Longitu

Benefits of linear mixed effects modelling:

- reduction in type I error rate compared to single time point (cross-sectional) analysis;
- able to cope with inconsistent sampling time points (e.g. from two different experiments) and/or irregularly-spaced data (e.g. no need to come on the week-end);
- it does account for time-correlation structure when treating time as continous;
- incomplete datasets due to randomly missing measurements or from incomplete time course resulting from an excessive tumour size can still be analysed;
- complex questions can be addressed by means of adequate contrast calculations, even in presence of not so balanced designs.

These advantages make mixed-effect modelling the standard method to statistically analyse tumor growth datasets. Yet, it relies the assumption for the nature of the relationship between tumour size and time. The current implementation only considers *linear* regression but can be applied on the raw or transformed response to accomodate the peculiarities of the data. Situations involving heterogeous datasets with non monotoneous behaviours for e.g. will be not be correctly addressed with this function: the users can reformulate their question differently with the `TumGrowth` survival and cross-sectional functionnalities (if not revisit their experimental set-up).

Settings Data selection:

1. treatment group of interests;
2. response variable amongst the several that could have been loaded to `TumGrowth`;
3. transformation of the response variable:

- None, the raw data
- Log, log-transformed response (zero's may be excluded)
- Sqrt, for the square root of the response.

Modelling:

1. a couple of things to add
2. outlier detection threshold - One round of outlier detection is performed to exclude automatically abberrant observations on the basis of Bonferroni-corrected p-value calculated from the residuals. `Default: p<0.1` is a not so stringent and reasonable cut-off. Note that aberrant animals are best excluded manually by the user before uploading the data by leaving empty the **Use** column in the raw datafile.

Output and interpretation Type II ANOVA: * `Time x Treat` correspond to the outcome of the global test underlying that there is the tumour growth curve slopes differ between treatment groups. If the test is positive, then the between pairwise comparison; * `Time` and `Treat` factors are solely meaningfull in the case of a non-significant `Time x Treat`. These to *Time+Treat* the model is like it

Pairwise comparisons: * Differences in slope between pairs of treatement groups <

Diagnostics plots: * `QQ-plot`: data points should lie as closely as possible to the straightline. Any *S* or *banana*-like shapes are likely to be caused by poor transformation of the response and straight segments of points may be *ceiling* effects due to a constant portion in a time course; * `Resid/Fit`: residuals of the models are plotted againts the fitted values (i.e. animal-level predictions). Data points are expected to be uniformly distributed around zero and at any value of the response. Issues observed in `QQ-Plot` can be outlined here; * `Fit`: overlay of the time courses (excluding outlying measuements) and back-transformed predicted growth curves (with 95% confidence intervals). It gives a visual insight into the adequacy of the modelling strategy; * `Resid/Mice`, `Resid/Grp`, `Resid/Tp`: distribution across time points and mice. This can help at hightlighting deviant animals, poorly sampled time points or non-typical treatment response. <

Model information: * Fixed effect coeff matrix; * Ids of any potentially excluded outliers;

Implementation blahblah

somne references here