Version 2.2-Results

# Results

* The table below (**table** ) shows the estimate, standard error, test statistic, and p-values associated with the fixed-effect slope parameter as estimated by each modeling method for the variable pairing.

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* The fixed effect slope parameter is being considered for comparison because we are interested in quantifying correlation between single-cell values at the subject level.
* Displayed in (**table** ), (**table** ) , and (**table** ) below are percent changes in: parameter estimates, standard errors, and test statistics (respectively) for the variable pairing as defined by:

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## Parameter Estimates

* Models LM and GEE have similar estimates
* Models LM-FE, LM-RI, and LM-RS are also all similar
* Estimates are less similar when comparing between the two clusters of similarity mentionioned
* Accounting for subject-specific outcomes results in a different estimate than when modeling population-averages, i.e. there is an effect from subject-level correlation
* The effect is more pronounced in the FBLN1~CD34 pairing than the MALAT1~CD19 pairing

## Standard Error Estimates

* The standard error of the fixed effect slope parameter estimate is highest for the random slope model
* The SE is lowest for the random intercept model
* The fixed-effect subject-specific intercept had a lower SE than either of the population-average parameter interpretaion models LM and GEE.

## Test Statistics

* Changes in test statistics for the fixed-effect main-effect slope were smaller between LM and GEE, as well as between LM-FE, LMM-RI, and LMM-RS with few exceptions.
* There were very small differences between LM and GEE
* Changes to the LMM-RS resulted in calculated p-value increases with two and three orders of magnitude.

## 

## Nested Model Comparisons

### Test for FE Subject Specific Intercept

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(**table** ) above is a nested model comparison, the result of which is an F-test statistic telling us that there is very strong evidence to support the inclusion of the subject-specific fixed-effect intercept into the LM model.

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### Test for RE Subject Specific Intercept

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(**table** ) above is a nested model comparison, the result of which is a likelihood ratio statistic telling us that there is very strong evidence to support the inclusion of the subject-specific random effect intercept into the LM model.

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### Test for RE Subject Specific Slope

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(**table** ) above is a nested model comparison, the result of which is a likelihood ratio statistic telling us that there is very strong evidence to support the inclusion of the subject-specific random effect slope into the LMM-RI model for the MALAT1~CD19 variable pairing. However, there is insufficient evidence to support the inclusion of the subject-specific random effect slope into the LMM-RI model for the FBLN~CD34 variable pairing.

# References