

Chances and challenges in the Bayesian analysis of translational animal experiments by meta-analytic predictive approaches

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The successful explanation of complex links between biological pathways and pathological phenotypes in translational research fundamentally depends on the sensitive contemplation of new data under past insights and expertise knowledge. The MAP (meta-analytic predictive) approach denotes the idea to set up a distribution on the parameters in historical related experiments and use this model as a predictive distribution in a Bayesian analysis of new data [1]. The value of Bayesian statistics has been recognized in pre-clinical research but an obstacle to their practical application resides in the fact that the results from historical experiments are usually unorganized and restricted to limited access. Meanwhile methods for Bayesian Meta-Analysis have been proposed to appropriately summarize historical information also in the context of only few, small clinical studies [2]. Still, the methods suggested in human clinical trials cannot be transferred straight forward to the application in animals. In this work, chances for the application of the MAP approach in the scenario of few, small experiments are discussed. The considerations are motivated by complex real world translational research examples. Special emphasis is put on the construction of prior distributions and on the incorporation of several control groups.

References

- [1] Beat Neuenschwander, Gorana Capkun-Niggli, Michael Branson, and David J Spiegelhalter. “Summarizing historical information on controls in clinical trials”. In: *Clinical Trials* 7.1 (2010), pp. 5–18.
- [2] Tim Friede, Christian Röver, Simon Wandel, and Beat Neuenschwander. “Meta-analysis of few small studies in orphan diseases”. In: *Research Synthesis Methods* 8.1 (2017), pp. 79–91.