**Bayesian statistics for longitudinal studies in biomedical research**

*Their application and use in biomedical research*

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## Paper outline

## Background

A longitudinal study is defined as one where a variable of interest is measured repeatedly in a group (or groups) of subjects. In biomedical research, this type of study is preferred when the intention is to observe the evolution of the effect of treatment across time, rather than analyzing the information at a single timepoint (a cross-sectional study). Clinical examples of this approach in biomedical research include studies on breast and neck cancer(Sio et al. [2016](#ref-sio2016); Kamstra et al. [2015](#ref-kamstra2015)); in the first case, weekly measurements of skin toxicities in patients with radiation-induced dermatitis were taken for up to 8 weeks; whereas in the latter mouth opening measured was assessed at 6,12, 18, 24 and 36 months after radiotherapy (RT). Longitudinal studies have used also to measure tumor response (Roblyer et al. [2011](#ref-roblyer2011); Tank et al. [2020](#ref-tank2020); Pavlov et al. [2018](#ref-pavlov2018); Demidov et al. [2018](#ref-demidov2018)), antibody expression(Ritter et al. [2001](#ref-ritter2001); Roth et al. [2017](#ref-roth2017)), and cell metabolism(Jones et al. [2018](#ref-jones2018); Skala et al. [2010](#ref-skala2010)). From a statistical standpoint, a longitudinal study presents advantages over a cross-sectional approach:it requires a lower number of subjects to reach a certain statistical power, and besides it being able to track the previously mentioned time-effect evolution on a group-by-group basis, it allows to determine the variability of the response within subjects (Guo et al. [2013](#ref-guo2013); Fitzmaurice, Laird, and Ware [2012](#ref-fitzmaurice2012)). In other words,a longitudinal study permits to quantify how the variable changes within each subject across time.

Researchers have typically employed a *frequentist* approach to analyze longitudinal data, a statistical view that derives its name from the fact that it regards probability as a limiting frequency [wagenmakers2008]. when applied to longitudinal, a frequentist analysis is based on a null hypothesis test using the *analysis of variance over repeated measures* (repeated measures ANOVA or rm-ANOVA). This methodology makes two key assumptions regarding longitudinal data: a constant correlation across same-subject measurements and complete observations from each subject (Schober and Vetter [2018](#ref-schober2018); Gueorguieva and Krystal [2004](#ref-gueorguieva2004)). The first condition is frequently unjustified as the correlation between measures diminishes when the time gap between them increases (Ugrinowitsch, Fellingham, and Ricard [2004](#ref-ugrinowitsch2004)), and in that case violating that assumption increases the type I error rate(Lane [2016](#ref-lane2016)). The reasons behind the second assumption being not met in biomedical research are varied: subjects can withdraw during the course of the study, attrition in animals due to injury or weight loss, or complications can arise that prevent the researcher from collecting measurements at a certain timepoint. When these issues arise, rm-ANOVA requires to exclude the subject with missing observations from the analysis, which can lead to increased costs for the study if the desired statistical power is not met with the remaining subjects, and can lead to the exclusion of valuable information.Additionaly, rm-ANOVA uses a *post hoc* analysis to assess significance in the differences between groups. Because a *post hoc* analysis is based in multiple repeated comparisons, it can inflate the false positivity rate(Liu, Cripe, and Kim [2010](#ref-liu2010)).

Recently, *linear mixed effects models* (LMEMs) have been used by certain groups to analyze biomedical longitudinal data (Vishwanath et al. [2009](#ref-vishwanath2009); Skala et al. [2010](#ref-skala2010)). Briefly, these models incorporate *fixed* effects, which correspond to the levels of experimental factors in the study (e.g. the different drug regimens in a clinical trial), and *random* effects, which account for random variation within the population (Pinheiro and Bates [2006](#ref-pinheiro2006)). These models are more flexible than rm-ANOVA as they can accommodate missing observations in the data, and allow different modeling strategies for the covariance(West, Welch, and Galecki [2014](#ref-west2014)). On the other hand, they impose restrictions in the distribution of the errors and of the random effects, and assume linearity between the response and the parameters(Schielzeth et al. [2020](#ref-schielzeth2020); Pinheiro and Bates [2006](#ref-pinheiro2006)).

The assumption of linearity is a key component of LMEMs and rm-ANOVA, and therefore both models restrict the inferences they can extract from longitudinal data when it does not follow a linear trend. In biomedical research, such behavior in longitudinal data does arise and has been exemplified in different studies, including response to radio/chemotherapy in preclinical and clinical settings (Vishwanath et al. [2009](#ref-vishwanath2009); Roblyer et al. [2011](#ref-roblyer2011); Tank et al. [2020](#ref-tank2020); Skala et al. [2010](#ref-skala2010); Demidov et al. [2018](#ref-demidov2018)), and wound healing and metabolism(Jones et al. [2018](#ref-jones2018); Grice et al. [2010](#ref-grice2010); Young and Grinnell [1994](#ref-young1994)). In such situations, an estimated model via rm-ANOVA or LMEMs may not provide a consistent fit with the observed variations in the variables of interest. Moreover, although it is possible to obtain a “significant” *p-value*( *p*<0.05) due to the well-known variability of this metric (Nuzzo [2014](#ref-nuzzo2014); Halsey [2019](#ref-halsey2019)), the model will lack predictive power and this in turn will compromise the extent of the inferences that can be derived from it.

Since both the *frequentist* (rm-ANOVA) and LMEM approaches are limited in the analysis of non-linear longitudinal information, there is a need for biomedical researchers to use statistical tools that allow the data to determine the fit of the model while enabling inferences that are both adequate and consistent from a statistical standpoint.

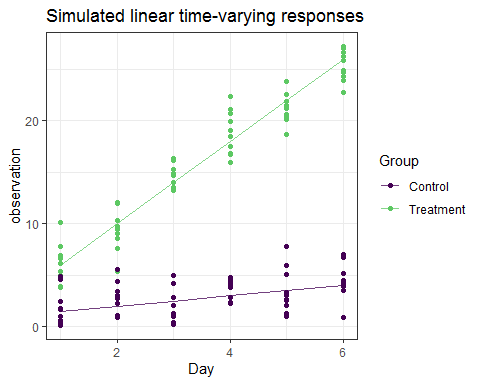
Generalized additive models (GAMs) are a subset of generalized linear models that use *smooth functions* (hencefort *smooths*) to estimate the parameters of a model. They have been used in palaeolimnology, ecology and clinical studies to model longitudinal data(Woolway et al. [2016](#ref-woolway2016); Hefley et al. [2017](#ref-hefley2017); **???**). Briefly, GAMs use a combination of multiple functions (basis functions)to construct the smooths of the model (Wood [2017](#ref-wood2017)). Their main advantage over LMEMs and rm-ANOVA is that the model specification is directed by the *smooths* rather than by a parametric relationship. This allows a consistent fit of the model with the data, and estimations of significance using the terms of the model. However, certain assumptions about the data are necessary: a normal distribution and constant variance of the residuals with the mean response. Therefore, GAMs provide a more suitable statistical method to analyze biomedical longitudinal data, when these assumptions are met.

If the assumptions of GAMs do not hold, the field of *Bayesian statistics* represents a relatively new area of Statistics that does not rely on *p-values* and hypothesis tests to analyze information. Bayesian statistics can work with missing observations, allow the data (and not an underlying assumed distribution) to determine the outcome in regard to significance and are able to expand the number of comparisons and inferences derived form the analysis. On the other hand, the shift that Bayesian statistics represent from the traditional *frequentist* statistical view in research, the computational tools required for its implementation, and the underlying mathematical theory have limited the use of this approach in the biomedical research community. However,Bayesian theory is intuitive and shares some principles with *frequentist* statistics, and there is an increasing use and recognition of the advantages of their use across different areas of biomedical research such as clinical trial design and imaging(Biswas et al. [2009](#ref-biswas2009); Kelter [2020](#ref-kelter2020); Kwon et al. [2020](#ref-kwon2020); Zhou [2017](#ref-zhou2017)). Additionaly,the current development in computational tools, specifically the programming language, enable a rapid implementation of Bayesian models.

To this end, the goals of this study are: a) to present the limitations of (rm-ANOVA) and LMEMs over longitudinal data, and demonstrate how these limitations in turn affect the results of the analysis b) introduce in a practical and amenable manner the theory of Bayesian statistics highlighting its applicability to biomedical research and c)Implement a Bayesian analysis over a set of simulated data that matches previously reported trends in longitudinal biomedical studies. With an emphasis on reproducibility by providing the code and dataset used, this will provide biomedical researchers a clear view of the advantages of Bayesian statistics for the analysis of longitudinal data.

* Why LMEMs are better than ANOVA
* How LMEMs (using splines) and a Bayesian analysis can be used to analyze longitudinal data

<https://www.frontiersin.org/articles/10.3389/fevo.2018.00149/full>



Simulated longitudinal data with a linear trend.

## Section 1:

### Challenges presented by longitudinal studies:

#### 1.1 the *frequentist* case for constant correlation (ANOVA limitations)

The first Missing observations, and correlation between measurements. How rm-ANOVA is limited by missing observations, and how both rm-ANOVA and LMEMs are limited with data that does not follow a linear trend (equations for both situations and the fit they produce.)

One of the key assumptions for rm-ANOVA is the constant correlation among measurements. This frequently not the case as the correlation reduces as the time interval between two measurements increases (Ugrinowitsch, Fellingham, and Ricard [2004](#ref-ugrinowitsch2004)). From a practical

#### 1.2 the case of LMEMs using splines and how they work and how they are better than rm-ANOVA

#### 1.3 Bayesian brief introduction, and compare the results of 1.2 to the results of Bayesian

* Section 2: Implementation of both LMEMs and Bayesian and their results

Present the implementation of a spline-fitted model in R, using data simulated from (Vishwanath et al. [2009](#ref-vishwanath2009))

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