

## MetaMutationalSigs

There are several packages available now for mutational signature analysis and they all use different approaches and give nontrivially different results. We created this package to facilitate comprehensive mutational signature analysis by creating a wrapper for different packages and creating a standard format for their outputs so that they can be effectively compared. We also create standard visualizations for the results of all packages to ensure easy analysis.

Commands: Run all packages and save the resulting data and visualizations in the output\_dir directory

```
Rscript meta_sig_main.R ./output_dir
```

Use hg38 reference genome. Default is hg19. `Rscript meta_sig_main.R ./output_dir hg38`