## Exploring LD decay with quantiles – a case study

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Abstract: Abstract text

Keywords: Keyword1; Keyword2; Keyword3.

## 1 Introduction and motivation

- Decreasing costs of genotyping  $\rightarrow$  data readily available
- More markers  $\rightarrow$  more information about genetic structure available
- More data available does not forcedly result in more information available. The sheer amount of data (Stichwort BIG DATA) might be a problem to deal commonly encountered. Even exploration is a challenge.
- manage  $\rightarrow$  explore  $\rightarrow$  analyse
- Here we focus on exploring/quantifying LD decay.
- As an exploratory tool we will be using quantile regression (general references).
- Data: (local) LD decay in Maize

## 2 Section 2

Text for the second section. This section will have no subsections.

We refer to Table 1 for a summary of our main results. Have a look to Table 2 for an additional example.

Finally a figure (in .pdf!)

We refer to Figure 1 for a graphical representation.

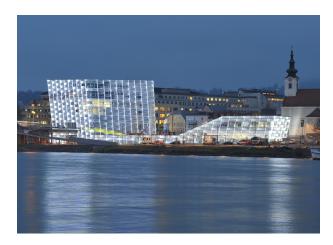


FIGURE 1. Caption text **BELOW** the figure.

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TABLE 1. Caption text **ABOVE** the table.

Title col1	Title col2	Title col3
	row1 col2	
row2 col1 row3 col1	row2 col2 row3 col2	

TABLE 2. Caption text  $\mathbf{ABOVE}$  the table.

	Title for cols 2 -3	
Title1	Title2	Title3
	a	c
	b	d
Total	a + b	n

Lee, Y. and Nelder, J.A. (1996). Hierarchical generalized linear models. *Journal of the Royal Statistical Society, Series B*, **58**, 619–678.

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