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**D-JRP7-5.2 / 2019 LISTADAPT  
training sessions**

**JRP7 - LISTADAPT**

**V0.1 15/02/2020**

Responsible Partner: Anses Maisons-Alfort



## GENERAL INFORMATION

<b>European Joint Programme full title</b>	Promoting One Health in Europe through joint actions on foodborne zoonoses, antimicrobial resistance and emerging microbiological hazards
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<b>JRP Deliverable/Report number</b>	D-JRP7-5.2
<b>Join Integrative/Research Project</b>	JRP7 – LISTADAPT
<b>JRP Leader / Report main redactor</b>	Sophie Roussel (Anses) / Laurent Guillier (Anses)
<b>Other contributors</b>	
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<b>Type</b> <i>R: Document, report</i> <i>DEC: Websites, patent filings, videos, etc.</i> <i>OTHER</i>	R
<b>Dissemination level</b> <i>PU: Public</i> <i>CO: confidential, only for members of the consortium (including the Commission Services)</i>	Public



# SLIDES PRESENTED DURING THE 2019 –TRAINING SESSION

**Illustrations of sampling strategies**

Case 2: Diversity characterization, source attribution  
 #1: existing strains collection from **passive surveillance**  
 #2: existing strains collection from **active surveillance**

#1 or #2: simple random sampling or stratified random sampling

Simple Random Sampling      Stratified Random Sampling

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**Illustrations of sampling strategies**

Random sampling:  
 - simple and convenient  
 - Might be non adapted if strains originated from passive surveillance

Region	Serotype	Systematic random sampling
A	II	X
A	II	
A	II	X
A	II	
A	II	X
A	IV	
B	II	X
C	II	
D	IV	X
D	IV	

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**Illustrations of sampling strategies**

Random sampling:  
 - Rather simple and convenient  
 - Better adapted for selecting strains originated from passive surveillance  
 - Limitations: number of strata and levels in strata

Region	I. Sampling region	Serotype	II. Random sampling in region strata
A		II	X
A		II	
A		II	
A	X	II	
A		II	
A		IV	
B	X	II	X
C	X	II	X
D	X	IV	X
D	X	IV	

**Method developed in the context of LISTADAPT: Cluster sampling based on metadata**

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**Sampling strains based on their metadata**

Training EJP LISTADAPT

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 09<sup>th</sup> April 2019

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**Strains to include in a scientific study**

Strains selection is not an easy task for scientist  
 Sampling is crucial for the pertinence/performance of the genomic analysis carried out.  
 Several strategies of sampling are available and the analyst must adapt to the global objective he has:

- Random sampling
- Stratified random sampling
- Cluster sampling

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**Illustrations of sampling strategies**

Case 1: exposure assessment  
 The analyst wants to assess to which strains consumers are exposed to.  
 Samples are taken proportionally to consumption data (if a food company presents 25% of sales, 25% of samples will be taken)

	% market	% samples
A	1	0
B	25	26
C	10	10
D	20	21
...	...	...
Z	8	8

**Illustrations of sampling strategies**

Case 1: exposure assessment  
 e.g. EFSA Baseline survey : most consumed product are samples

Resulting strain collection is representative of exposure  
 Use in risk assessment (Fritsch et al. 2019, MRA)

CC	Number of serotypes	Total	Violence group
DC1	1		
DC2	4		
DC6	10		
DC7	8	37 (12.6%)	Hyper
DC8	6		
DC101	7		
DC401	1		
DC3	9		
DC5	1		
DC8	49		
DC14	5		
DC26	4		
DC21	1	105 (35.7%)	Medium
DC9	6		
DC117	1		
DC155	24		
DC483	4		
New CC	1		
DC8	37		
DC101	59		
DC16	3		
DC15	5	162 (51.7%)	Hypo
DC163	4		
DC204	8		
DC24	2		
Total	204		







**Gower distance**

Do strains  $i$  and  $j$  share the same information for metadata  $k$ ?

$$S_{ijk} = \begin{cases} 0 & \text{if } X_{ik} = X_{jk} \\ 1 & \text{if } X_{ik} \neq X_{jk} \end{cases}$$

Across the  $K$  different metadata, differences are summarized with Gower's metric

$$S_{ij} = \frac{\sum_{k=1}^K w_{ijk} S_{ijk}}{\sum_{k=1}^K w_{ijk}}$$


(user-defined weights can be attributed to metadata)





Thank you for your attention!

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<https://github.com/laurentguillier/LISTADAPT/tree/master/trainings>

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## 2019-Training session Information

Organizers	Date	Domain	Subject	Tools	Support	Maximum number of attendees (LISTADAPT members, NRL Lm, EJP OH member)	Contact persons
<b>ANSES Maisons-Alfort</b>	9 <sup>th</sup> April 2019	Sampling	Sampling strains according to metadata	R	Meeting, script	8	Laurent Guillier, Yann Sevellec, Benjamin Felix

