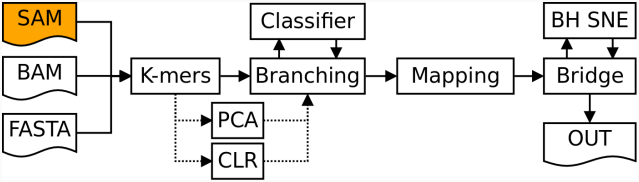


Implementation



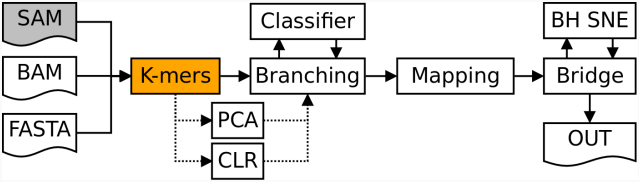
1	0	1	483	42	100M	*	0	0	GCAGTCGCGTATTCATCGCG	IIIIIIIIIIIIIIIIIIII
2	16	1	372	42	100M	*	0	0	TGCTCGAACGTCTGCAAAAG	IIIIIIIIIIIIIIIIIIII
3	0	1	646	42	100M	*	0	0	CAGCGCCGCTGATGGCGCGG	IIIIIIIIIIIIIIIIIIII
4	16	2	61	42	100M	*	0	0	GAGTTTTAACGACGAACGTG	IIIIIIIIIIIIIIIIIIII
5	0	2	390	42	100M	*	0	0	AGCGGATGAGCTTTGCGCTG	IIIIIIIIIIIIIIIIIIII

Implementation



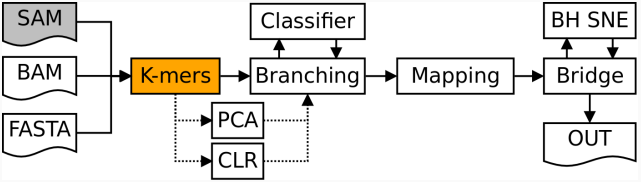
1	0	1	483	42	100M	*	0	0	GCAGTCGCGTATTCATCGCG	IIIIIIIIIIIIIIIIIIII
2	16	1	372	42	100M	*	0	0	TGCTCGAACGTCTGCAAAAG	IIIIIIIIIIIIIIIIIIII
3	0	1	646	42	100M	*	0	0	CAGCGCCGCTGATGGCGCGG	IIIIIIIIIIIIIIIIIIII
4	16	2	61	42	100M	*	0	0	GAGTTTTAACGACGAACGTG	IIIIIIIIIIIIIIIIIIII
5	0	2	390	42	100M	*	0	0	AGCGGATGAGCTTTGCGCTG	IIIIIIIIIIIIIIIIIIII

Implementation



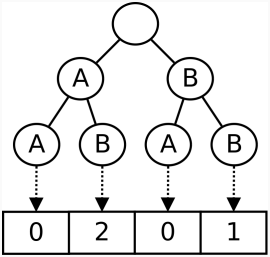
1	0	1	483	42	100M	*	0	0	GCAGTCGCGTATTCATCGCG	IIIIIIIIIIIIIIIIIIII
2	16	1	372	42	100M	*	0	0	TGCTCGAACGTCTGCAAAAG	IIIIIIIIIIIIIIIIIIII
3	0	1	646	42	100M	*	0	0	CAGCGCCGCTGATGGCGCGG	IIIIIIIIIIIIIIIIIIII
4	16	2	61	42	100M	*	0	0	GAGTTTTAACGACGAACGTG	IIIIIIIIIIIIIIIIIIII
5	0	2	390	42	100M	*	0	0	AGCGGATGAGCTTTGCGCTG	IIIIIIIIIIIIIIIIIIII

Implementation



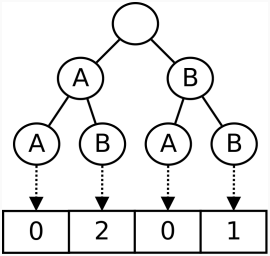
GCAGTCGCGTATTCATCGCG
TGCTCGAACGTCTGCAAAAG
CAGCGCCGCTGATGGCGCGG
GAGTTTTAACGACGAACGTG
AGCGGATGAGCTTTGCGCTG

Implementation



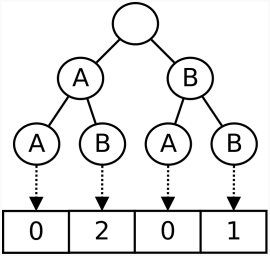
GCAGTCGCGTATTCATCGCG
TGCTCGAACGTCTGCAAAAG
CAGCGCCGCTGATGGCGCGG
GAGTTTTAACGACGAACGTG
AGCGGATGAGCTTTGCGCTG

Implementation



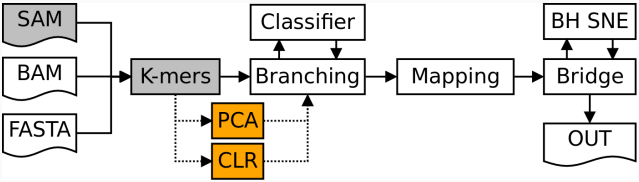
AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	...
0	0	0	0	0	0	0	0	...
2	1	1	0	0	0	1	0	...
0	0	0	0	0	0	0	0	...
0	2	0	0	0	0	3	0	...
0	0	0	0	0	0	0	0	...

Implementation



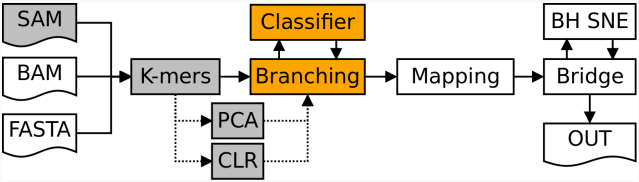
AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	...
0	0	0	0	0	0	0	0	...
0.111	0.056	0.056	0	0	0	0.056	0	...
0	0	0	0	0	0	0	0	...
0	0.111	0	0	0	0	0.167	0	...
0	0	0	0	0	0	0	0	...

Implementation



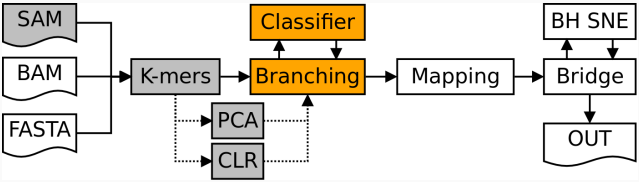
AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	...
0	0	0	0	0	0	0	0	...
0.111	0.056	0.056	0	0	0	0.056	0	...
0	0	0	0	0	0	0	0	...
0	0.111	0	0	0	0	0.167	0	...
0	0	0	0	0	0	0	0	...

Implementation



AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	...
0	0	0	0	0	0	0	0	...
0.111	0.056	0.056	0	0	0	0.056	0	...
0	0	0	0	0	0	0	0	...
0	0.111	0	0	0	0	0.167	0	...
0	0	0	0	0	0	0	0	...

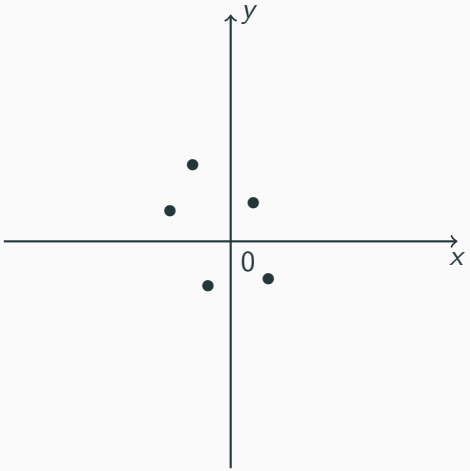
Implementation



ID	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	...
1	0	0	0	0	0	0	0	0	...
2	0.111	0.056	0.056	0	0	0	0.056	0	...
3	0	0	0	0	0	0	0	0	...
4	0	0.111	0	0	0	0	0.167	0	...
5	0	0	0	0	0	0	0	0	...

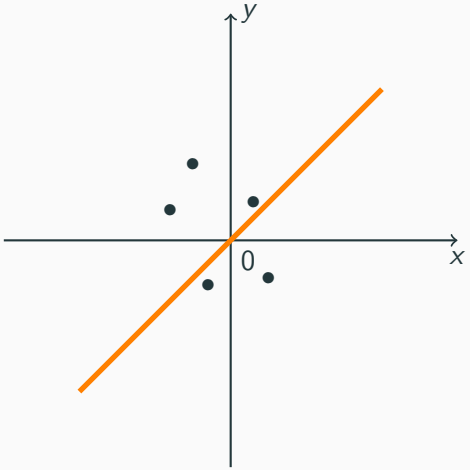
Implementation

1,2,3,4,5

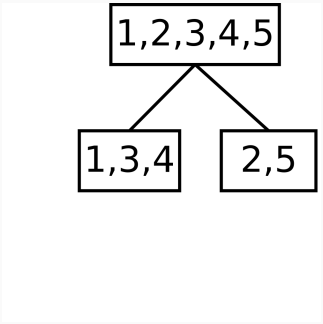


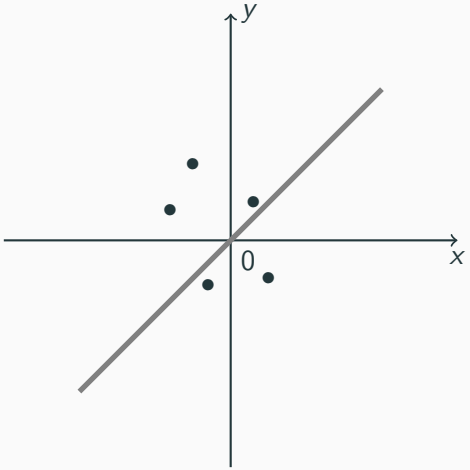
Implementation

1,2,3,4,5

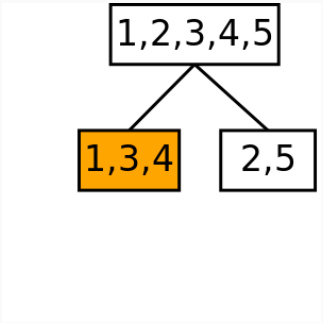


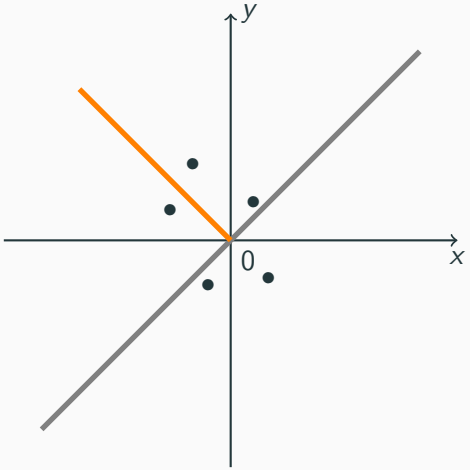
Implementation



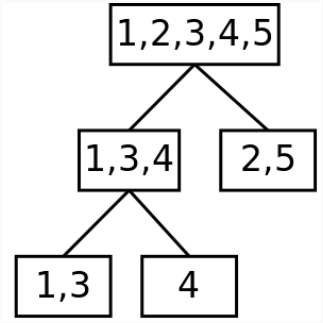


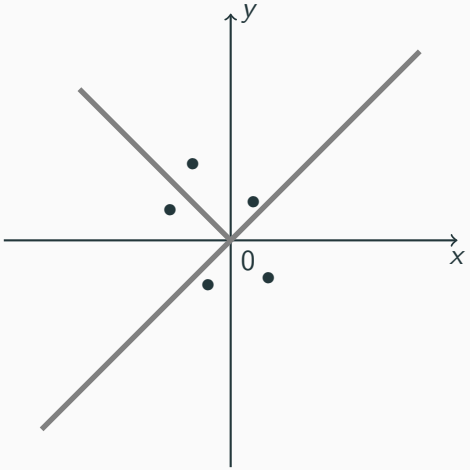
Implementation





Implementation





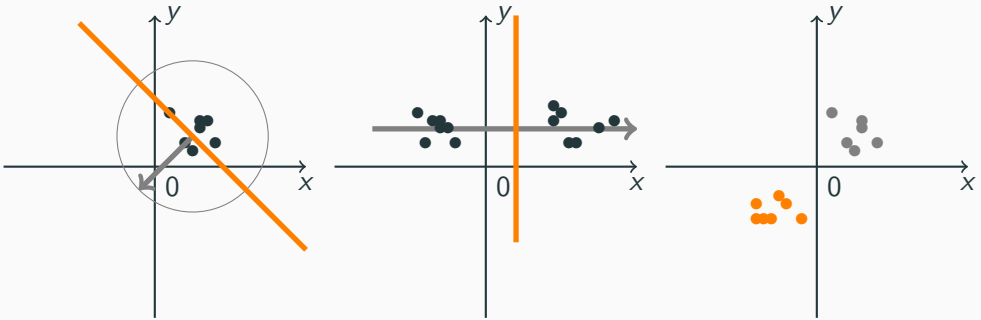
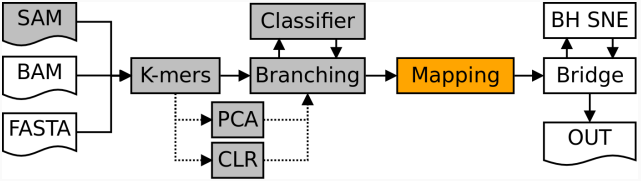


Figure 3: Mean classifier (left), Variance classifier (middle), 2-means (right)

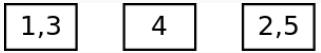
Implementation



Implementation

1	0	1	483	42	100M	*	0	0	GCAGTCGCGTATTCATCGCG	IIIIIIIIIIIIIIIIIIII
2	16	1	372	42	100M	*	0	0	TGCTCGAACGTCTGCAAAAG	IIIIIIIIIIIIIIIIIIII
3	0	1	646	42	100M	*	0	0	CAGCGCCGCTGATGGCGCGG	IIIIIIIIIIIIIIIIIIII
4	16	2	61	42	100M	*	0	0	GAGTTTTAACGACGAACGTG	IIIIIIIIIIIIIIIIIIII
5	0	2	390	42	100M	*	0	0	AGCGGATGAGCTTTGCGCTG	IIIIIIIIIIIIIIIIIIII

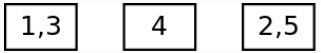
Contig ID	Read IDs
1	1, 2, 3
2	4 ,5



Implementation

Contig ID	Subspace 1	Subspace 2	Subspace 3
1	2 reads	0 reads	1 reads
2	0 reads	1 reads	1 reads

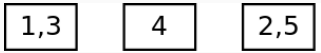
Contig ID	Read IDs
1	1, 2, 3
2	4 ,5



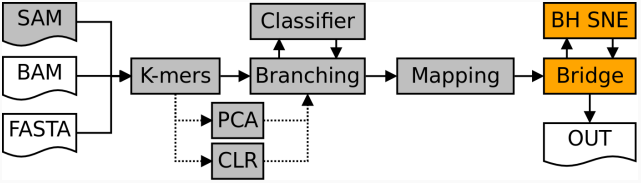
Implementation

	x1	x2	x3
Contig 1	2	0	1
Contig 2	0	1	1

Contig ID	Read IDs
1	1, 2, 3
2	4 ,5

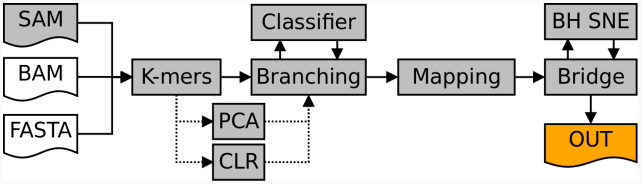


Implementation



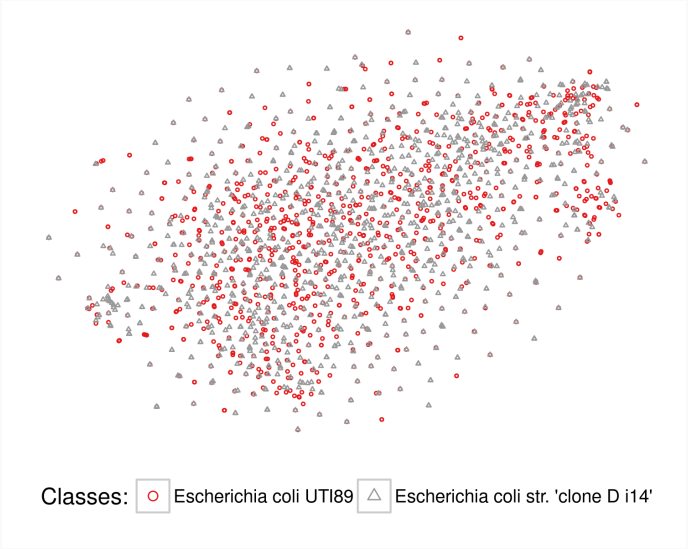
	x1	x2	x3
Contig 1	2	0	1
Contig 2	0	1	1

Implementation

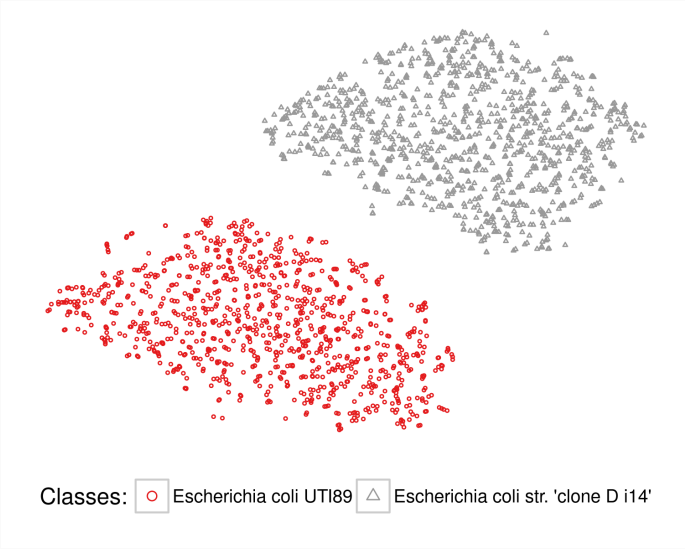


	x	y
Contig 1	0.345	1.234
Contig 2	-0.456	2.341

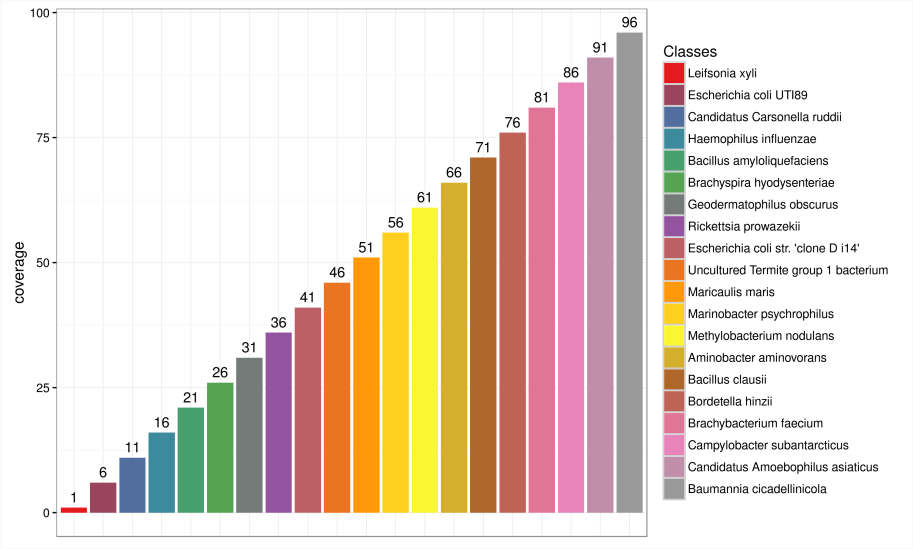
Two classes


Classes:
Escherichia coli UTI89
Escherichia coli str. 'clone D i14'

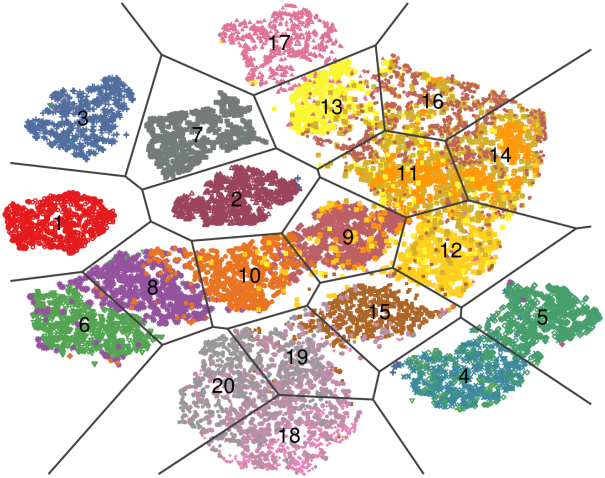
Two classes


Classes:
Escherichia coli UTI89
Escherichia coli str. 'clone D i14'

Data Set 1 (Linear)



Data Set 1 (Linear)



Classes:

- (1) Leifsonia xyli
- (2) Escherichia coli UTI89
- (3) Candidatus Carsonella ruddii
- (4) Haemophilus influenzae
- (5) Bacillus amyloliquefaciens
- (6) Brachyspira hyodysenteriae
- (7) Geodermatophilus obscurus
- (8) Rickettsia prowazekii
- (9) Escherichia coli str. 'clone D i14'
- (10) Uncultured Termite group 1 bacterium
- (11) Maricaulis maris
- (12) Marinobacter psychrophilus
- (13) Methylobacterium nodulans
- (14) Aminobacter aminovorans
- (15) Bacillus clausii
- (16) Bordetella hinzii
- (17) Brachybacterium faecium
- (18) Campylobacter subantarcticus
- (19) Candidatus Amoebophilus asiaticus
- (20) Baumannia cicadellinicola

Data Set 1 (Linear)

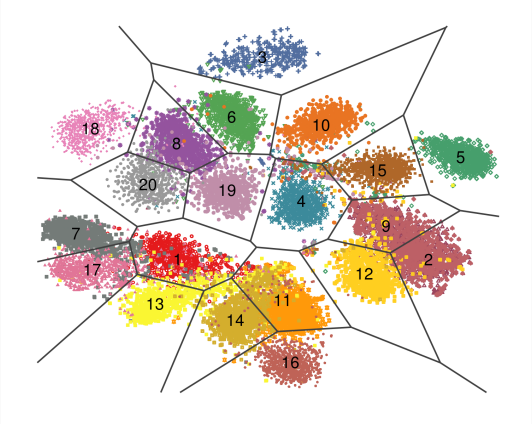


Figure 4: VizBin

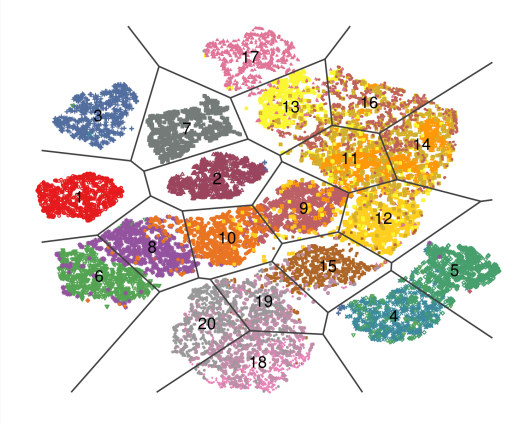


Figure 5: Implementation

Data Set 1 (Linear)

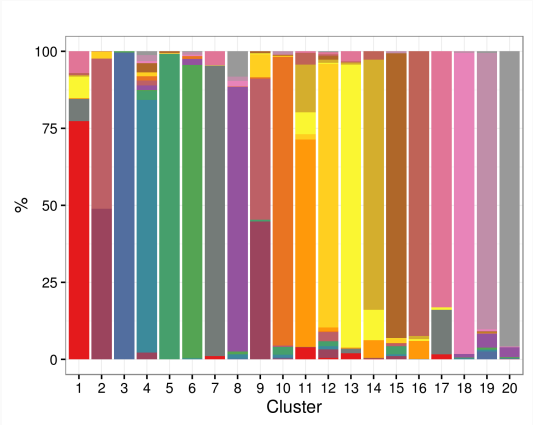


Figure 6: VizBin (Mean: 84.97%)

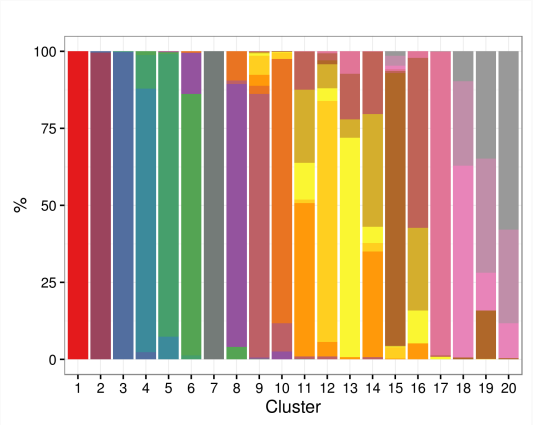
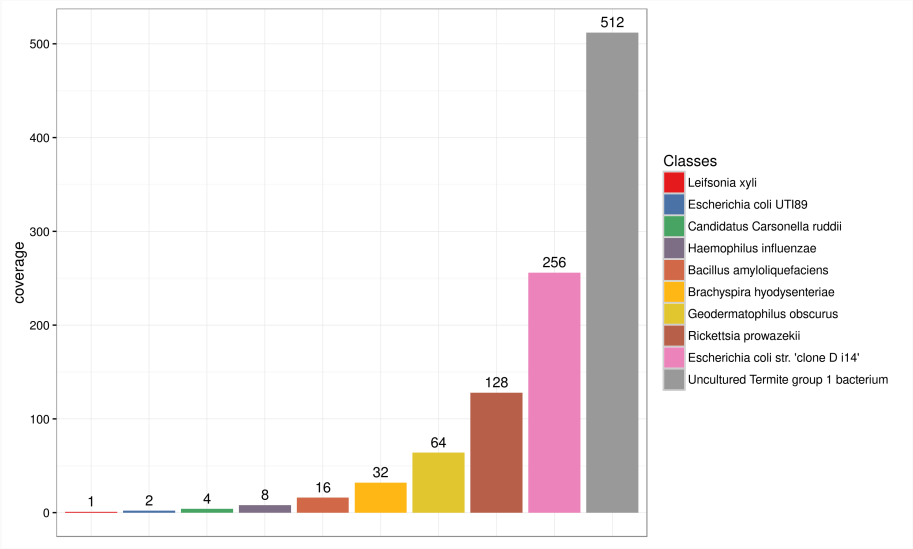
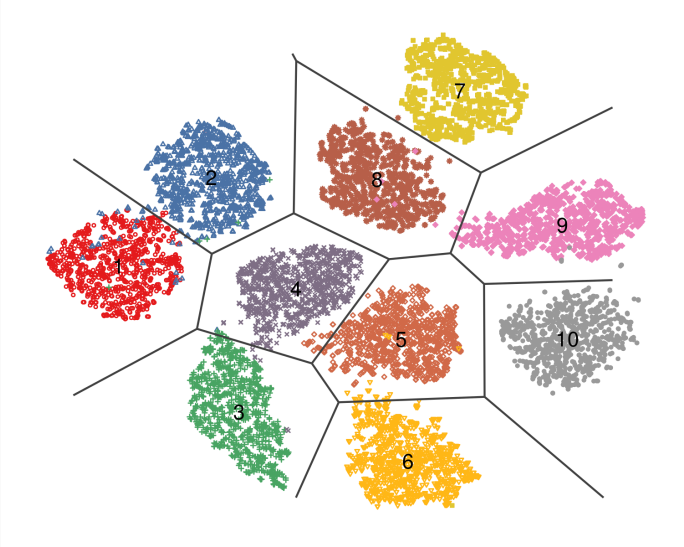


Figure 7: Implementation (Mean: 77.67%)

Data Set 2 (Exponential)



Data Set 2 (Exponential)



Classes:

- (1) Leifsonia xyli
- (2) Escherichia coli UTI89
- (3) Candidatus Carsonella ruddii
- (4) Haemophilus influenzae
- (5) Bacillus amyloliquefaciens
- (6) Brachyspira hyodysenteriae
- (7) Geodermatophilus obscurus
- (8) Rickettsia prowazekii
- (9) Escherichia coli str. 'clone D i14'
- (10) Uncultured Termite group 1 bacterium

Data Set 2 (Exponential)

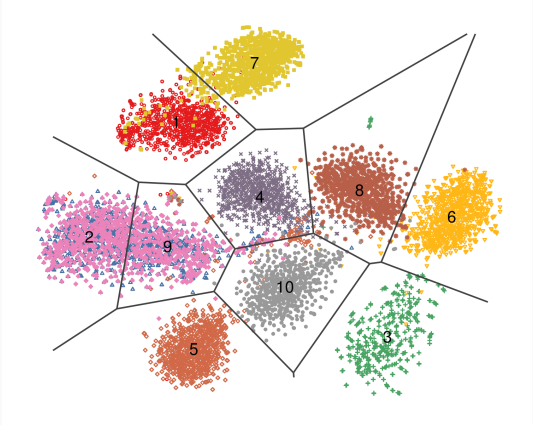


Figure 8: VizBin

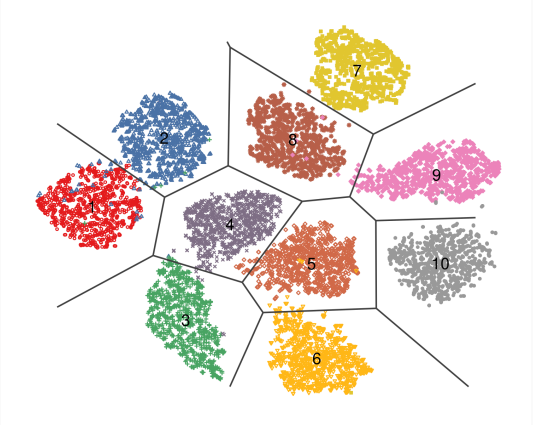


Figure 9: Implementation

Data Set 2 (Exponential)

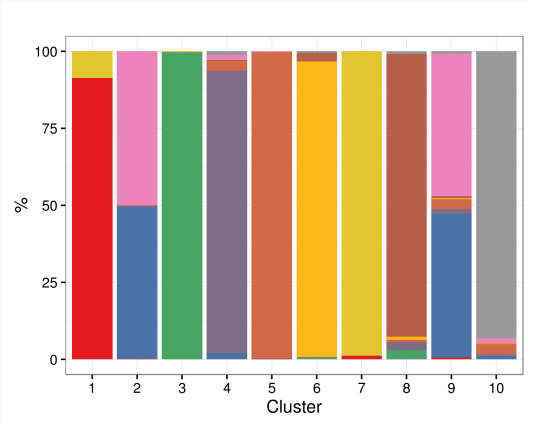


Figure 10: VizBin (Mean: 85.78%)

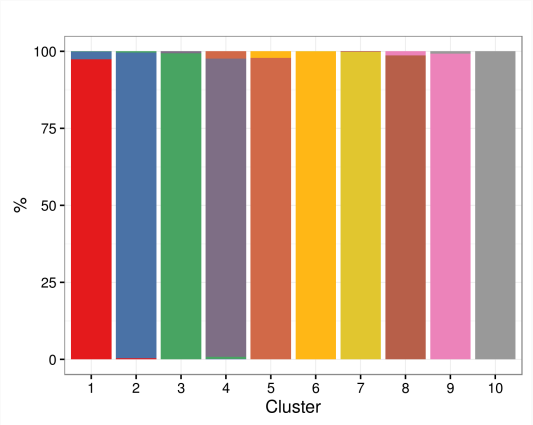
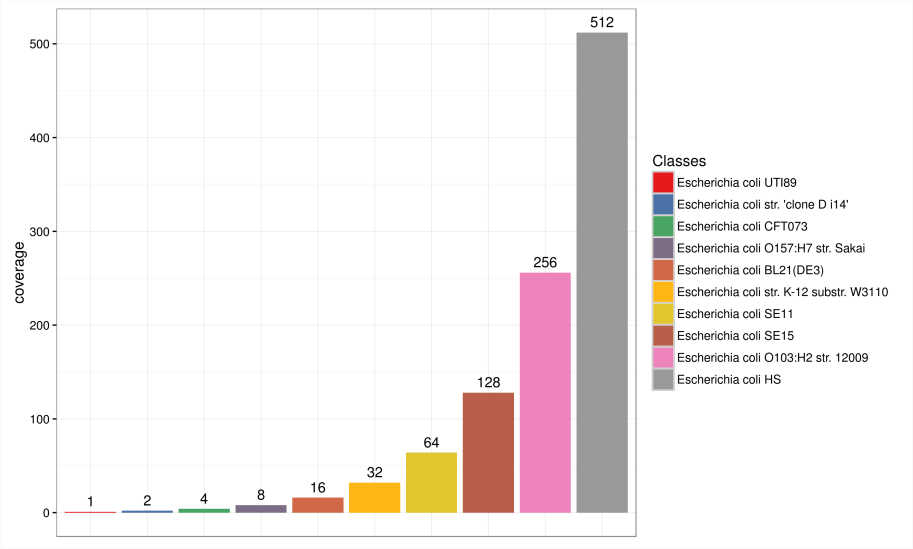
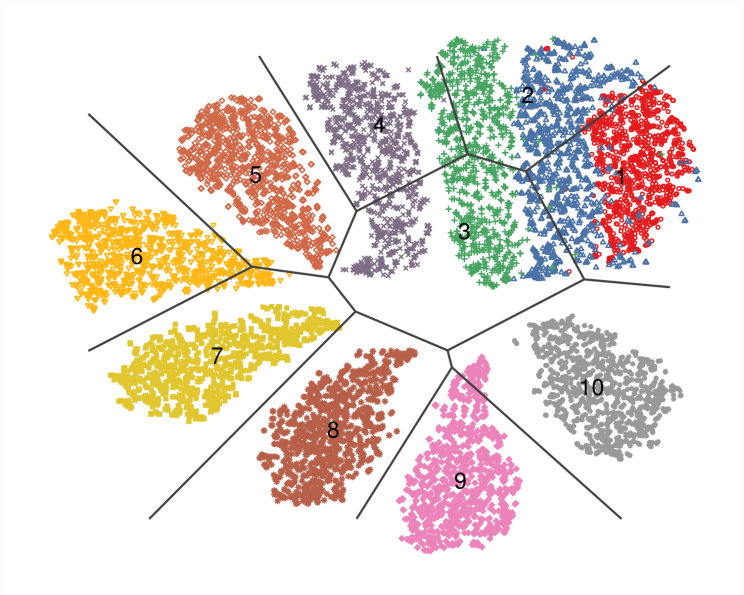


Figure 11: Implementation (Mean: 98.83%)

Data Set 3 (Similar Organisms)



Data Set 3 (Similar Organisms)



Classes:

- (1) Escherichia coli UTI89
- (2) Escherichia coli str. 'clone D i14'
- (3) Escherichia coli CFT073
- (4) Escherichia coli O157:H7 str. Sakai
- (5) Escherichia coli BL21(DE3)
- (6) Escherichia coli str. K-12 substr. W3110
- (7) Escherichia coli SE11
- (8) Escherichia coli SE15
- (9) Escherichia coli O103:H2 str. 12009
- (10) Escherichia coli HS

Data Set 3 (Similar Organisms)

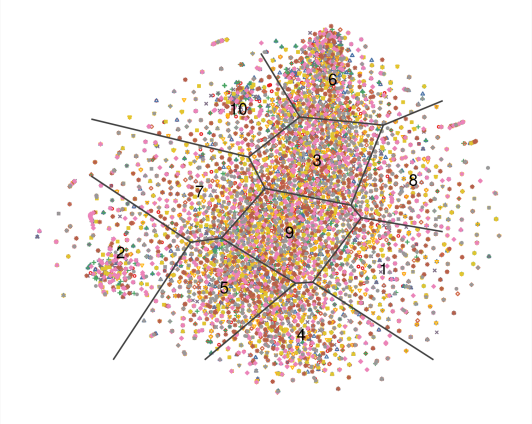


Figure 12: VizBin

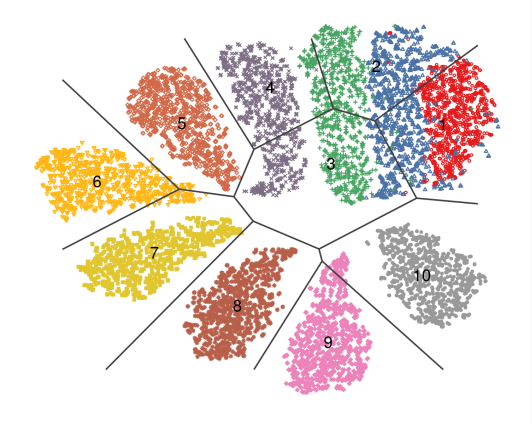


Figure 13: Implementation

Data Set 3 (Similar Organisms)

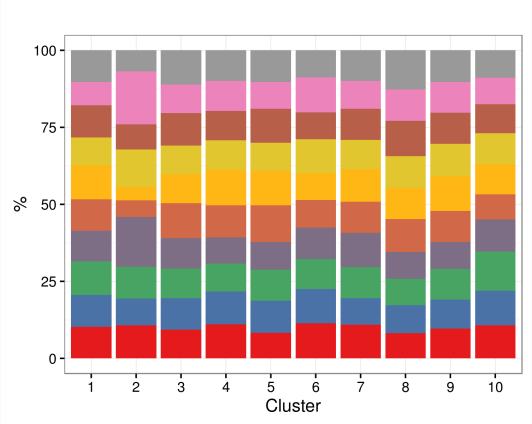


Figure 14: VizBin (Mean: 9.83%)

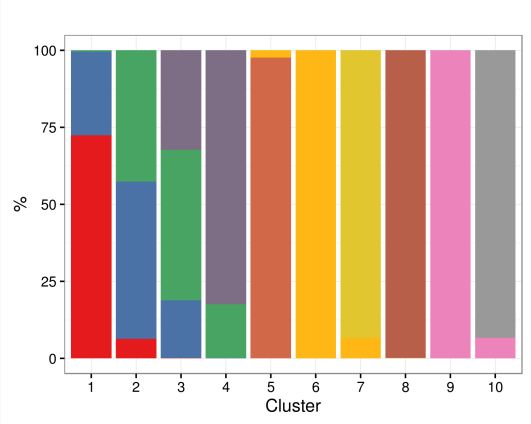
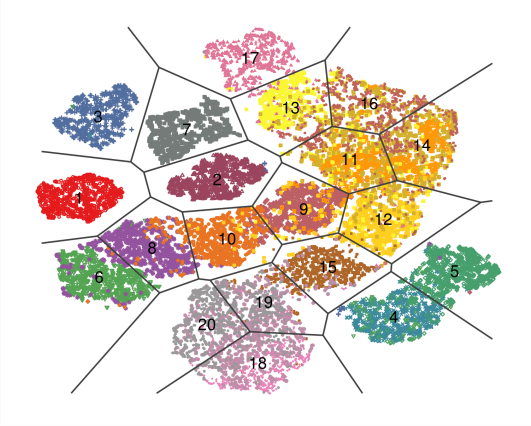
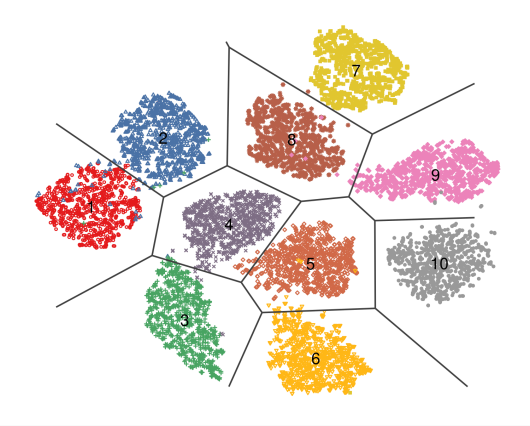


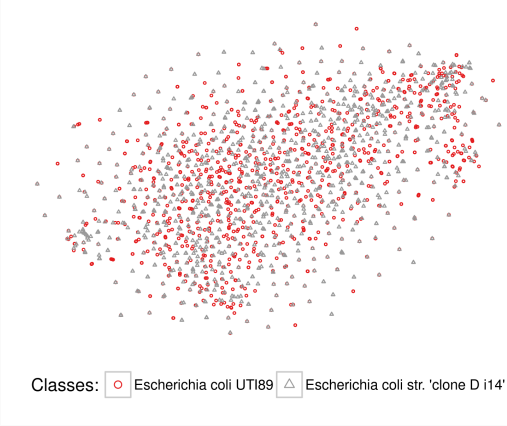
Figure 15: Implementation (Mean: 83.89%)

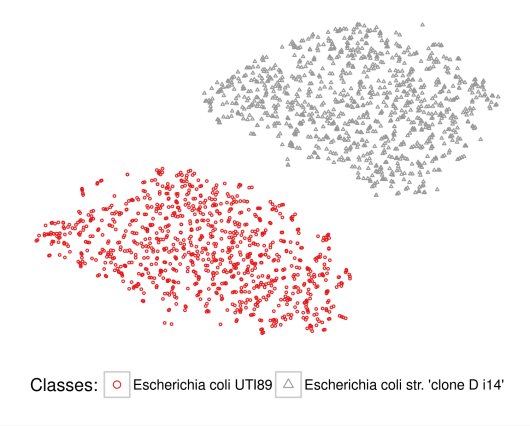
Conclusion





Conclusion


Classes:
Escherichia coli UTI89
Escherichia coli str. 'clone D i14'


Classes:
Escherichia coli UTI89
Escherichia coli str. 'clone D i14'

References i

Noble PA, Citek RW and Ogunseitan OA.
Tetranucleotide frequencies in microbial genomes.
Electrophoresis
19(4), p. 528–35

Yu-Wei Wu, Yung-Hsu Tang, Susannah G Tringe, Blake A Simmons and Steven W Singer
MaxBin: an automated binning method to recover individual genomes from metagenomes using an expectation-maximization algorithm.
Microbiome
2:26


J.Alneberg et al.
Binning metagenomic contigs by coverage and composition.
Nature Methods
11, p. 1144–1146

Appendix

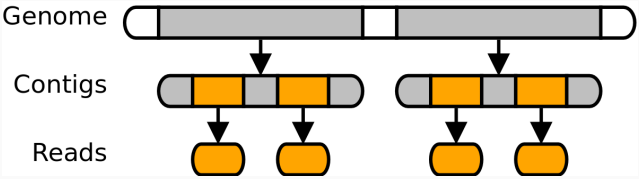
Name	Assembly Accession
Leifsonia xyli CTCB07	GCF_000007665.1_ASM766v1
Candidatus Carsonella ruddii HT	GCF_000287295.1_ASM28723v1
Haemophilus influenzae 86–028NP	GCF_000016485.1_ASM1648v1
Bacillus amyloliquefaciens TA208	GCF_000195515.1_ASM19551v1
Brachyspira hyodysenteriae WA1	GCF_000022105.1_ASM2210v1
Geodermatophilus obscurus DSM 43160	GCF_000025345.1_ASM2534v1
Rickettsia prowazekii Dachau	GCF_000277225.1_ASM27722v1
Uncultured Termite group 1 bacterium Rs-D17	GCF_000146025.2_ASM14602v1
Maricaulis maris MCS10	GCF_000014745.1_ASM1474v1
Marinobacter psychrophilus 20041	GCF_001043175.1_ASM104317v1
Methylobacterium nodulans ORS 2060	GCF_000022085.1_ASM2208v1
Aminobacter colombiense DSM 12261	GCF_000025885.1_ASM2588v1
Bacillus clausii KSM-16	GCF_000009825.1_ASM982v1
Bordetella hinzii F582	GCF_001078275.1_ASM107827v1
Brachybacterium faecium DSM 4810	GCF_000023405.1_ASM2340v1
Campylobacter subantarcticus LMG 24374	GCF_000816265.1_ASM81626v1
Candidatus Amoebophilus asiaticus 5a2	GCF_000020565.1_ASM2056v1
Candidatus Baumannia cicadellinicola Hc	GCF_000013185.1_ASM1318v1

continued on next slide

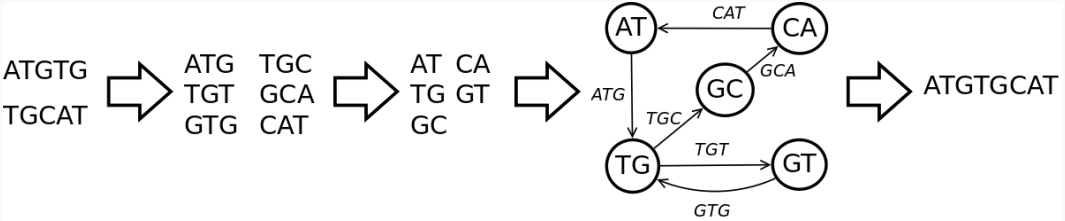
Appendix

Name	Assembly Accession
Escherichia coli UTI89	GCF_000013265.1_ASM1326v1
Escherichia coli clone D i14	GCF_000233895.1_ASM23389v1
Escherichia coli CFT073	GCF_000007445.1_ASM744v1
Escherichia coli O157:H7 str. Sakai	GCF_000008865.1_ASM886v1
Escherichia coli BL21(DE3)	GCF_000009565.1_ASM956v1
Escherichia coli str. K-12 substr. W3110	GCF_000010245.2_ASM1024v1
Escherichia coli SE11	GCF_000010385.1_ASM1038v1
Escherichia coli SE15	GCF_000010485.1_ASM1048v1
Escherichia coli O103:H2 str. 12009	GCF_000010745.1_ASM1074v1
Escherichia coli HS	GCF_000017765.1_ASM1776v1

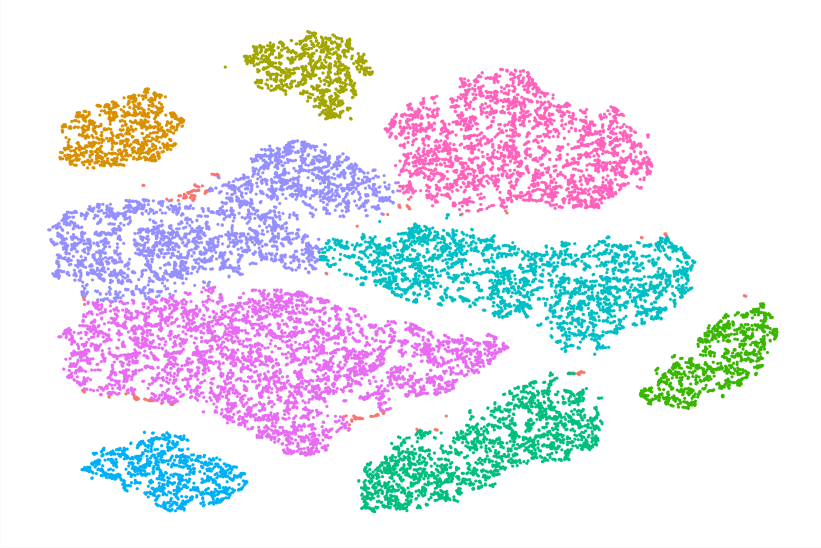
Appendix



Appendix


ATGTG
TGCAT
ATG TGC
TGT GCA
GTG CAT
AT CA
TG GT
GC
AT
CA
GC
TG
GT
CAT
GCA
ATG
TGC
TGT
GTG
ATGTGCAT

Appendix



Appendix

High Dimensional:

$$p_{i|i} = 0 \qquad p_{j|i} = \frac{\exp -d(x_i, x_j)^2 / 2\sigma_i^2}{\sum_{k \neq i} \exp -d(x_i, x_k)^2 / 2\sigma_i^2} \tag{1}$$

$$p_{ij} = \frac{p_{j|i} + p_{i|j}}{2N} \tag{2}$$

Low Dimensional (Student-t):

$$q_{ij} = \frac{\left(1 + ||y_i - y_j||^2\right)^{-1}}{\sum_{k \neq l} \left(1 + ||y_k - y_l||^2\right)^{-1}} \tag{3}$$

Combined:

$$\mathrm{KL}(P||Q) = \sum_{i \neq j} p_{ij} \log \frac{p_{ij}}{q_{ij}} \tag{4}$$