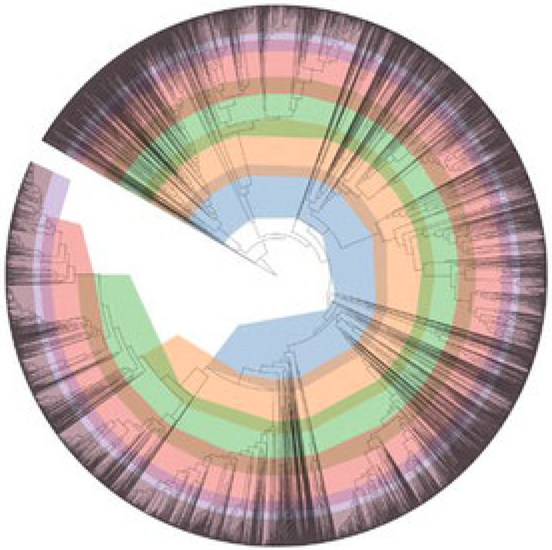
ENVIRONMENTAL METAGENOMICS

Physalia course, online, 11-15 November 2024

Read-based taxonomic profiling

Nikolay Oskolkov, Lund University, NBIS SciLifeLab
Luis Pedro Coelho, Queensland University of Technology



NB: original course material courtesy:
Dr. Antti Karkman, University of Helsinki
Dr. Igor Pessi, Finnish Environment Institute (SYKE)

Typical analysis methods used in metagenomics

1) Alignment:

BOW TIE

BWA

stands for

Burrows Wheeler Aligner

Abbreviations.com

HOPS

2) Classification:

KRAKEN

Centrifuge

MetaPhlan

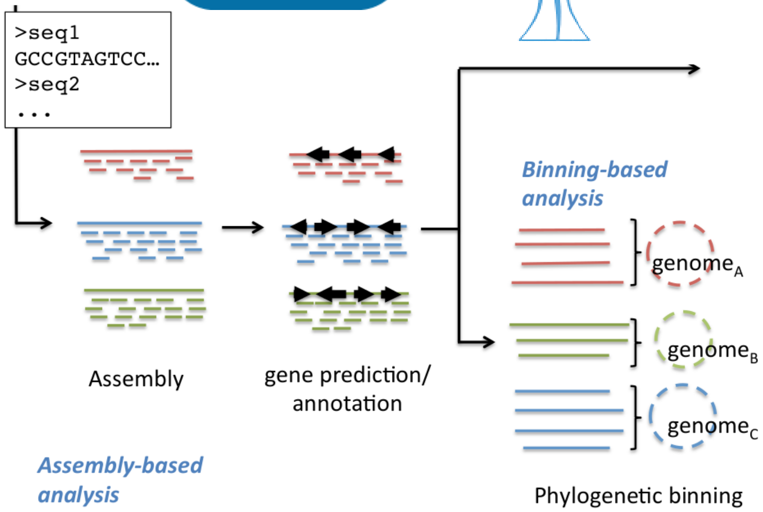
Clark

Reference based:
assume similarity to reference

3) De-novo assembly:

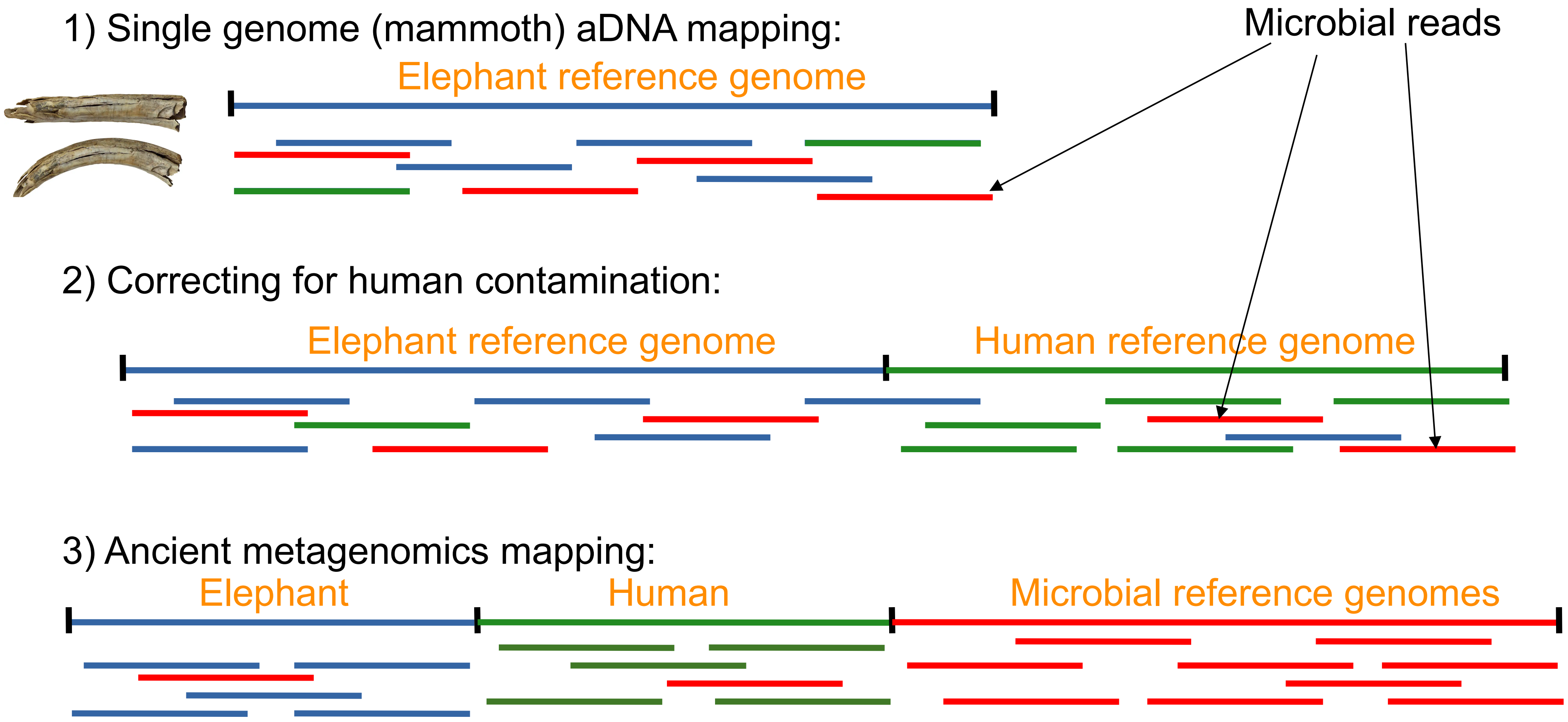
MEGA HIT

meta



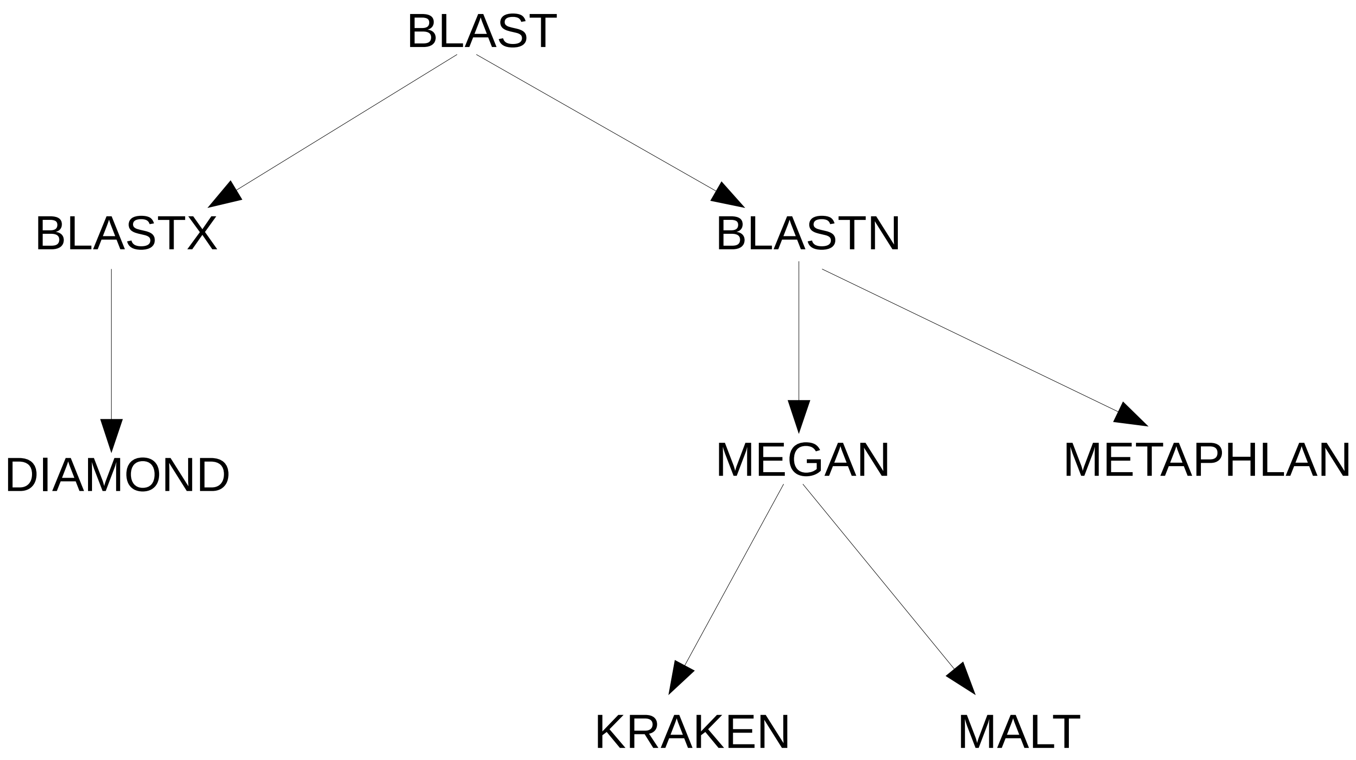
Reference free:
unbiased but challenging

What is competitive mapping and why you should do it



Competitive mapping is absolutely central for metagenomic analysis!

Evolution of taxonomic profilers (my view)



K-mer based taxonomic profiling: Kraken family of tools

Wood *et al. Genome Biology* (2019) 20:257
https://doi.org/10.1186/s13059-019-1891-0

Genome Biology

SHORT REPORT Open Access

Improved metagenomic analysis with Kraken 2

Check for updates

Derrick E. Wood[1,2], Jennifer Lu[2,3] and Ben Langmead[1,2*]

Abstract

Although Kraken's *k*-mer-based approach provides a fast taxonomic classification of metagenomic sequence data, its large memory requirements can be limiting for some applications. Kraken 2 improves upon Kraken 1 by reducing memory usage by 85%, allowing greater amounts of reference genomic data to be used, while maintaining high accuracy and increasing speed fivefold. Kraken 2 also introduces a translated search mode, providing increased sensitivity in viral metagenomics analysis.

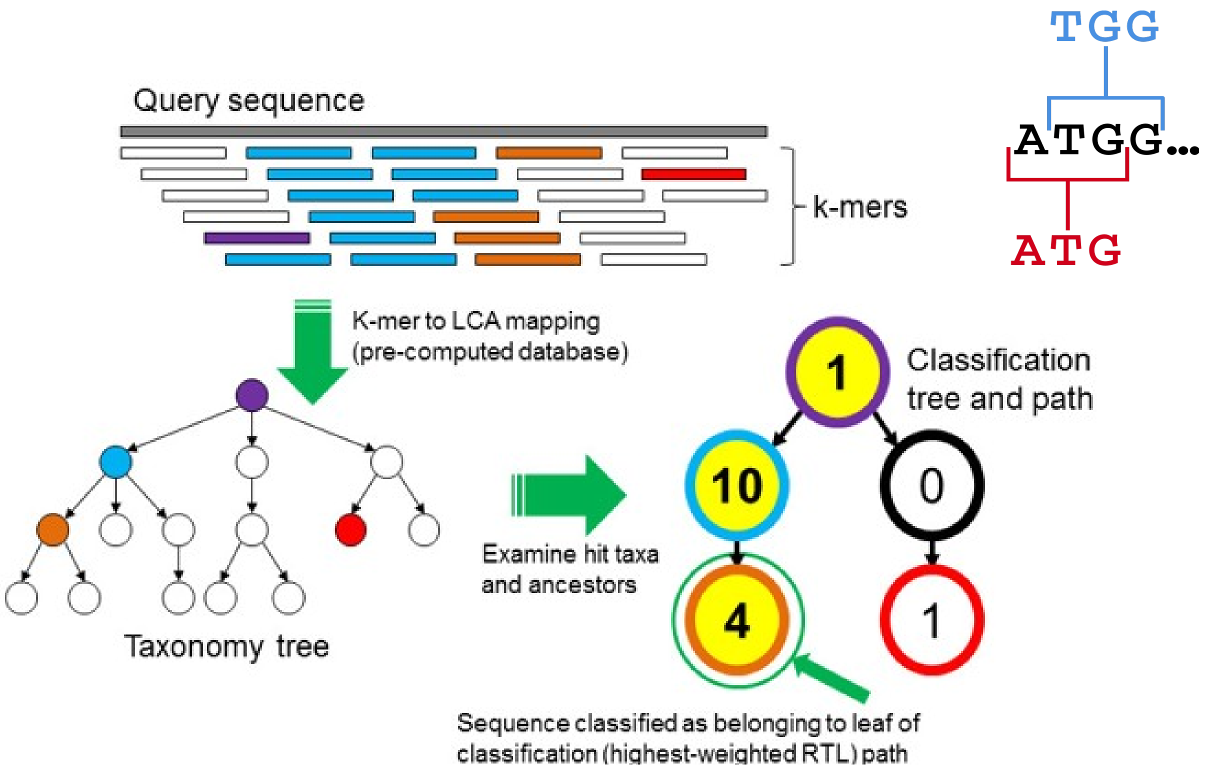
Keywords: Metagenomics, Metagenomics classification, Microbiome, Probabilistic data structures, Alignment-free methods, Minimizers

Assigning taxonomic labels to sequencing reads is an important part of many computational genomics pipelines for metagenomics projects. Recent years have seen several approaches to accomplish this task in a time-efficient manner [1–3]. One such tool, Kraken [4], uses a memory-intensive algorithm that associates short genomic substrings (*k*-mers) with the lowest common ancestor (LCA) taxa. Kraken and related tools like KrakenUniq [5] have proven highly efficient and accurate in independent tool comparisons [6, 7]. But Kraken's high memory requirements force many researchers to either use a reduced-sensitivity MiniKraken database [8, 9] or to build and use many indexes over subsets of the reference sequences [10,11]. Its memory requirements can easily exceed 100 GB [7], especially when the reference data includes large eukaryotic genomes [12,13]. Here, we introduce Kraken 2, which provides a major reduction in memory usage as well as faster classification, a spaced seed searching scheme, a translated search mode for matching in amino acid space, and continued compatibility with the Bracken [14] species-level sequence abundance estimation algorithm.

Kraken 2 addresses the issue of large memory requirements through two changes to Kraken 1's data structures and algorithms. While Kraken 1 used a sorted list of *k*-mer/LCA pairs indexed by minimizers [15], Kraken 2 introduces a probabilistic, compact hash table to map minimizers to LCAs. This table uses one third of the memory of a standard hash table, at the cost of some specificity and accuracy. Additionally, Kraken 2 only stores minimizers (of length ℓ, $\ell \le k$) from the reference sequence library in its data structure, whereas Kraken 1 stored all *k*-mers. This change means that, during classification, the minimizer (ℓ-mer) is the substring compared against a reference set in Kraken 2, while Kraken 1 compared *k*-mers (Fig. 1a, b). Kraken 2's index for a specific reference database with 9.1 Gbp of genomic sequences uses 10.6 GB of memory when classifying. Kraken 1's index for the same reference uses 72.4 GB of memory for classification (Fig. 2a, Additional file 1: Table S1). In general, a Kraken 2 database is about 85% smaller than a Kraken 1 database over the same references (Additional file 2: Figure S1).

Kraken 2's approach is faster than Kraken 1's because only distinct minimizers from the query (read) trigger accesses to the hash table. A similar minimizer-based approach has proven useful in accelerating read alignment [16]. Kraken 2 additionally provides a hash-based subsampling approach that reduces the set of minimizer/LCA pairs included in the table, allowing the user to specify a target hash table size; smaller hash tables yield lower memory usage and higher classification

* Correspondence: langmea@cs.jhu.edu
[1] Department of Computer Science, Whiting School of Engineering, Johns Hopkins University, Baltimore, MD, USA
[2] Center for Computational Biology, Johns Hopkins University, Baltimore, MD, USA
Full list of author information is available at the end of the article



Physalia
Courses

Advantage of classification over alignment: speed, Kraken2 is very fast!

Why exactly do we need LCA?

Same genus

sequence 1 ATGGTCGGGCAGGACGTTGCGAGT — Species 1
sequence 2 CGAGAAGGGCAGGACGCCACGTAC — Species 2

Ambiguous reads

- Ignore ambiguous reads (loose many reads)
- Keep them for quantifying abundance on genus level (LCA)
- Align genus reads to your species of interest ref genome (isn't it too risky?)

Physalia Courses

Krestovka.merged.trimmed.fastq.gz_kraken2.output - LibreOffice Calc

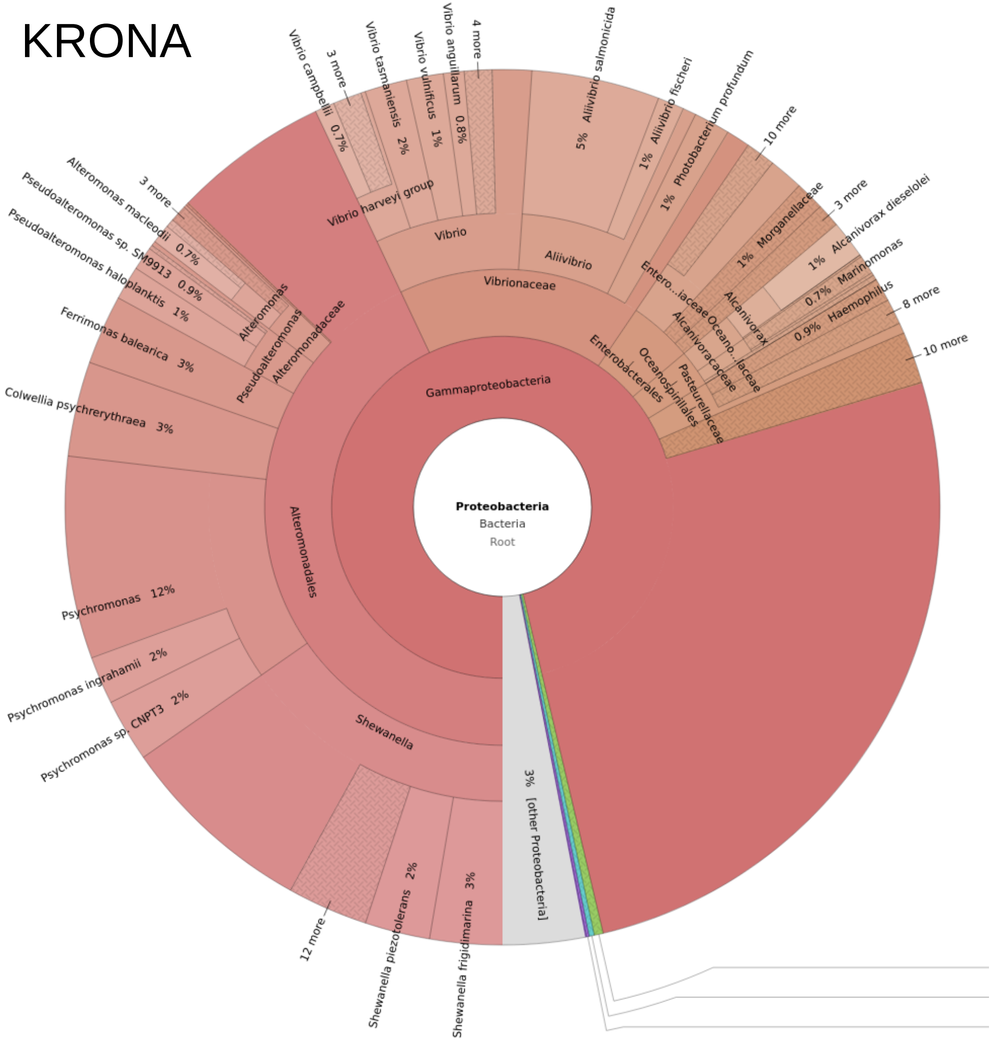
% of reads	reads	taxReads	n_minimizer	n_distinct_minimizer	rank	taxID	Name
85.76	229988348	229988348	0	0	U	0	unclassified
14.24	38188511	317329	229258315	10956342	R	1	root
14.1	37814928	553677	223347668	10689204	R1	131567	cellular organisms
13.35	35791835	861918	201695602	8612373	D	2	Bacteria
10.84	29060274	1196943	151278879	5085202	P	1224	Proteobacteria
8.22	22056723	407757	106202766	1185104	C	28216	Betaproteobacteria
7.82	20984490	1268537	97499372	1030255	O	80840	Burkholderiales
6	16081257	2224086	68602917	538180	F	80864	Comamonadaceae
2.23	5974652	286945	22944027	90448	G	52972	Polaromonas
1.11	2971020	18648	10967489	38279	S	216465	Polaromonas naphthalenivorans
1.1	2952372	2952372	10917548	38245	S1	365044	Polaromonas naphthalenivorans CJ2
0.95	2560665	1058948	9078851	43621	G1	2638319	unclassified Polaromonas
0.55	1465800	1465800	4741406	23365	S	296591	Polaromonas sp. JS666
0	8327	8327	23317	17	S	1840289	Polaromonas sp. H4N
0	7639	7639	40303	221	S	1840293	Polaromonas sp. H6N
0	7127	7127	35955	154	S	1840301	Polaromonas sp. W10N
0	3429	3429	14648	74	S	1840297	Polaromonas sp. H8N
0	2336	2336	10159	219	S	1840303	Polaromonas sp. W11N
0	1757	1757	7805	272	S	1869339	Polaromonas sp.
0	1251	1251	2288	2	S	1840287	Polaromonas sp. H3N
0	956	956	4451	96	S	1840283	Polaromonas sp. H1N
0	770	770	1317	8	S	416605	Polaromonas sp. A10
0	721	721	1823	1	S	1840281	Polaromonas sp. H12N
0	628	628	712	5	S	2268087	Polaromonas sp. SP1
0	255	255	812	64	S	1840267	Polaromonas sp. E5S
0	245	245	745	49	S	1840265	Polaromonas sp. E3S
0	222	222	1167	24	S	1840239	Polaromonas sp. E10S
0	163	163	405	2	S	480424	Polaromonas sp. GM1
0	20	20	374	1	S	1840257	Polaromonas sp. E19S
0	15	15	51	5	S	642193	Polaromonas sp. RB76
0	15	15	57	20	S	1840275	Polaromonas sp. E9S
0	9	9	28	16	S	1840323	Polaromonas sp. W9N
0	8	8	8	1	S	1705699	Polaromonas sp. 277

Krestovka.merged.trimmed.fastq.gz_kraken2

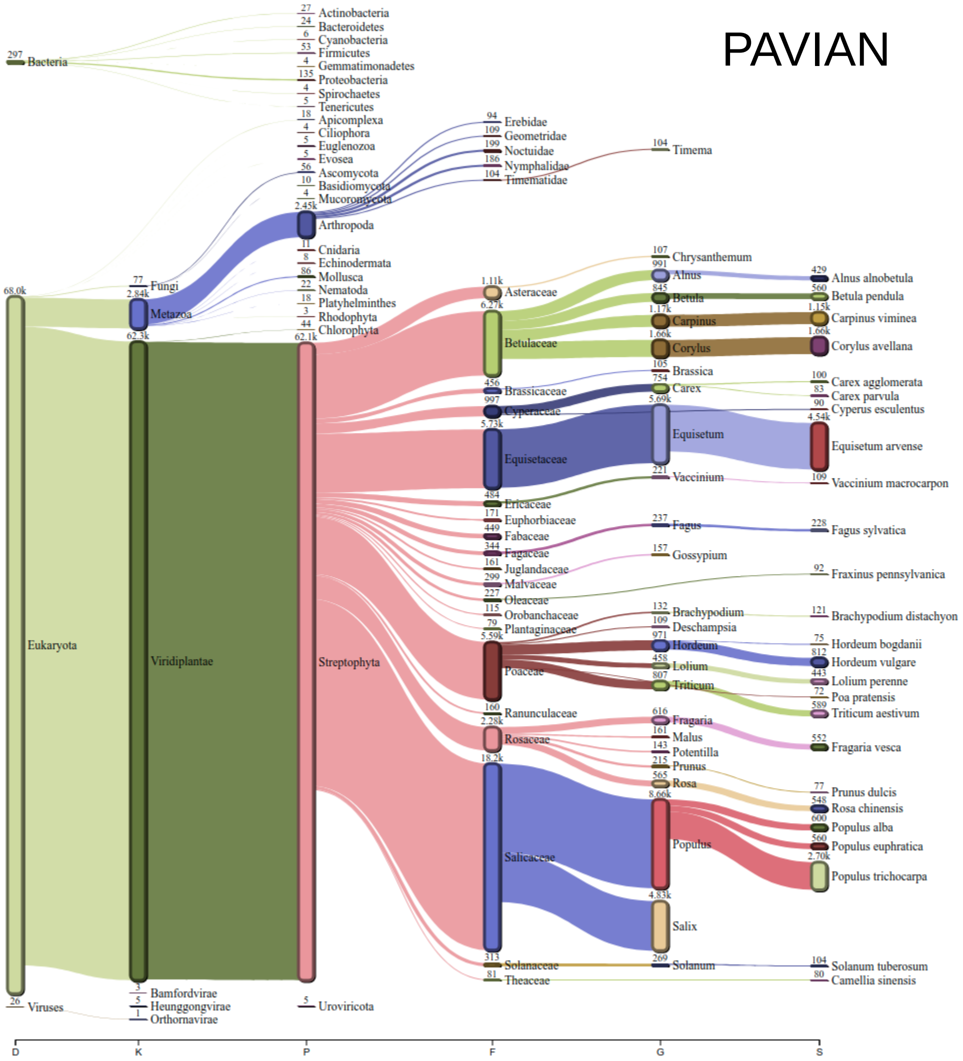
Sheet 1 of 1

Ways to visualize and interpret taxonomic profilers outputs

KRONA



PAVIAN



How you see false-positives: Kraken2 with NT database

	A	B	C	D	E	F
1	Percent_Reads	Reads	TaxReads	Rank	TaxID	Name
2	0.12	6438	6438	S	1009846	Burkholderia cepacia GG4
3	0.09	4683	4683	S	1395570	Burkholderia cepacia JBK9
4	0.09	4685	4685	S	1417228	Paraburkholderia phytofirmans OLGA172
5	0.05	2483	2483	S	1249668	Burkholderia ubonensis MSMB22
6	0.05	2736	2736	S	339670	Burkholderia ambifaria AMMD
7	0.04	2193	2193	S	391038	Paraburkholderia phymatum STM815
8	0.04	2317	2317	S	9615	Canis lupus familiaris
9	0.03	1738	1738	S	754502	Paraburkholderia sprentiae WSM5005
10	0.03	1640	1640	S	1229205	Paraburkholderia phenoliruptrix BR3459a
11	0.03	1664	1664	S	1416914	Pandoraea pnomenusa 3kgm
12	0.03	1785	1785	S	1112204	Gordonia polyisoprenivorans VH2
13	0.02	871	871	S	395019	Burkholderia multivorans ATCC 17616
14	0.02	919	919	S	398577	Burkholderia ambifaria MC40-6
15	0.02	955	955	S	398527	Paraburkholderia phytofirmans PsJN
16	0.02	982	982	S	266265	Paraburkholderia xenovorans LB400
17	0.02	973	973	S	272630	Methylorubrum extorquens AM1
18	0.02	1143	1143	S	223781	Aquila chrysaetos chrysaetos
19	0.02	1192	1192	S	202946	Apteryx mantelli mantelli
20	0.01	755	755	S	406425	Burkholderia cenocepacia MC0-3
21	0.01	623	623	S	32009	Burkholderia gladioli pv. gladioli
22	0.01	581	581	S	999541	Burkholderia gladioli BSR3
23	0.01	772	772	S	1323664	Paraburkholderia caribensis MBA4
24	0.01	536	536	S	264198	Cupriavidus pinatubonensis JMP134
25	0.01	752	752	S	882378	Paraburkholderia rhizoxinica HKI 454
26	0.01	546	546	S	1034807	Flavobacterium branchiophilum FL-15
27	0.01	587	587	S	112262	Ovis canadensis canadensis

Look like reasonable microbes so far ...

This was a blank!

Give me one best metagenomic taxonomic classifier

AMERICAN SOCIETY FOR MICROBIOLOGY | mSystems®

RESEARCH ARTICLE
Ecological and Evolutionary Science

Check for updates

Selection of Appropriate Metagenome Taxonomic Classifiers for Ancient Microbiome Research

Irina M. Velsko,[a*] Laurent A. F. Frantz,[a,b] Alexander Herbig,[c] Greger Larson,[a] Christina Warinner[c,d,e]

[a]Palaeogenomics and Bio-Archaeology Research Network, Research Laboratory for Archaeology and the History of Art, University of Oxford, Oxford, United Kingdom
[b]School of Biological and Chemical Sciences, Queen Mary University of London, London, United Kingdom
[c]Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Jena, Germany
[d]Department of Anthropology, University of Oklahoma, Norman, Oklahoma, USA
[e]Department of Periodontics, University of Oklahoma Health Sciences Center, Oklahoma City, Oklahoma, USA

ABSTRACT Metagenomics enables the study of complex microbial communities from myriad sources, including the remains of oral and gut microbiota preserved in archaeological dental calculus and paleofeces, respectively. While accurate taxonomic assignment is essential to this process, DNA damage characteristic of ancient samples (e.g., reduction in fragment size and cytosine deamination) may reduce the accuracy of read taxonomic assignment. Using a set of *in silico*-generated metagenomic data sets, we investigated how the addition of ancient DNA (aDNA) damage patterns influences microbial taxonomic assignment by five widely used profilers: QIIME/UCLUST, MetaPhlAn2, MIDAS, CLARK-S, and MALT. *In silico*-generated data sets were designed to mimic dental plaque, consisting of 40, 100, and 200 microbial species/strains, both with and without simulated aDNA damage patterns. Following taxonomic assignment, the profiles were evaluated for species presence/absence, relative abundance, alpha diversity, beta diversity, and specific taxonomic assignment biases. Unifrac metrics indicated that both MIDAS and MetaPhlAn2 reconstructed the most accurate community structure. QIIME/UCLUST, CLARK-S, and MALT had the highest number of inaccurate taxonomic assignments; false-positive rates were highest by CLARK-S and QIIME/UCLUST. Filtering out species present at <0.1% abundance greatly increased the accuracy of CLARK-S and MALT. All programs except CLARK-S failed to detect some species from the input file that were in their databases. The addition of ancient DNA damage resulted in minimal differences in species detection and relative abundance between simulated ancient and modern data sets for most programs. Overall, taxonomic profiling biases are program specific rather than damage dependent, and the choice of taxonomic classification program should be tailored to specific research questions.

IMPORTANCE Ancient biomolecules from oral and gut microbiome samples have been shown to be preserved in the archaeological record. Studying ancient microbiome communities using metagenomic techniques offers a unique opportunity to reconstruct the evolutionary trajectories of microbial communities through time. DNA accumulates specific damage over time, which could potentially affect taxonomic classification and our ability to accurately reconstruct community assemblages. It is therefore necessary to assess whether ancient DNA (aDNA) damage patterns affect metagenomic taxonomic profiling. Here, we assessed biases in community structure, diversity, species detection, and relative abundance estimates by five popular metagenomic taxonomic classification programs using *in silico*-generated data sets with and without aDNA damage. Damage patterns had minimal impact on the taxonomic profiles produced by each program, while false-positive rates and biases were intrinsic to each program. Therefore, the most ap-

Received 29 May 2018 **Accepted** 20 June 2018 **Published** 17 July 2018

Citation Velsko IM, Frantz LAF, Herbig A, Larson G, Warinner C. 2018. Selection of appropriate metagenome taxonomic classifiers for ancient microbiome research. mSystems 3:e00080-18. https://doi.org/10.1128/mSystems.00080-18.

Editor Thomas J. Sharpton, Oregon State University

Address correspondence to Christina Warinner, warinner@shh.mpg.de.

* Present address: Irina M. Velsko, Department of Biological Sciences, Clemson University, Clemson, South Carolina, USA.

Taxonomic classification of ancient metagenomes is minimally affected by DNA damage patterns

PeerJ

Benchmarking metagenomics classifiers on ancient viral DNA: a simulation study

Yami Ommar Arizmendi Cárdenas[1,2], Samuel Neuenschwander[1,3] and Anna-Sapfo Malaspinas[1,2]

[1] Department of Computational Biology, University of Lausanne, Lausanne, Switzerland
[2] Swiss Institute of Bioinformatics, Lausanne, Switzerland
[3] Vital-IT, Swiss Institute of Bioinformatics, Lausanne, Switzerland

ABSTRACT

Owing to technological advances in ancient DNA, it is now possible to sequence viruses from the past to track down their origin and evolution. However, ancient DNA data is considerably more degraded and contaminated than modern data making the identification of ancient viral genomes particularly challenging. Several methods to characterise the modern microbiome (and, within this, the virome) have been developed; in particular, tools that assign sequenced reads to specific taxa in order to characterise the organisms present in a sample of interest. While these existing tools are routinely used in modern data, their performance when applied to ancient microbiome data to screen for ancient viruses remains unknown. In this work, we conducted an extensive simulation study using public viral sequences to establish which tool is the most suitable to screen ancient samples for human DNA viruses. We compared the performance of four widely used classifiers, namely Centrifuge, Kraken2, DIAMOND and MetaPhlAn2, in correctly assigning sequencing reads to the corresponding viruses. To do so, we simulated reads by adding noise typical of ancient DNA to a set of publicly available human DNA viral sequences and to the human genome. We fragmented the DNA into different lengths, added sequencing error and C to T and G to A deamination substitutions at the read termini. Then we measured the resulting sensitivity and precision for all classifiers. Across most simulations, more than 228 out of the 233 simulated viruses were recovered by Centrifuge, Kraken2 and DIAMOND, in contrast to MetaPhlAn2 which recovered only around one third. Overall, Centrifuge and Kraken2 had the best performance with the highest values of sensitivity and precision. We found that deamination damage had little impact on the performance of the classifiers, less than the sequencing error and the length of the reads. Since Centrifuge can handle short reads (in contrast to DIAMOND and Kraken2 with default settings) and since it achieve the highest sensitivity and precision at the species level across all the simulations performed, it is our recommended tool. Regardless of the tool used, our simulations indicate that, for ancient human studies, users should use strict filters to remove all reads of potential human origin. Finally, we recommend that users verify which species are present in the database used, as it might happen that default databases lack sequences for viruses of interest.

Submitted 12 April 2021
Accepted 21 December 2021
Published 24 March 2022

Corresponding authors
Samuel Neuenschwander, samuel.neuenschwander@unil.ch
Anna-Sapfo Malaspinas, annasapfo.malaspinas@unil.ch

Academic editor
Joseph Gillespie

Additional Information and Declarations can be found on page 26

DOI 10.7717/peerj.12784

microorganisms MDPI

Article

Benchmarking Metagenomic Classifiers on Simulated Ancient and Modern Metagenomic Data

Vaidehi Pusadkar [1,2] and Rajeev K. Azad [1,2,3,*]

[1] Department of Biological Sciences, University of North Texas, Denton, TX 76203, USA; vaidehipusadkar@my.unt.edu
[2] BioDiscovery Institute, University of North Texas, Denton, TX 76203, USA
[3] Department of Mathematics, University of North Texas, Denton, TX 76203, USA
* Correspondence: rajeev.azad@unt.edu

Abstract: Taxonomic profiling of ancient metagenomic samples is challenging due to the accumulation of specific damage patterns on DNA over time. Although a number of methods for metagenome profiling have been developed, most of them have been assessed on modern metagenomes or simulated metagenomes mimicking modern metagenomes. Further, a comparative assessment of metagenome profilers on simulated metagenomes representing a spectrum of degradation depth, from the extremity of ancient (most degraded) to current or modern (not degraded) metagenomes, has not yet been performed. To understand the strengths and weaknesses of different metagenome profilers, we performed their comprehensive evaluation on simulated metagenomes representing human dental calculus microbiome, with the level of DNA damage successively raised to mimic modern to ancient metagenomes. All classes of profilers, namely, DNA-to-DNA, DNA-to-protein, and DNA-to-marker comparison-based profilers were evaluated on metagenomes with varying levels of damage simulating deamination, fragmentation, and contamination. Our results revealed that, compared to deamination and fragmentation, human and environmental contamination of ancient DNA (with modern DNA) has the most pronounced effect on the performance of each profiler. Further, the DNA-to-DNA (e.g., Kraken2, Bracken) and DNA-to-marker (e.g., MetaPhlAn4) based profiling approaches showed complementary strengths, which can be leveraged to elevate the state-of-the-art of ancient metagenome profiling.

Keywords: microorganisms; microbial DNA; ancient metagenomics; taxonomic profiling; benchmarking

check for updates

Citation: Pusadkar, V.; Azad, R.K. Benchmarking Metagenomic Classifiers on Simulated Ancient and Modern Metagenomic Data. *Microorganisms* **2023**, *11*, 2478. https://doi.org/10.3390/microorganisms11102478

Academic Editor: Renmao Tian

Received: 18 July 2023
Revised: 28 September 2023
Accepted: 29 September 2023
Published: 2 October 2023

1. Introduction

The evolutionary history of genetic information of all extant microorganisms goes back up to billions of years in time. Advances in metagenome sequencing have enabled the reconstruction of evolutionary trajectories to understand how microbial communities have evolved through time. Such studies have highlighted the emergence and evolution of microbes involved in infectious diseases [1,2], ancient pandemics [3], and migrations that happened in the past. Ancient metagenomics refers to the analysis of complex genomic content which is retrieved from degraded biological material of ancient or extinct microorganisms. Research in this field is commonly focused on adding a new perspective to our understanding of the past and providing exciting sources of information for modern metagenomics studies. With the decrease in sequencing cost and increase in coverage depth, thanks to the next-generation high throughput sequencing technologies, reliable estimation of the relative abundance of organisms (or taxa) dwelling in an environment is now possible [4]. Popular methods for profiling microbial communities use sequence data obtained using either 16S rRNA amplicon sequencing or whole shotgun metagenome sequencing. The former targets the 16S rRNA gene for taxonomic profiling, while the latter targets the entire complement of genomic information in a community to profile

Are we comparing classifiers or filtering strategies of their outputs?

Why is it important to do filtering of Kraken output?

%	reads	taxReads	kmers	dup	cov	taxID	rank	taxName
87.090	222111	222111	3577712	1.00	9.593e-03	0	no rank	unclassified
12.910	32934	331	329116	1.17	3.026e-06	1	no rank	root
12.780	32603	3	324663	1.16	3.032e-06	131567	no rank	cellular organisms
7.002	17859	7	111728	1.43	1.388e-06	2759	superkingdom	Eukaryota
6.998	17849	0	111664	1.43	1.729e-06	33154	clade	Opisthokonta
6.998	17847	0	111664	1.43	1.918e-06	33208	kingdom	Metazoa
6.998	17847	0	111664	1.43	1.919e-06	6072	clade	Eumetazoa
6.998	17847	0	111664	1.43	1.935e-06	33213	clade	Bilateria
6.996	17844	0	111664	1.43	2.365e-06	33511	clade	Deuterostomia
6.996	17844	0	111664	1.43	2.392e-06	7711	phylum	Chordata
6.996	17844	0	111664	1.43	2.399e-06	89593	subphylum	Craniata
6.996	17844	0	111664	1.43	2.399e-06	7742	clade	Vertebrata
6.996	17844	1	111664	1.43	2.402e-06	7776	clade	Gnathostomata
6.996	17843	0	111640	1.43	2.410e-06	117570	clade	Teleostomi
6.996	17843	12	111640	1.43	2.410e-06	117571	clade	Euteleostomi
6.973	17785	0	111127	1.43	4.908e-06	8287	superclass	Sarcopterygii
6.973	17785	0	111127	1.43	4.920e-06	1338369	clade	Dipnotetrapodomorpha
6.973	17785	3	111127	1.43	4.920e-06	32523	clade	Tetrapoda
6.972	17781	47	111095	1.43	5.185e-06	32524	clade	Amniota
6.945	17714	1	110030	1.44	7.432e-06	40674	class	Mammalia

rank = species

%	reads	taxReads	kmers	dup	cov	taxID	rank	taxName
4.7660000	12155	5002	72665	1.45	1.342e-03	9785	species	Loxodonta africana
0.0019600	5	0	48	1.00	1.719e-03	99490	species	Loxodonta cyclotis
0.0337200	86	0	335	1.19	[illegible]	[illegible]	[illegible]	Elephas maximus
0.0003921	1	0	8	1.00	[illegible]	[illegible]	[illegible]	Mammuthus primigenius
0.3937000	1004	9	3984	1.08	[illegible]	[illegible]	[illegible]	Trichechus manatus
0.0172500	44	0	130	1.30	[illegible]	[illegible]	[illegible]	Dugong dugon
0.1380000	352	25	1388	1.14	[illegible]	[illegible]	[illegible]	Procavia capensis
0.0003921	1	0	4	1.00	[illegible]	[illegible]	[illegible]	Dendrohyrax arboreus
0.0200000	51	3	188	1.14	[illegible]	[illegible]	[illegible]	Echinops telfairi
0.0047050	12	0	33	1.21	[illegible]	[illegible]	[illegible]	Orycteropus afer
0.0019600	5	1	38	1.00	[illegible]	[illegible]	[illegible]	Chrysochloris asiatica
0.0003921	1	0	6	1.00	[illegible]	[illegible]	[illegible]	Amblysomus hottentotus
0.0011760	3	0	12	1.00	[illegible]	[illegible]	[illegible]	Elephantulus edwardii
0.0003921	1	1	2	1.00	3.333e-04	237658	species	Petrosaltator rozeti
0.1313000	335	3	1351	1.01	8.105e-07	9612	species	Canis lupus
0.0294100	75	2	277	1.06	5.837e-07	9657	species	Lutra lutra
0.0007842	2	0	10	1.00	7.836e-07	34882	species	Enhydra lutris
0.0007842	2	1	10	1.00	8.168e-07	76717	species	Lontra canadensis
0.0019600	5	0	16	1.00	8.997e-07	9715	species	Mirounga leonina
0.0011760	3	1	10	1.00	4.989e-07	9720	species	Phoca vitulina

kmers = 1000

%	reads	taxReads	kmers	dup	cov	taxID	rank	taxName
4.7660	12155	5002	72665	1.45	1.342e-03	9785	species	Loxodonta africana
0.3937	1004	9	3984	1.08	1.020e-04	9778	species	Trichechus manatus
0.1380	352	25	1388	1.14	6.428e-04	9813	species	Procavia capensis
0.1313	335	3	1351	1.01	8.105e-07	9612	species	Canis lupus
0.1686	430	430	1794	1.00	1.212e-06	9606	species	Homo sapiens
5.1680	13180	12862	178949	1.01	5.993e-03	1491	species	Clostridium botulinum

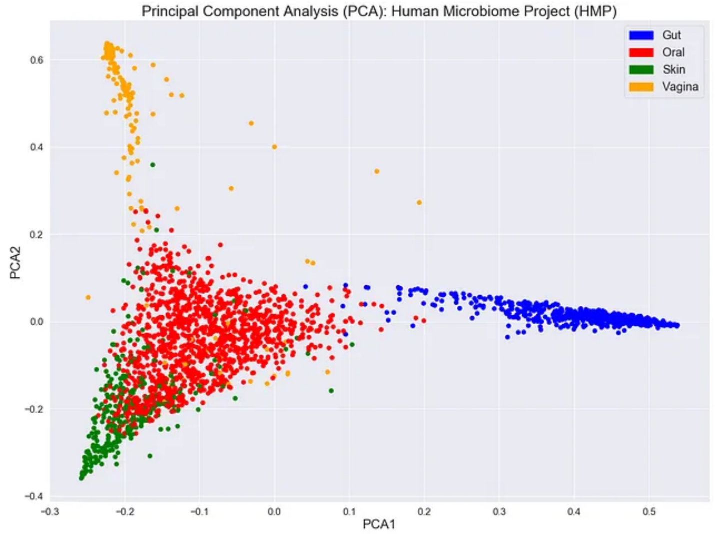
taxReads = 200

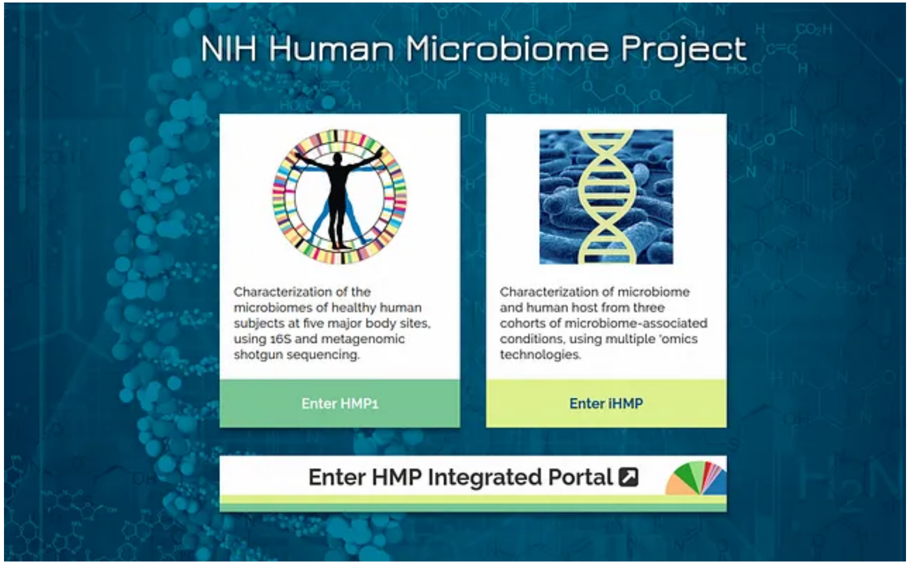
%	reads	taxReads	kmers	dup	cov	taxID	rank	taxName
4.7660	12155	5002	72665	1.45	1.342e-03	9785	species	Loxodonta africana
0.1686	430	430	1794	1.00	1.212e-06	9606	species	Homo sapiens
5.1680	13180	12862	178949	1.01	5.993e-03	1491	species	Clostridium botulinum

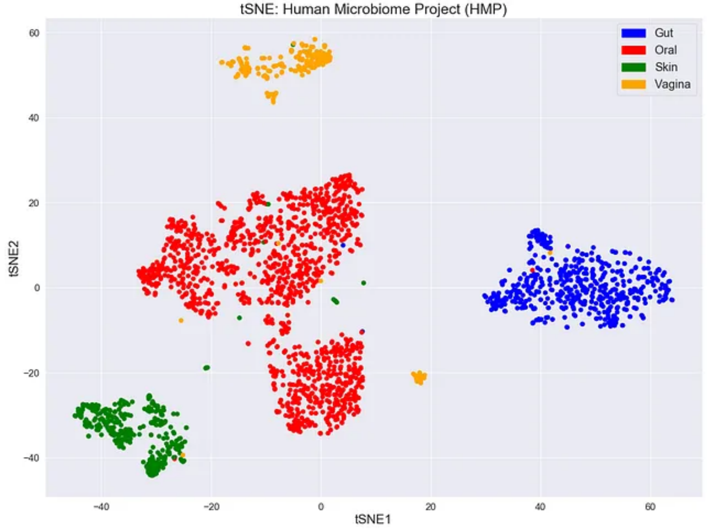
Filtering is critical for understanding content of metagenomic samples!

How can we use microbial abundance matrix from Kraken?

	sample1	sample2	sample3	sample4	sample5	sample6	sample7	sample8	sample9	sample10
Ralstonia solanacearum	3628	3751	619	1804	1384	1608	1375	0	1112	749
Mycobacterium avium	8236	8546	273	265	3221	4808	7750	6382	0	0
Burkholderia pseudomallei	7095	0	0	0	13082	0	4885	1456	0	7310
Salmonella enterica	4356	4471	4205	3588	0	13854	0	0	1959	2560
Pseudomonas chlororaphis	296	1024	0	977	374	677	276	0	0	294
Neisseria meningitidis	465	502	0	0	7341	0	0	3268	5643	0
Yersinia pestis	0	0	0	7174	957	0	11485	6461	0	11553



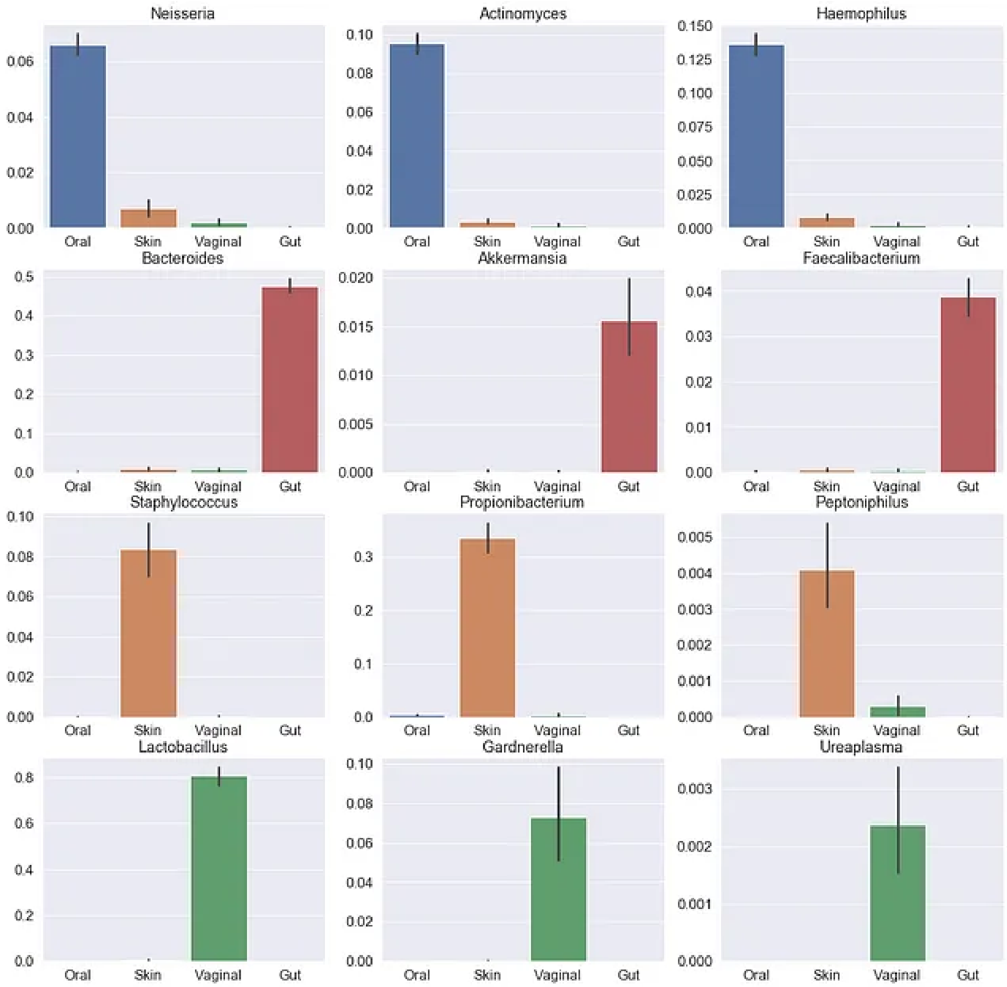




Physalia
Courses

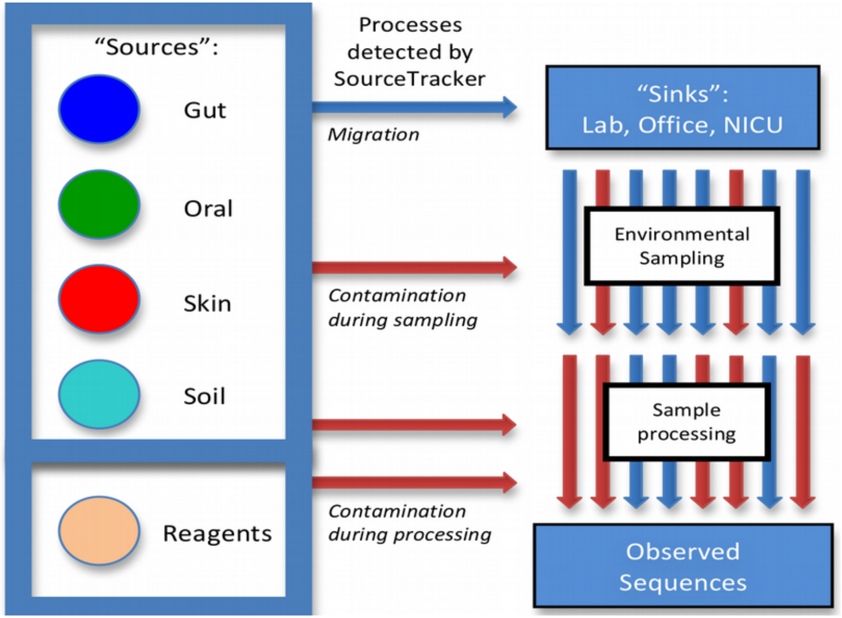
Understanding marker microbes for different environments

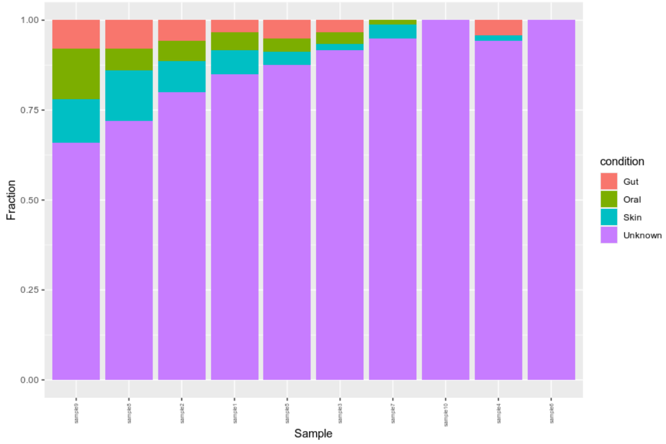
	Oral	Gut	Skin	Vagina
0	Neisseria	Blautia	Staphylococcus	Mobiluncus
1	Veillonella	Faecalibacterium	Peptoniphilus	Sphingopyxis
2	Actinomyces	Bacteroides	Citrobacter	Ureaplasma
3	Haemophilus	Dorea	Enhydrobacter	Caulobacter
4	Rothia	Akkermansia	Finegoldia	Gardnerella
5	Leptotrichia	Clostridium	Propionibacterium	Chlamydia
6	Cardiobacterium	Ruminococcus	Acinetobacter	Asticcacaulis
7	Capnocytophaga	Subdoligranulum	Massilia	Mycobacterium
8	Oribacterium	Oxalobacter	Hymenobacter	Herbaspirillum
9	Alloprevotella	Oscillibacter	Corynebacterium	Lactobacillus
10	Gemella	Eubacterium	Bacillus	Achromobacter
11	Fusobacterium	Bilophila	Micrococcus	Atopobium

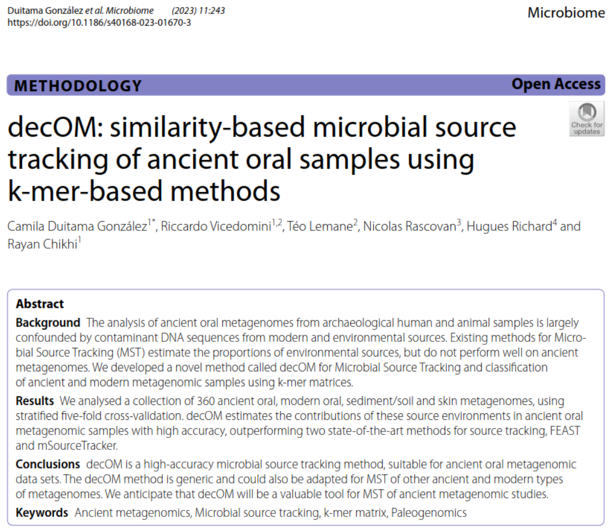


Physalia Courses

Microbial source tracking







Duitama González *et al. Microbiome* (2023) 11:243
https://doi.org/10.1186/s40168-023-01670-3
Microbiome
METHODOLOGY Open Access

decOM: similarity-based microbial source tracking of ancient oral samples using k-mer-based methods

Camila Duitama González[1*], Riccardo Vicedomini[1,2], Téo Lemane[2], Nicolas Rascovan[3], Hugues Richard[4] and Rayan Chikhi[1]

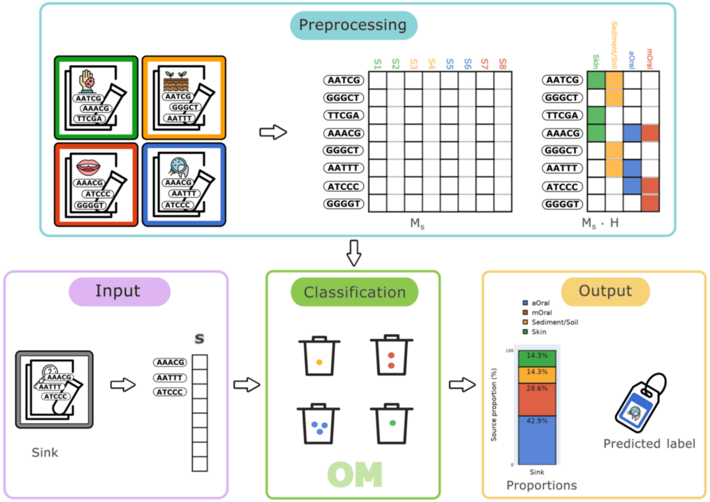
Abstract

Background The analysis of ancient oral metagenomes from archaeological human and animal samples is largely confounded by contaminant DNA sequences from modern and environmental sources. Existing methods for Microbial Source Tracking (MST) estimate the proportions of environmental sources, but do not perform well on ancient metagenomes. We developed a novel method called decOM for Microbial Source Tracking and classification of ancient and modern metagenomic samples using k-mer matrices.

Results We analysed a collection of 360 ancient oral, modern oral, sediment/soil and skin metagenomes, using stratified five-fold cross-validation. decOM estimates the contributions of these source environments in ancient oral metagenomic samples with high accuracy, outperforming two state-of-the-art methods for source tracking, FEAST and mSourceTracker.

Conclusions decOM is a high-accuracy microbial source tracking method, suitable for ancient oral metagenomic data sets. The decOM method is generic and could also be adapted for MST of other ancient and modern types of metagenomes. We anticipate that decOM will be a valuable tool for MST of ancient metagenomic studies.

Keywords Ancient metagenomics, Microbial source tracking, k-mer matrix, Paleogenomics



Physalia Courses