A sheep with listeriosis was detected in a Spanish farm in region X. A ***Listeria monocytogenes* cgMLST type L1-SL1-ST1-CT8169** **(clonal complex CC1, serogroup IVb)** was isolated from the **sheep brain**. Following this report, you and your colleagues decide to investigate the occurrence of Listeria spp. in nearby farms, as studies have shown that CC1 is the most **prevalent clinical clone** in industrialized countries and **the most pathogenic**, causing severe listeriosis cases in humans. A total of 425 *Listeria* isolates are obtained across the farms sampled and sequenced. You need to **report the findings** to the authorities.

**1.** **Access this dataset** on the <https://bigsdb.pasteur.fr/listeria> **isolates database** and search for the project **GenEpiBio-Exercise** (change the form with  to be able to see the project filter, if needed,). Display the metadata of the entire dataset to get familiar with it. The farm id can be found in the field ‘other\_source\_info’. Use Une image contenant texte, Police, capture d’écran, blanc

Description générée automatiquement to **explore the data**.

1. 19 farms were sampled. In how many farms did you detect *Listeria*?
2. Which *Listeria* species were found? Which of those are pathogenic (hint: look for LIPI-1)? Are they expected to be capable of causing invasive disease (hint: look for inlA and inlB genes)?
3. No other animal shown listeriosis symptoms. Were there any pathogenic *Listeria* found in the animals? In which type of sample? How do you interpret this result?
4. Which were the most prevalent *L. monocytogenes* clonal complex(es)? Is that concerning?

**2.** Filter the dataset to focus only on *L. monocytogenes.* Using theUne image contenant texte, Police, capture d’écran, ligne

Description générée automatiquement plugin in BIGSdb and an allelic cut-off of **7 allelic differences**, **summarize the clusters** in your dataset (output: partions\_summary.tsv) and visualize the straindiversity with GrapeTree (color nodes by farm id).

**a.** how many clusters did you identify?

**b.** what can you say about their locations, timespans and seasonality?

**c.** Did you find other cgMLST type L1-SL1-ST1-CT8169 isolate? What can you say about its dispersion?

**3.** Using the  plugin in BIGSdb look for the presence of **antibiotic resistance** genes and **stress islands**.

**a.**which are intrinsic *L. monocytogenes* antibiotic resistance genes?

**b**. is there any isolate with acquired antibiotic resistance genes or stress islands? Do the genes found compromise listeriosis treatment (typically: AMP, GEN or STX)? Select one isolate id, export its genome from BIGSdb with . Are any of acquired resistances located in plasmids?

**c.** If time permitting, represent any desired traits with proksee or other tool of your choice outside BIGSdb.