

vs\_sup

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## Virtual screening for high affinity guests for synthetic supramolecular receptors

### Original literature

<https://doi.org/10.1039/C5SC00534E>

### Function used in this analysis

I don't have a R data science package(library) yet...

### Replication of our analysis in the manuscript using python

We load and clean data from the supporting information

```
df = read.csv("tab_gold_wt.csv", header = TRUE)
```

### Run some exploratory data analysis

#### Data summary

```
summary(df)
```

```
##      Guest      Ligand_clash      Ligand_torsion      Part_buried
##  Min.   : 1      Min.   :0.00000      Min.   :0.0000      Min.   : -4.621
## 1st Qu.:18      1st Qu.:0.00000      1st Qu.:0.0000      1st Qu.: -3.046
## Median :35      Median :0.00000      Median :0.0000      Median : -2.193
## Mean   :35      Mean   :0.02582      Mean   :0.0650      Mean   : -2.027
## 3rd Qu.:52      3rd Qu.:0.00000      3rd Qu.:0.0016      3rd Qu.: -1.708
## Max.   :69      Max.   :1.78130      Max.   :1.0855      Max.   :  8.908
##  Non.polar      Ligand_flexibility      logKexp
##  Min.   : -72.20      Min.   :0.0000      Min.   : -1.000
## 1st Qu.: -49.49      1st Qu.:0.0000      1st Qu.:  1.860
## Median : -40.64      Median :0.0000      Median :  3.600
## Mean   : -42.43      Mean   :0.7971      Mean   :  3.167
## 3rd Qu.: -34.32      3rd Qu.:1.0000      3rd Qu.:  4.300
## Max.   : -22.77      Max.   :7.0000      Max.   :  8.000
```

we still have guest number the data frame we will remove it

```
df <- df[-c(1)]  
summary(df)
```

```
##   Ligand_clash    Ligand_torsion    Part_buried    Non.polar  
##   Min.      :0.00000    Min.      :0.0000    Min.      :-4.621    Min.      :-72.20  
##   1st Qu.:0.00000    1st Qu.:0.0000    1st Qu.: -3.046    1st Qu.: -49.49  
##   Median :0.00000    Median :0.0000    Median : -2.193    Median : -40.64  
##   Mean   :0.02582    Mean   :0.0650    Mean   : -2.027    Mean   : -42.43  
##   3rd Qu.:0.00000    3rd Qu.:0.0016    3rd Qu.: -1.708    3rd Qu.: -34.32  
##   Max.    :1.78130    Max.    :1.0855    Max.     : 8.908    Max.     :-22.77  
##   Ligand_flexibility    logKexp  
##   Min.      :0.0000    Min.      :-1.000  
##   1st Qu.:0.0000    1st Qu.: 1.860  
##   Median :0.0000    Median : 3.600  
##   Mean   :0.7971    Mean   : 3.167  
##   3rd Qu.:1.0000    3rd Qu.: 4.300  
##   Max.    :7.0000    Max.     : 8.000
```

```
col_names = colnames(df)  
print(ncol(df))
```

```
## [1] 6
```

```
print(col_names[1])
```

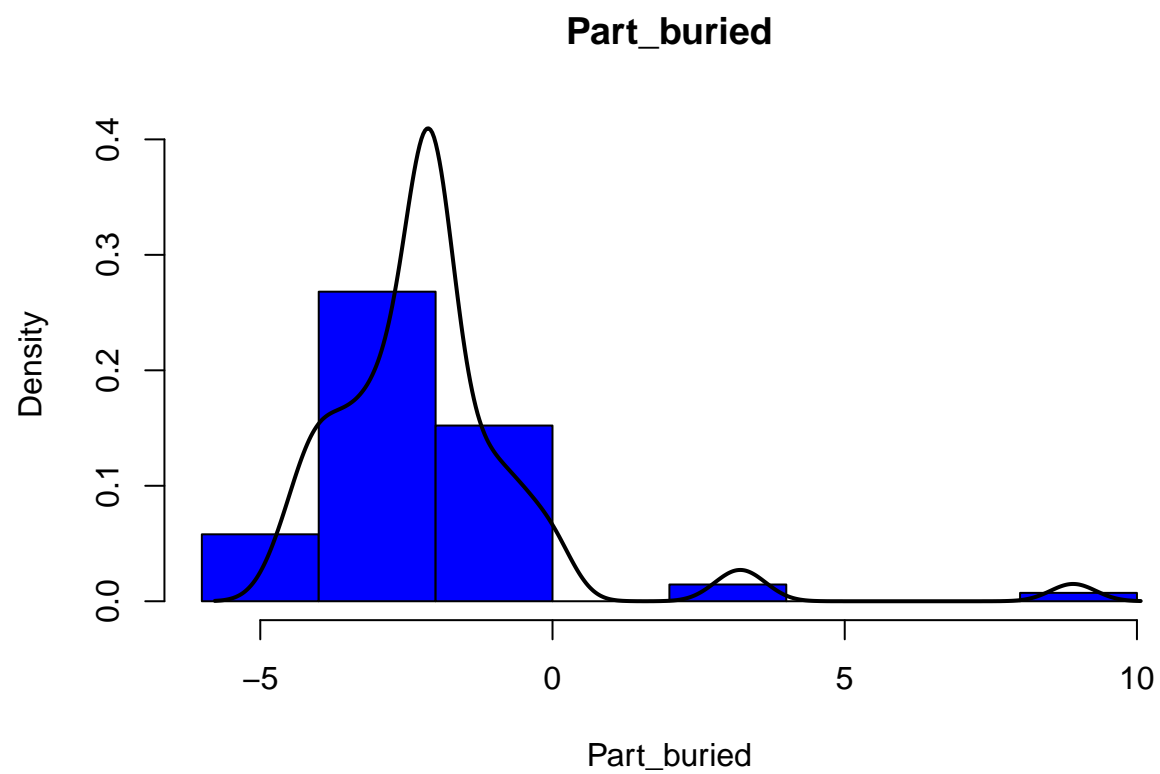
```
## [1] "Ligand_clash"
```

```
int_made_even(3)
```

```
## [1] 4
```

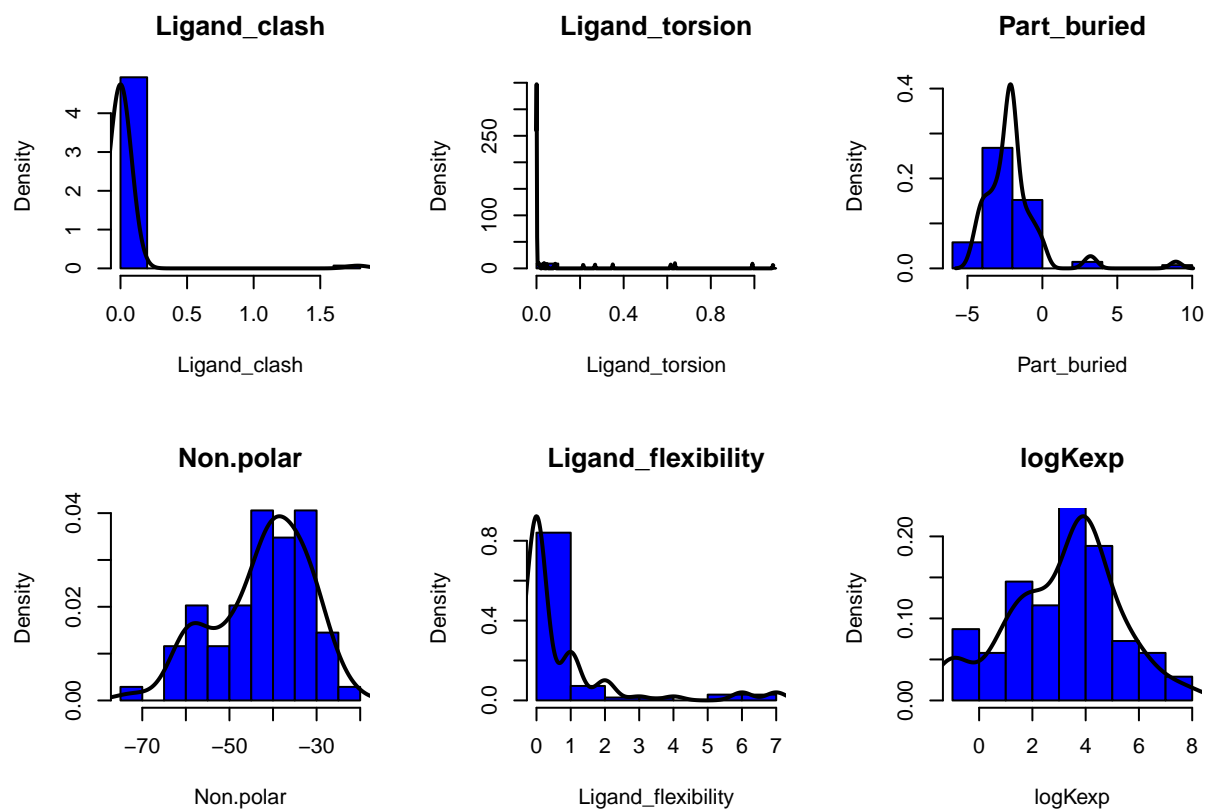
Colored Histogram with KDE line for clarity

```
hist_kde(df, "Part_buried")
```



```
multi_plot(df, hist_kde)
```

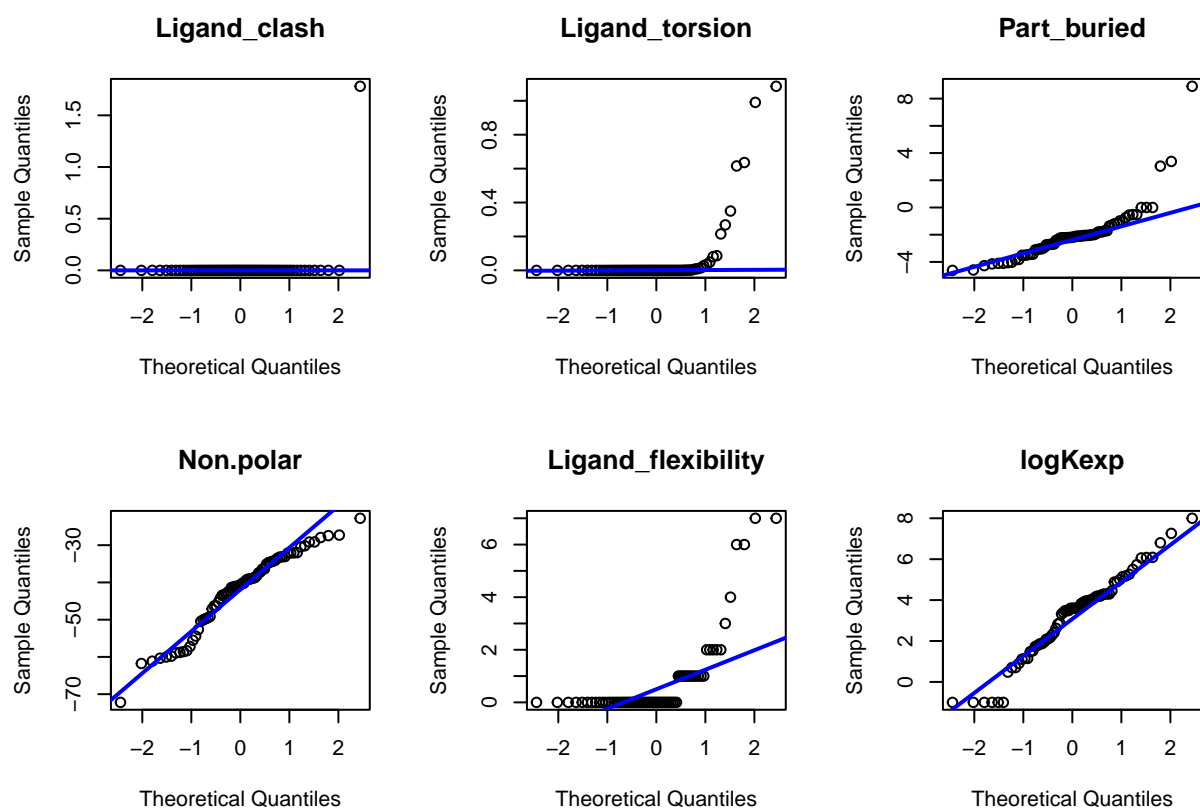
```
## [1] 6  
## [1] 6  
## [1] 6
```



### Quantile quantile plots Our quantile quantile plots show us whether our data fits to a theoretical distribution

```
multi_plot(df, q_q_plot)
```

```
## [1] 6
## [1] 6
## [1] 6
```



This is experimental data from 69 individual data points our team generated so we don't really expect it to fit a normal distribution. We would expect the replicates of **logKexp** to fit a normal distribution and the error quoted in the manuscript is at 95% confidence.