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Association between somatic cell count dynamics and pathogens for clinical mastitis in dairy cows

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Background

Mastitis is a common problem in modern dairy herds worldwide. It is often caused by infections with contagious and environmental bacteria. The **somatic cell count** (**SCC**) is routinely measured on cow level during milking, and a high SCC indicates **inflammation** in the udder. Thus, the SCC increases after infection. The **aim** of this study was to **investigate the association between the SCC and clinical infection with different pathogens.**

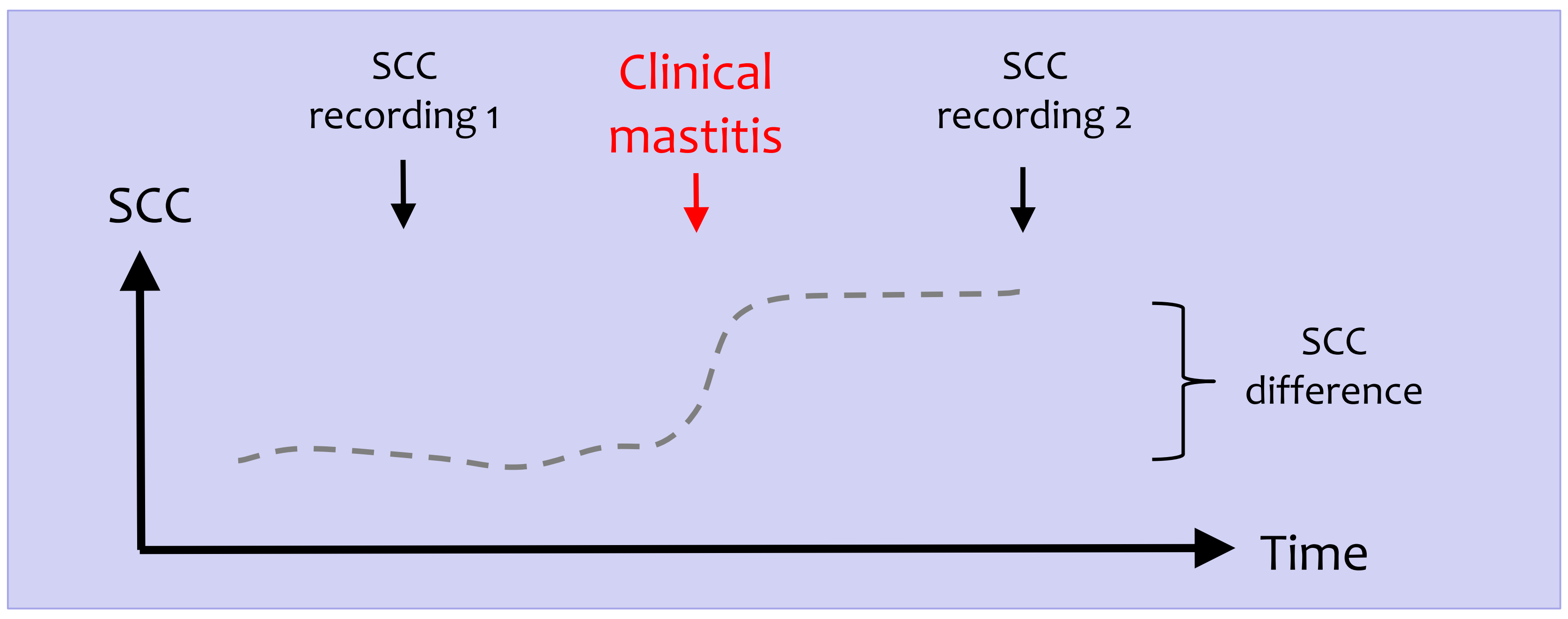
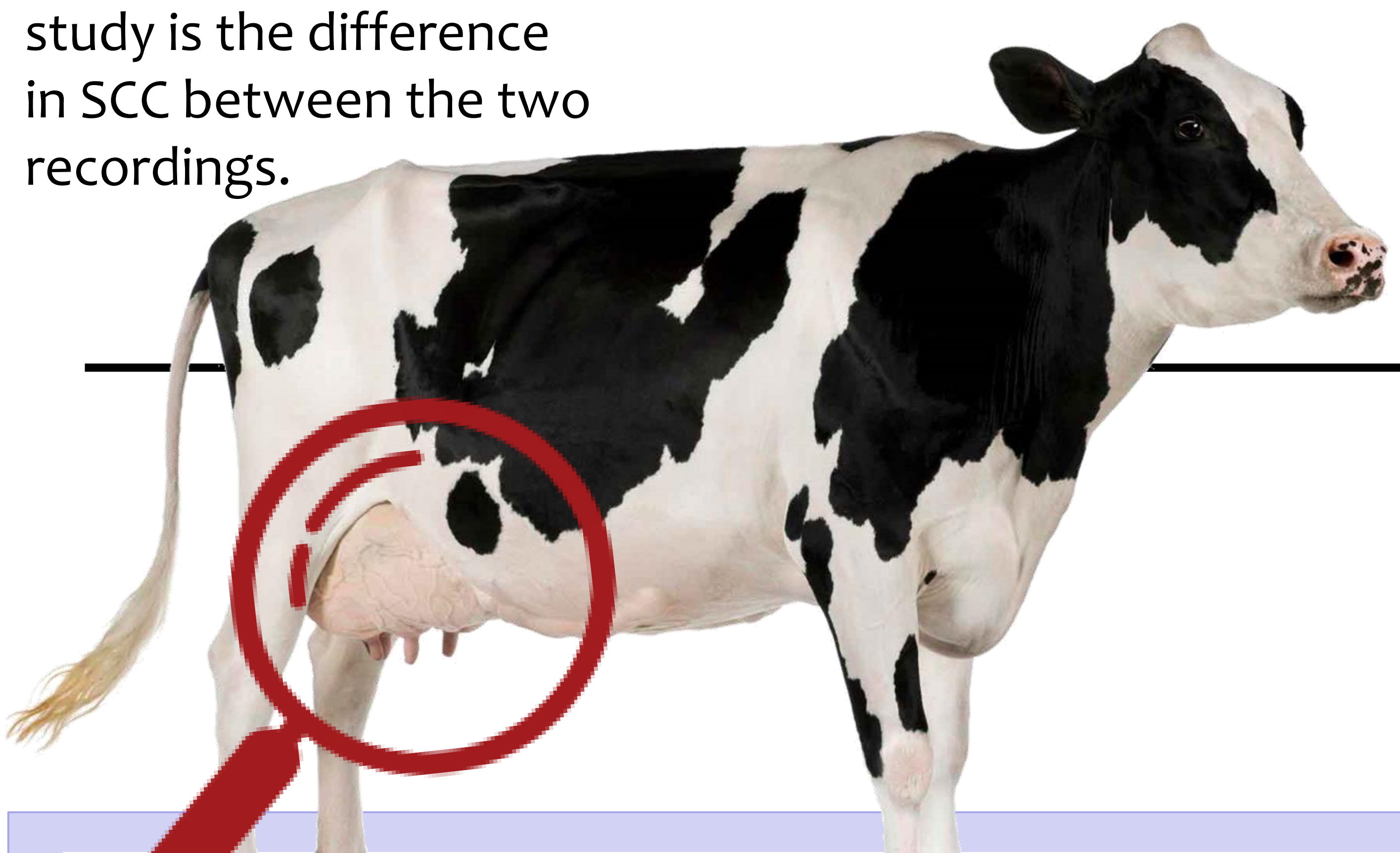


Figure 1. Theoretical response of SCC to a clinical infection occurring between two SCC measurements. The outcome variable in the study is the difference in SCC between the two recordings.



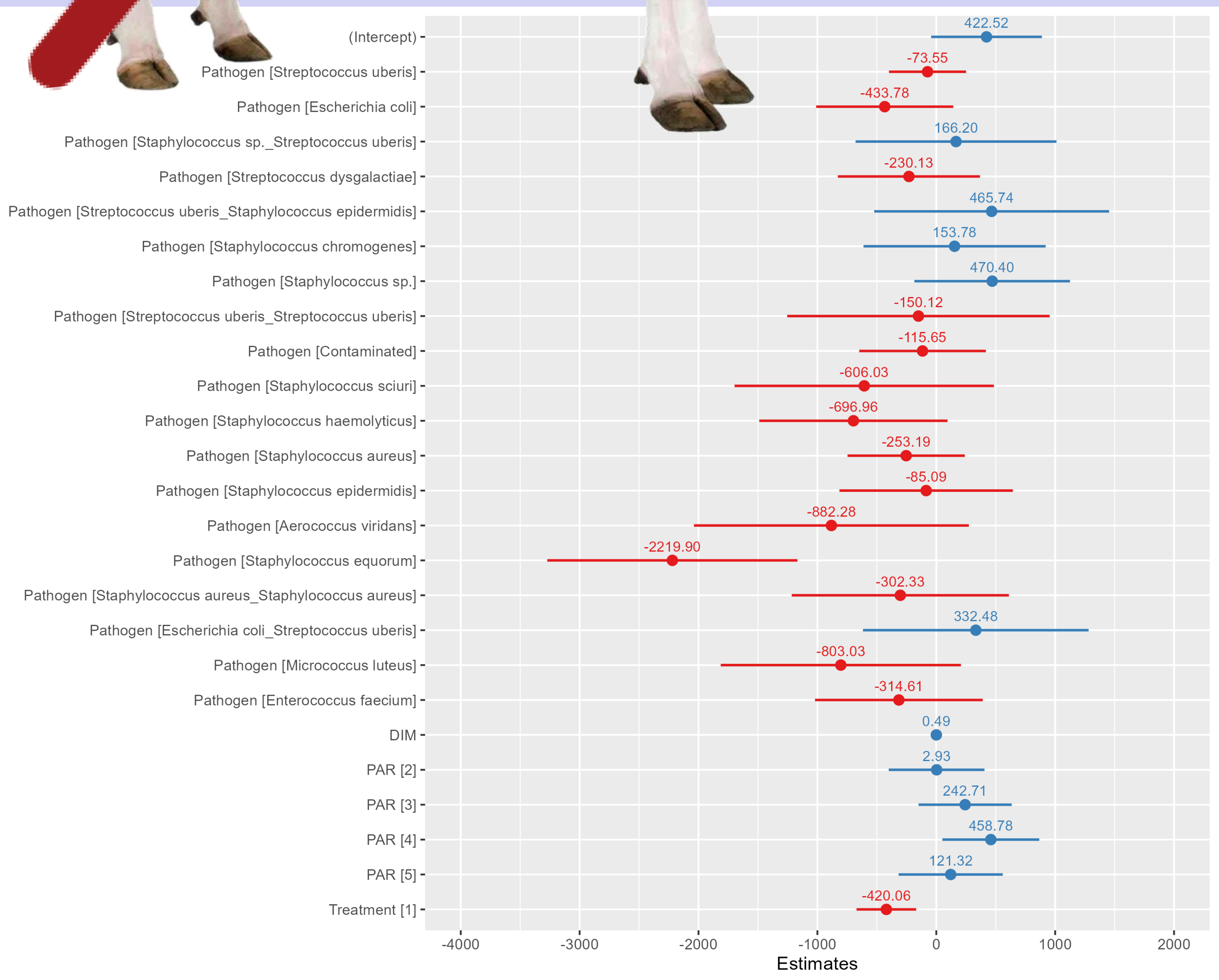
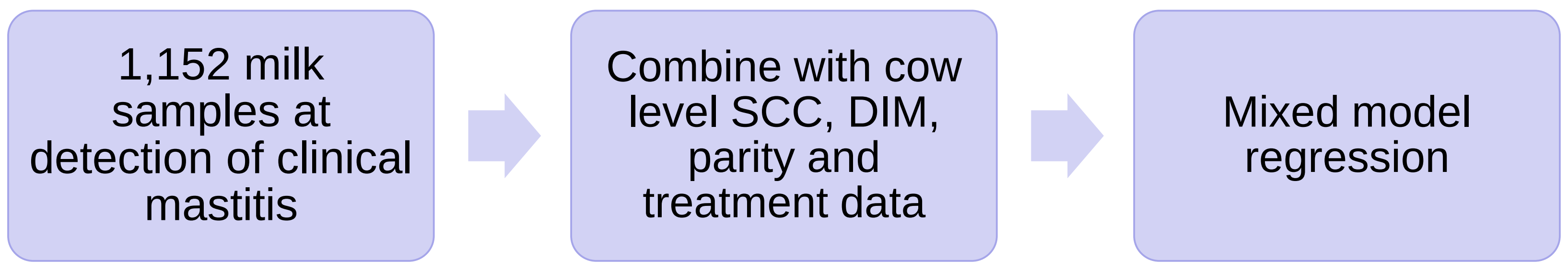


Figure 2. The estimated association between explanatory variables and the difference in SCC (x 1,000) before and after clinical mastitis detection. The reference is samples from untreated cows in first parity with no bacterial growth. Blue color shows positive and red color shows negative estimates in relation to the reference.

Methods

Cows on 12 farms were monitored for clinical mastitis according to the IDF guidelines. We acquired milk samples from cows with a mild to moderate clinical infection, and tested for pathogens using bacterial culture, and MALDI-TOF for confirmation. Samples were considered contaminated if more than two pathogen species were found in the same quarter. Then we combined this data with routinely recorded cow-level register data on somatic cell count, and treatment records related to the infection. **Our outcome variable was the difference in somatic cell count between the last recording before, and the first sample after clinical infection**. We only included pathogens that were found in at least 10 samples.



1,152 milk samples at detection of clinical mastitis

Combine with cow level SCC, DIM, parity and treatment data

Mixed model regression

We used a mixed regression model with a random effect of herd, to investigate the effect of pathogen and pathogen combinations, DIM, parity (1 to 5+) and treatment status (treated/not treated) on the difference in SCC before and after clinical mastitis detection.

Results

Table 1. Number of cow-level samples used in the study, specified per pathogen or pathogen combination, and treatment status.

Pathogen	No treatment	Treatment
No bacterial growth	333	105
Streptococcus uberis	52	203
Contaminated sample	43	10
Staphylococcus aureus	33	32
Escherichia coli	26	16
Staphylococcus epidermidis	20	6
Enterococcus faecium	15	12
Staphylococcus chromogenes	15	8
Staphylococcus haemolyticus	15	8
Staphylococcus sp.	15	16
Streptococcus dysgalactiae	14	28
Staphylococcus aureus + Staphylococcus aureus	13	4
Aerococcus viridans	12	0
Micrococcus luteus	11	2
Staphylococcus equorum	9	3
Staphylococcus sciuri	8	3
Escherichia coli + Streptococcus uberis	5	9
Streptococcus uberis + Streptococcus uberis	5	12
Staphylococcus sp. + Streptococcus uberis	2	16
Streptococcus uberis + Staphylococcus epidermidis	2	11

Take home messages

- ❖ Clinical mastitis detection was associated with a **mean 422.000 increase in SCC**
- ❖ **Treatment significantly reduced SCC** after clinical mastitis detection with **mean 420.000 SCC difference**
- ❖ We found **variation in the SCC difference** at clinical detection related to pathogens, but with overlap
- ❖ Infection with ***Staph. equorum*** was associated with a large **reduction in SCC** after clinical mastitis detection
- ❖ The **difference in SCC increased with increasing parity**, except for parity 5+ cows

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