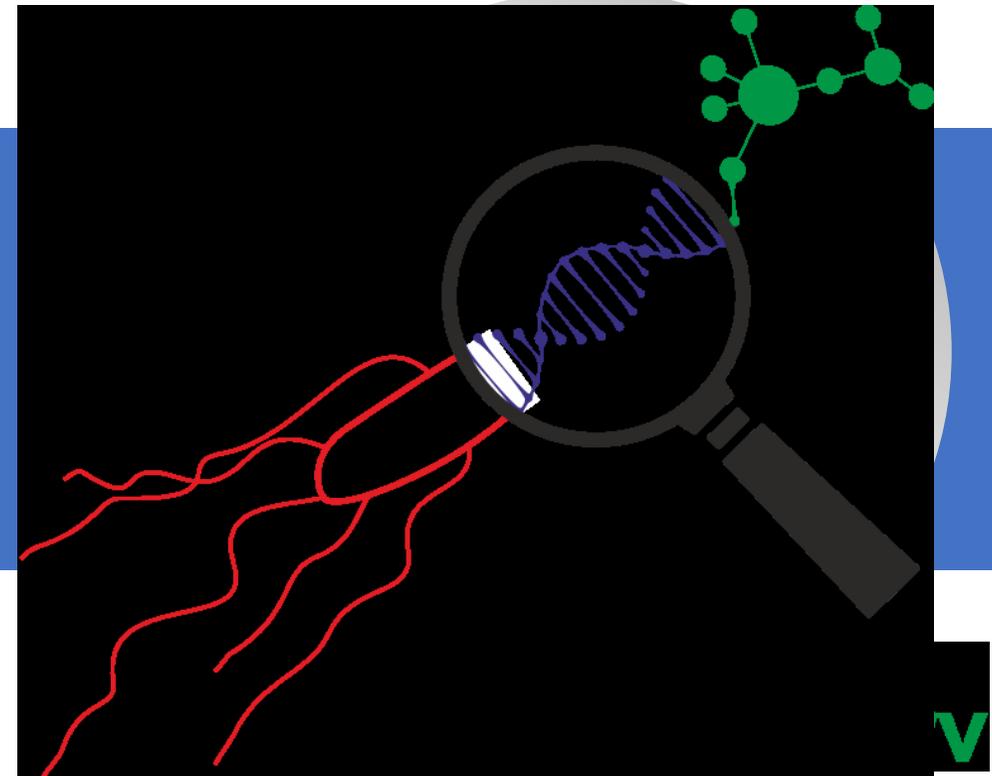


# GenoSalmSurv screencasts



# GenoSalmSurv screencasts

das Projekt 1

die Pipelines

AQUAMIS und die QC Entscheidung

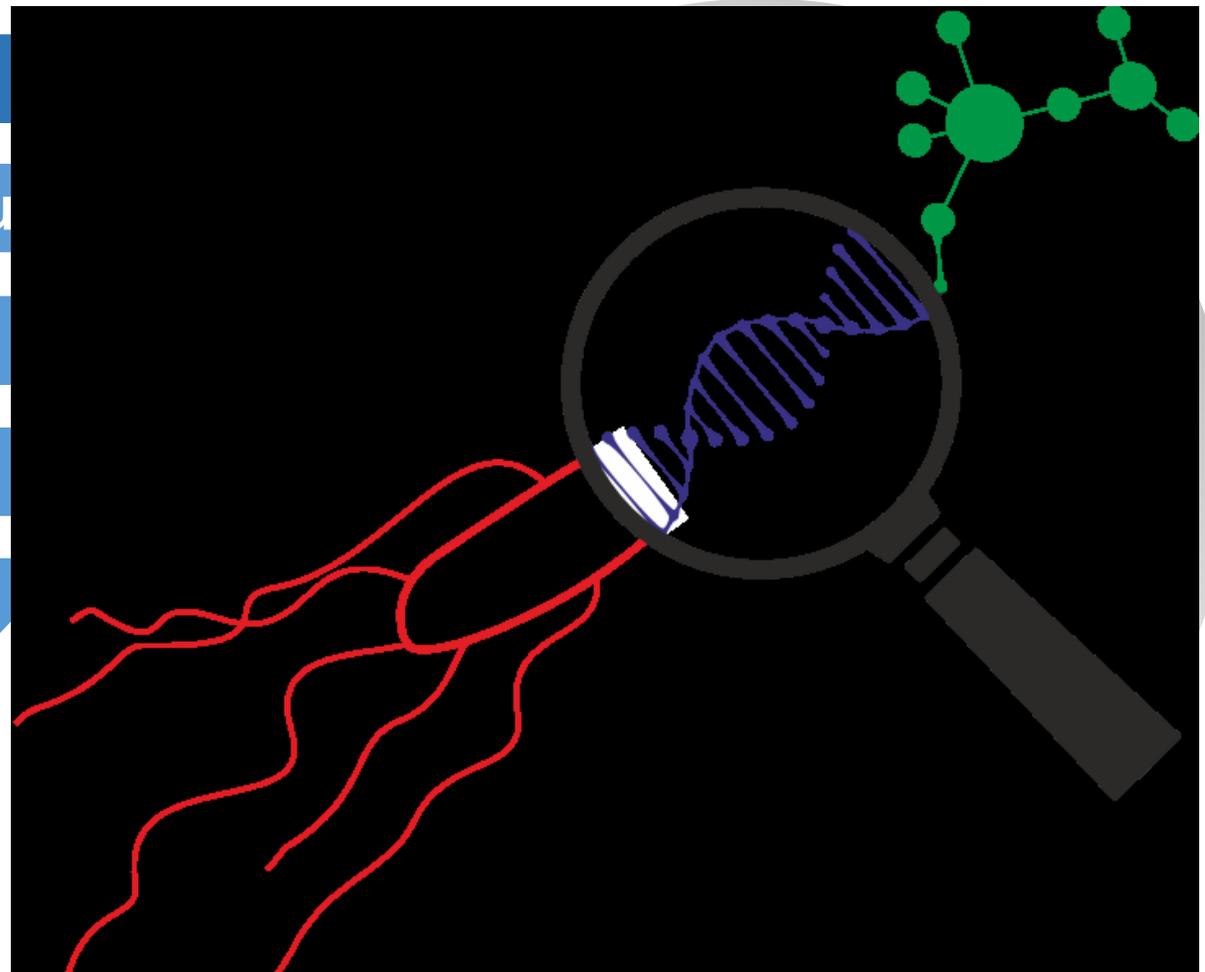
Allele calling mit chewieSnake

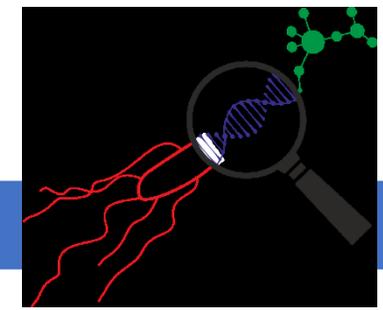
Gemeinsame GenoSalmSurv Datenbank

Metachewiereport + Interpretation 6

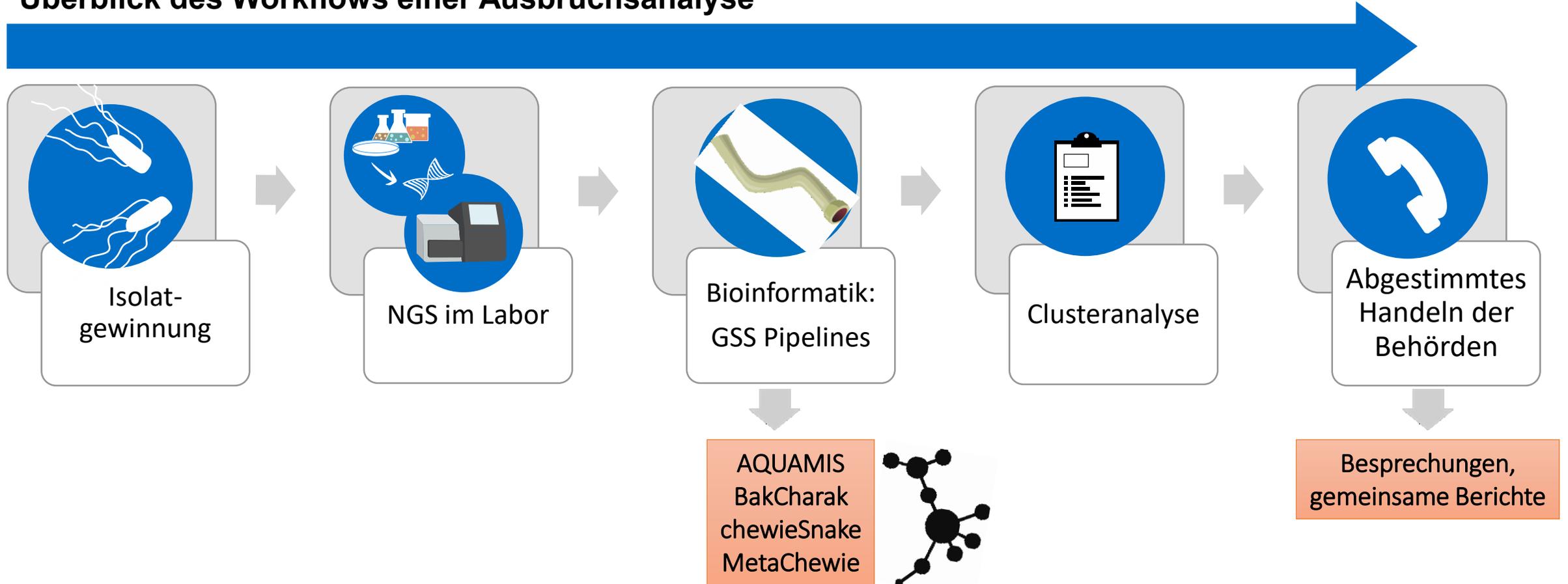
Demo einer Ausbruchsanalyse 7

Installationshilfe 8



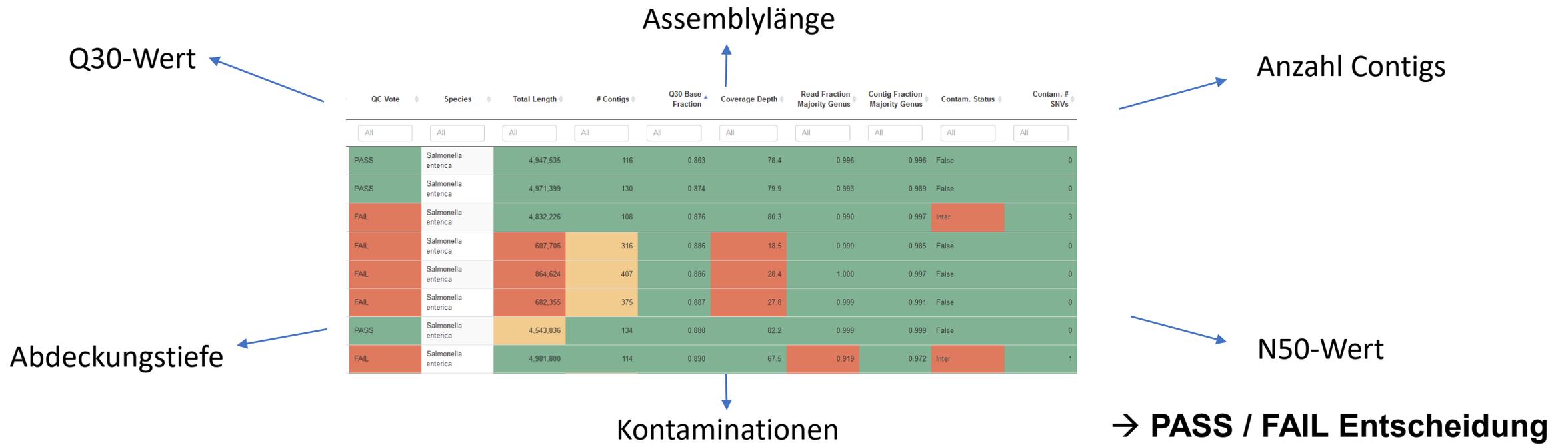


### Überblick des Workflows einer Ausbruchsanalyse



### AQUAMIS

Assembly-based QUality Assessment for Microbial Isolate Sequencing



### BakCharak

### Bakterielle Charakterisierung

Virulenzgene

Serovargene

MLST Typ

Sample	Details	MLST_ST	MLST_Formula_short	mash_serovar	serovar	serovar_cgmlst	count_resgenes	resgenes	count_plasmids	plasmids	count_vf
19-SA00026-0	<a href="#">Details</a>	11	5.2.3.7.6.6.11	Ententidis	Ententidis	Ententidis	0	None found	2	ColRNAI_1,IncFIB(S)_1	133
19-SA00037-0	<a href="#">Details</a>	11	5.2.3.7.6.6.11	Ententidis	Ententidis	Ententidis	0	None found	1	IncFIB(S)_1	132
19-SA00077-0	<a href="#">Details</a>	11	5.2.3.7.6.6.11	Ententidis	Ententidis	Ententidis	2	blaTEM-1,qnrS1	3	IncFIB(S)_1,Inc1_1_Alpha,IncX1_1	133
19-SA00078-0	<a href="#">Details</a>	11	5.2.3.7.6.6.11	Ententidis	Ententidis	Ententidis	2	blaTEM-1,qnrS1	3	IncFIB(S)_1,Inc1_1_Alpha,IncX1_1	133
19-SA00097-0	<a href="#">Details</a>	183	5.2.3.7.60.6.11	Ententidis	Ententidis	Ententidis	0	None found	1	IncFII(S)_1	129
19-SA00100-0	<a href="#">Details</a>	183	5.2.3.7.60.6.11	Ententidis	Ententidis	Ententidis	0	None found	1	IncFII(S)_1	129

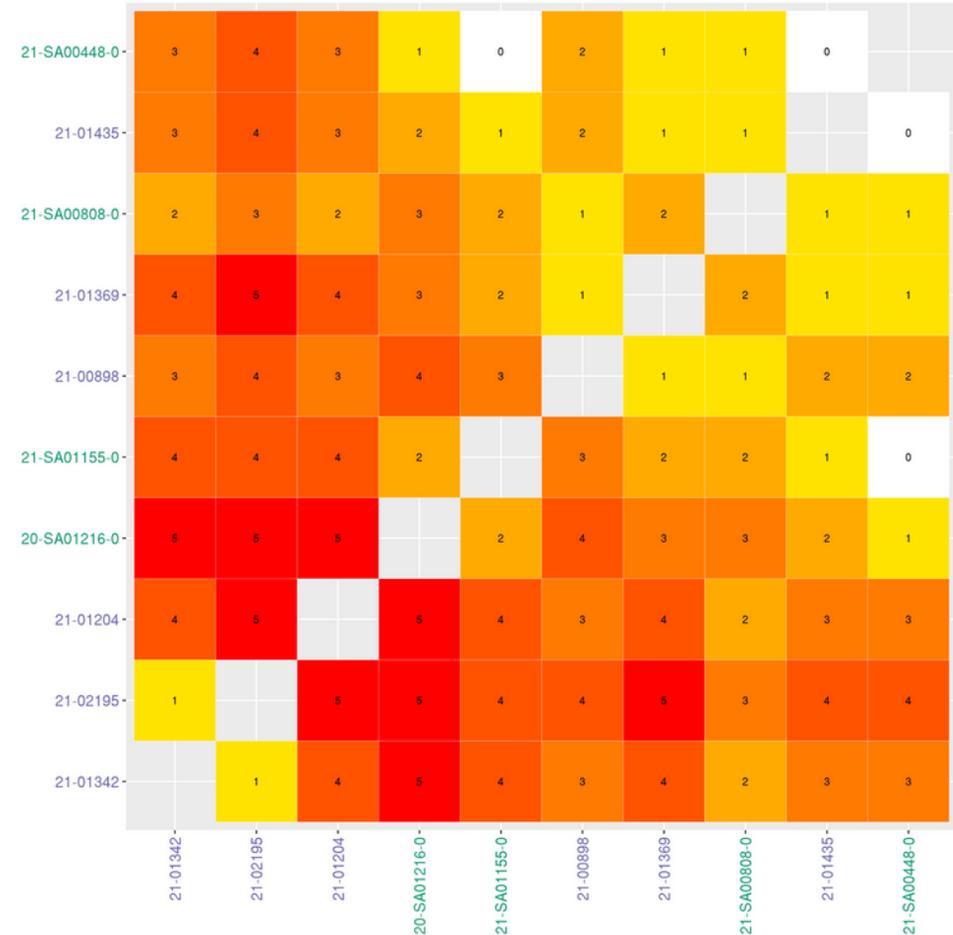
Plasmide

Antibiotikaresistenzgene

Referenzsuche

### chewieSnake

Genomvergleich mit core-genome Multi Locus  
Sequence Typing (cgMLST)

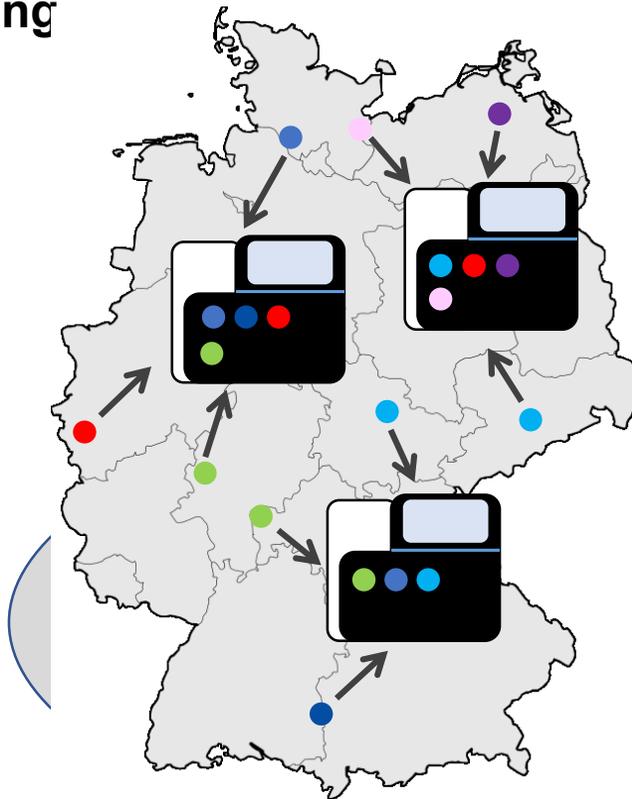


[https://gitlab.com/bfr\\_bioinformatics/chewieSnake](https://gitlab.com/bfr_bioinformatics/chewieSnake)

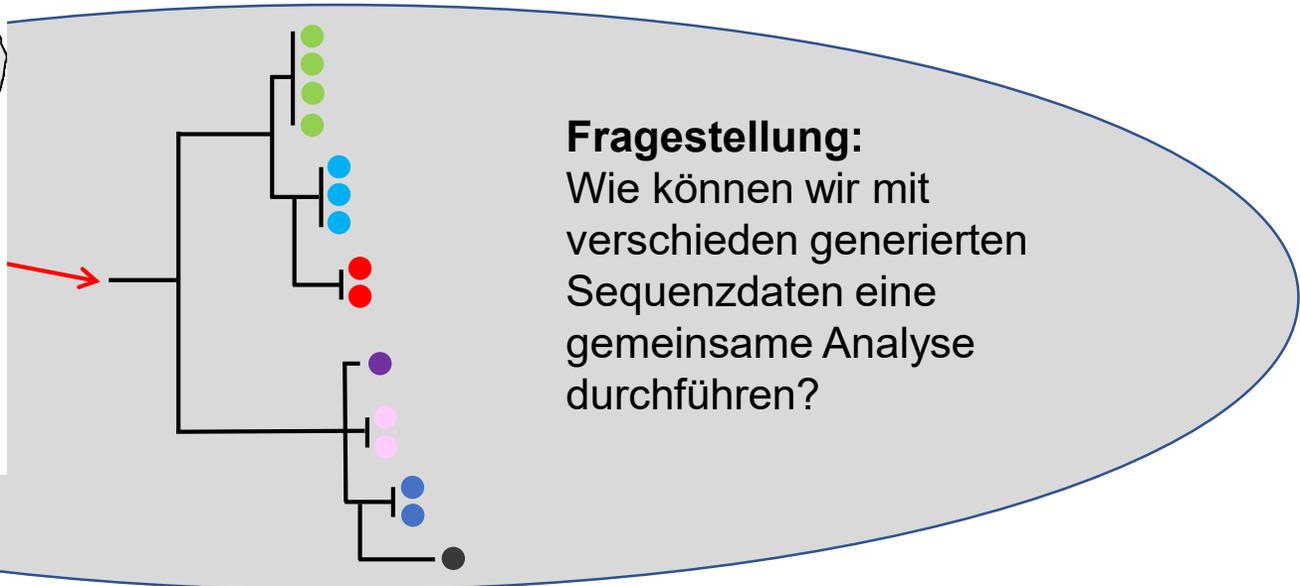
### Cluster-report

cluster name	serovar	count samples	count BfR	count RKI	count LGL	which min diff	min diff	timestamp mostrecent
<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text"/>	<input type="text" value="All"/>					
Aristonicus:Eucherius:Vindonius	Typhimurium	89	45	42	2	BfR-RKI	0	2021-04-09
Agathocles:Antidamas	Enteritidis	80	25	49	6	BfR-RKI	0	2021-04-09
Antiphon	Enteritidis	73	14	58	1	BfR-RKI	0	2021-04-09
Paterius:Rutilius	Choleraesuis;Imonella Subspez. I;Subspec. I Rauform;Subspez. I	58	50	8	0	BfR-RKI	1	2021-03-06
Fridugisus:Maximianus	Choleraesuis;Subspec. I Rauform;Subspez. I	53	47	6	0	BfR-RKI	0	2021-02-26
Auspicius:Ptolemais	Enteritidis	45	9	36	0	BfR-RKI	0	2021-04-09
Aelianus	Typhimurium	42	3	37	2	LGL-RKI	0	2021-03-25
Libanius	Enteritidis	37	37	0	0			2021-03-25
Arabius	Enteritidis	36	1	35	0	BfR-RKI	10	2021-04-09
Baudovinia	Enteritidis	33	0	27	6	LGL-RKI	1	2021-01-13

### Problemstellung

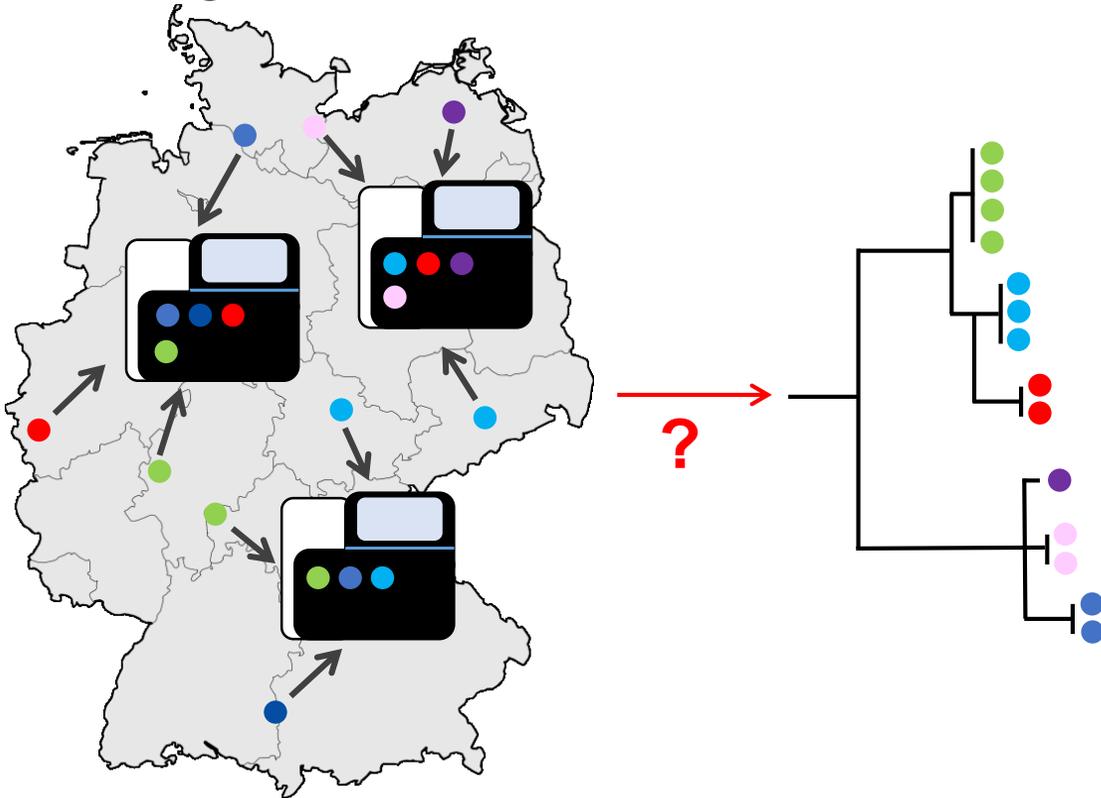


Gesamtgenomsequenzierung  
der Isolate in unterschiedlichen  
Einrichtungen



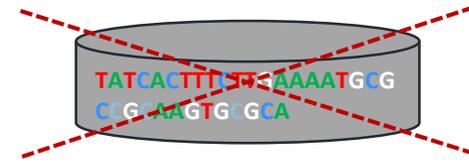
**Fragestellung:**  
Wie können wir mit  
verschieden generierten  
Sequenzdaten eine  
gemeinsame Analyse  
durchführen?

### Lösungsidee



### Idee A:

#### Sequenzrohdaten - Datenbank



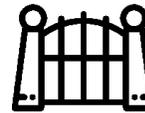
→ keine Sektor-übergreifende  
Zusammenführung von WGS Daten  
zur einheitlichen Interpretation



große  
Datenmengen



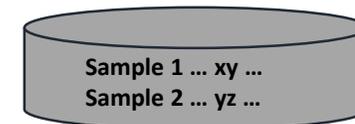
Regulationen

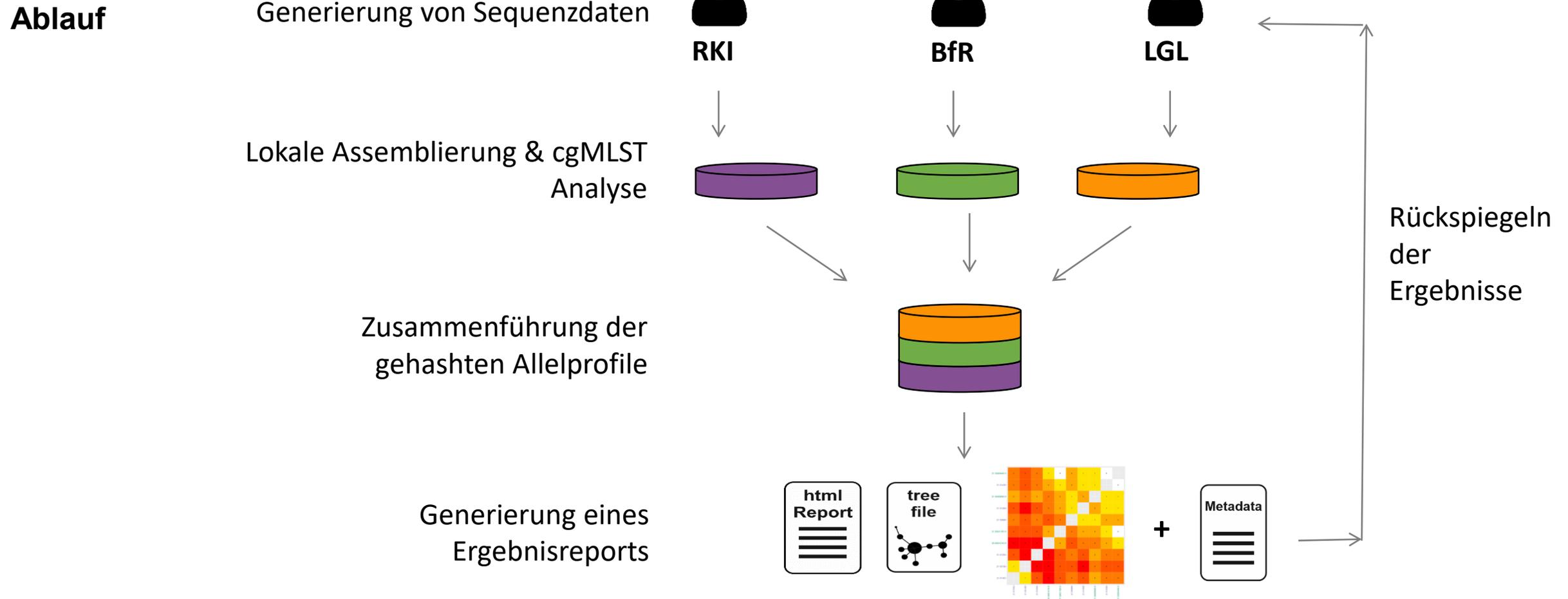


eigene  
Forschungs-  
interessen

### Idee B:

#### Ergebnisdaten - Datenbank





# GenoSalmSurv screencasts

das Projekt

1

die Pipelines

AQUAMIS und die QC Entscheidung

Allele calling with chewieSnake

Gemeinsame GenoSalmSurv Datenbank

Metachewiereport + Interpretation

6

Demo einer Ausbruchsanalyse

7

Installationshilfe

8

