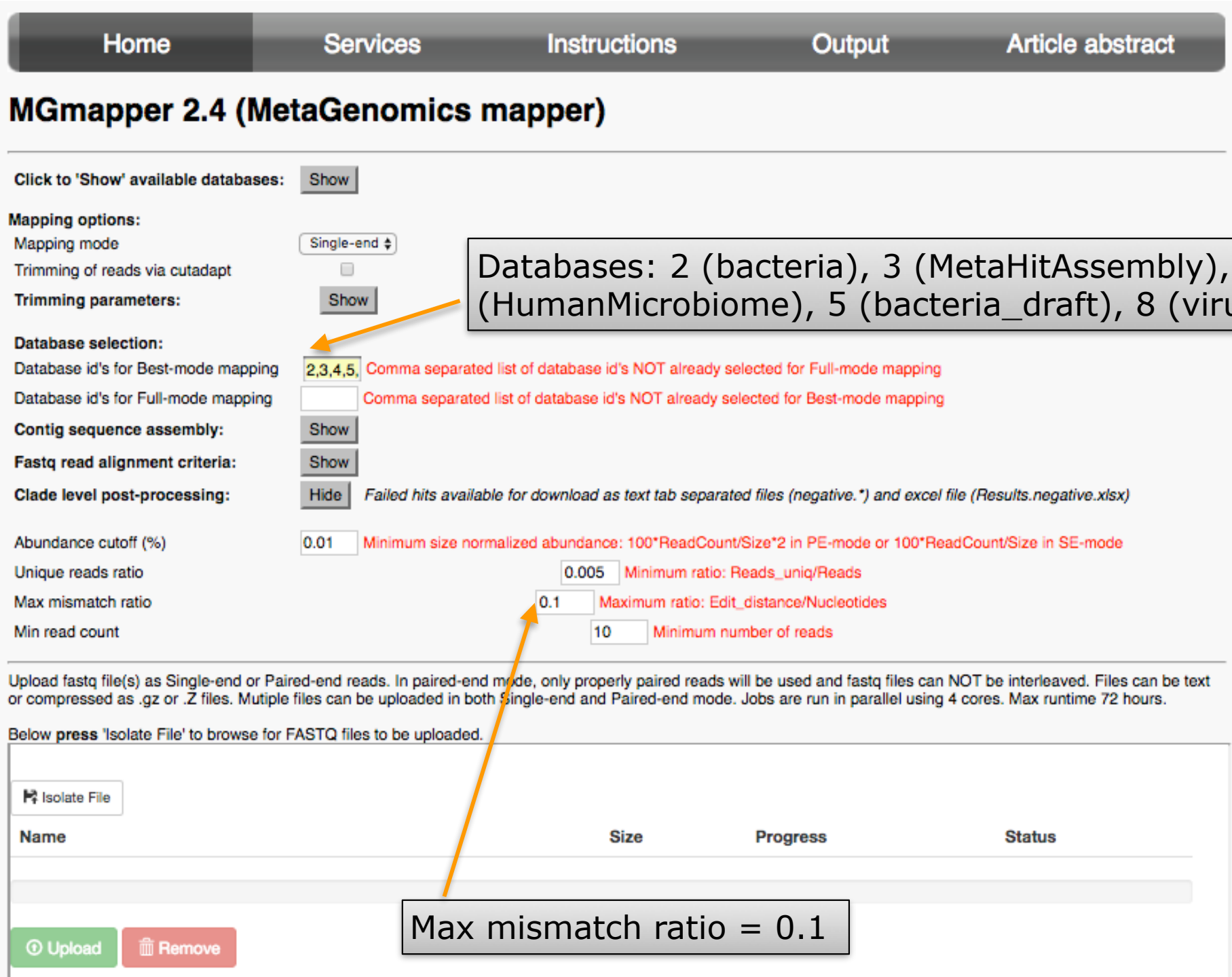
Wrap-up Exercise 6

MGMapper input



MGMapper output

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Running time in single-end mode:

Job start	Job end
Mon Sep 18 10:48:55 2017	Mon Sep 18 11:03:50 2017

Table 1. Start and end times for running MGmapper.

File statistics:

Counter	FileName	Reads in
1	outbreak_matrix_pathogen.fastq	109804
1	/home/data1/services/MGmapper/MGmapper-2.4/IO/2_18_9_2017_103_864_173355/uploads/outbreak_matrix_pathogen.fastq	109804

Table 2. Statistics for input fastq files. Last line sums up number of fastq files and total number of reads.

Summary file statistics:

Biological relevant reads = 109804

Fastq files	Reads read	After cleaning
1	109804	109804

Table 3. The number 'After cleaning' represents reads with a biological origin, after removing potential Illumina PhiX control reads (http://www.illumina.com/products/phix_control_v3.html).

Reference sequence databases:

Database	Version	No of sequence	No of nucleotides
Bacteria	20151124	6969	19137675153
MetaHitAssembly	20140111	41126	908004652
HumanMicrobiome	20140409	42928	2831377980
Bacteria_draft	20151124	137980	7972498520
Virus	20151124	6640	196732536

Table 4. Reference database statistics. 'Version' is the date at which reference sequences was updated.

MGMapper output

Overall mapping results before post-processing:

Mapping mode	Database	Percent mapped	No reads
Fullmode	notPhiX	100.00	109804
Bestmode	Bacteria	8.808	9671
Bestmode	MetaHitAssembly	0.008	9
Bestmode	HumanMicrobiome	0.027	30
Bestmode	Bacteria_draft	58.751	64511
Bestmode	Virus	0.049	54
-	Unmapped	32.357	35529

Table 5. The percentages are in relation to the number of reads ('After cleaning') as shown in Table 3..

Statistics - Bestmode mapping (Max top 5 hits are shown below):

Database	Ref Seq	S_Abundance (%)	R_Abundance (%)	Size (bp)	Seq_count	Nucleotides	Covered positions	Coverage	Depth	ReadCount	Rea u
Database	Ref Seq	S_Abundance (%)	R_Abundance (%)	Size (bp)	Seq_count	Nucleotides	Covered positions	Coverage	Depth	ReadCount	Rea u
Database	Ref Seq	S_Abundance (%)	R_Abundance (%)	Size (bp)	Seq_count	Nucleotides	Covered positions	Coverage	Depth	ReadCount	Rea u

Database	Ref Seq	S_Abundance (%)	R_Abundance (%)	Size (bp)	Seq_count	Nucleotides	Covered positions	Coverage	Depth	ReadCount	R
Bacteria_draft	AKVP01000102.1	1559.539	12.953	912	1	4112826	901	0.988	4509.678	14223	1
Bacteria_draft	AKVP01000085.1	1295.931	24.655	2089	1	9656894	1704	0.816	4622.735	27072	2
Bacteria_draft	AKVP01000087.1	818.636	13.122	1760	1	5842575	1760	1.000	3319.645	14408	1
Bacteria_draft	AKVP01000114.1	436.377	2.611	657	1	979948	518	0.788	1491.549	2867	2
Bacteria_draft	AKVP01000128.1	133.778	0.548	450	1	193722	450	1.000	430.493	602	6

Database	Ref Seq	S_Abundance (%)	.....	Virus	Vi
				Mismatches	Description
Virus	NC_001489.1	0.722		1969	Hepatitis A virus, complete genome

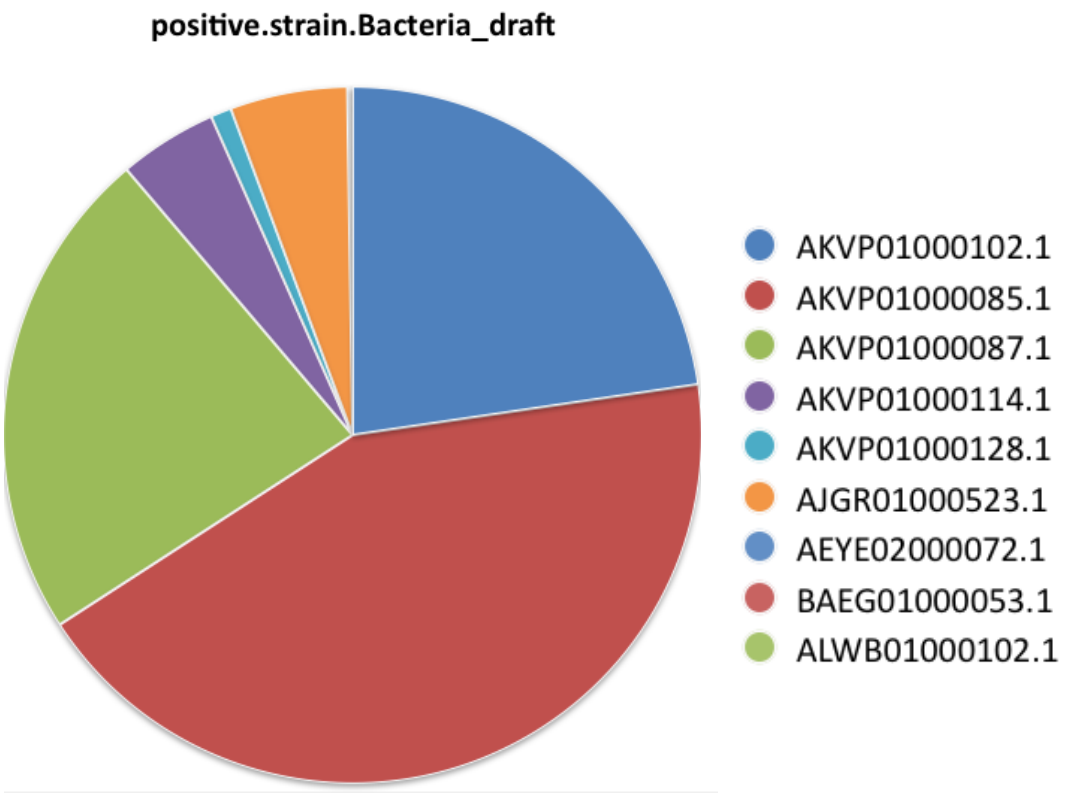
Results in Excel

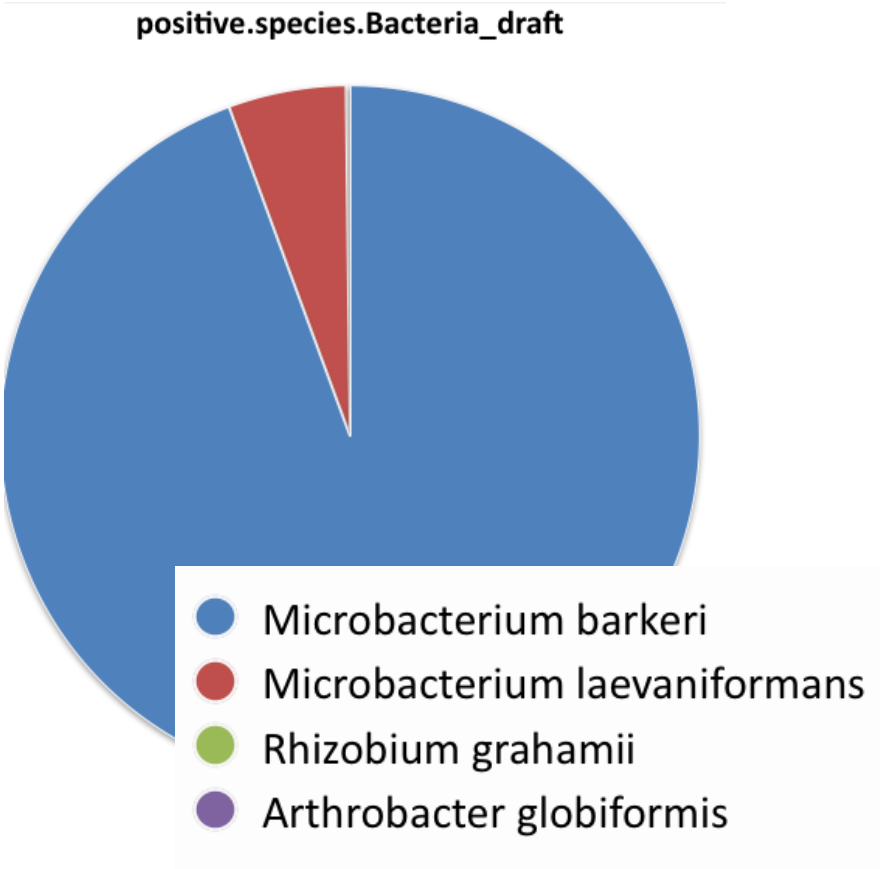
Download excel workbook result files incl graphics:

Results.xlsx

Results.negative.xlsx

Note: Results are both given for individual hits to reference sequences (strain level) and on species-level, where statistics for all references sequences of the same species are lumped together





Depth and Coverage

positive.species.HumanMicrobiom			positive.strain.Bacteria_draft			positive.species.Bacteria_draft
D	E	F	G	H	I	J
_Abundar	Size (bp)	Seq_count	Nucleotides	Covered_positions	Coverage	Depth
53,894	7285	6	20786230	5428	0,745	2853,292
3,106	37303	2	1358134	6533	0,175	36,408
0,061	397	1	5159	392	0,987	12,995
0,042	525	1	2102	129	0,246	4,004

Depth = Nucleotides / Size (bp) = 20786230 / 7285 = 2853.292 (depth of coverage)

Coverage = Covered_positions / Size (bp) = 5428 / 7285 = 0.745

Viral pathogen

- Which viral pathogen is present in the sample?

  Hepatitis A

- How many reads map to the viral pathogen?

  54

- Would the viral pathogen have been reported, if Max mismatch ratio = 0.01?

  Mismatch ratio = mismatched (edit distance)/ nucleotide = 1969/21859 = 0.090

Nucleotides	Covered_pc	Coverage	Depth	Reads	Reads_unic	Edit_distan	Description
21859	6814	0,911	2,923	54	54	1969	Hepatitis A