

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 → data readily available
- More markers → 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 → explore → 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.

Acknowledgments: This case study was performed while the first and third author were visiting at Biometris at Wageningen University and Research Centre in winter 2014/2015. We are indebted to the group of Prof. Dr. Ruedi Fries, from Technische Universität München, for the SNP genotyping of the parental lines, which was funded by the German Federal Ministry of Education and Research (BMBF) within the AgroClustEr SynbreedSynergistic plant and animal breeding (FKZ:0315528d).

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

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

TABLE 2. Caption text **ABOVE** the table.

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

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