

Import the unaltered medial axis data.

```
## [1] TRUE
```

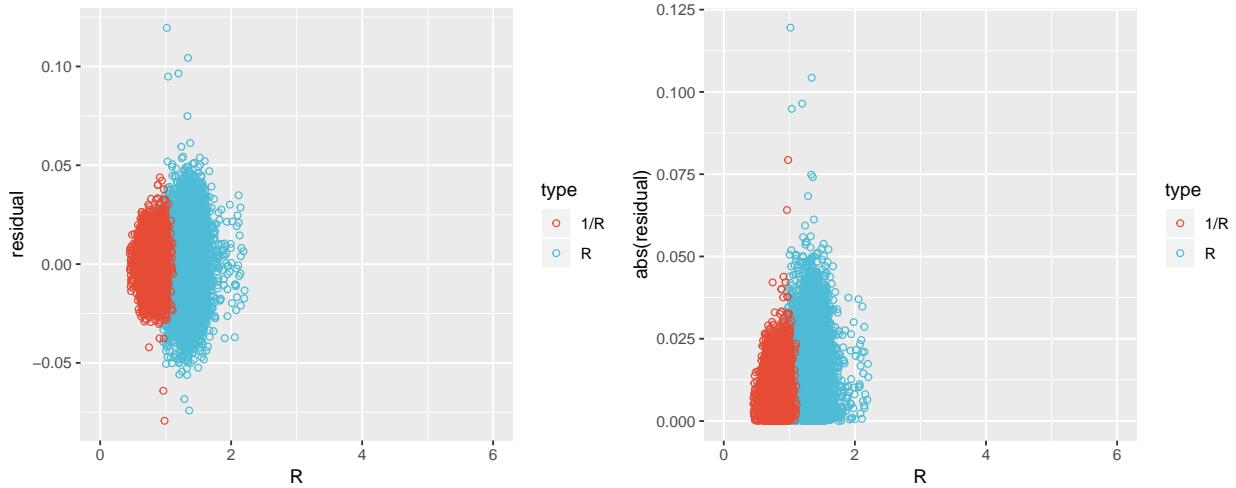
| R | residual | individual | type | lambda | experiment | location |
|----------|------------|------------|------|--------|------------|-------------|
| 1.070923 | 0.0077718 | 1 | R | 3.9 | tbuooh | medial_axis |
| 1.064363 | -0.0058960 | 1 | R | 3.9 | tbuooh | medial_axis |
| 1.095505 | 0.0255295 | 1 | R | 3.9 | tbuooh | medial_axis |
| 1.043605 | -0.0299668 | 1 | R | 3.9 | tbuooh | medial_axis |
| 1.047435 | -0.0129234 | 1 | R | 3.9 | tbuooh | medial_axis |
| 1.096380 | -0.0005029 | 1 | R | 3.9 | tbuooh | medial_axis |

Import the inverted medial axis data.

```
## [1] TRUE
```

| R | residual | individual | type | lambda | experiment | location |
|-----------|------------|------------|------|--------|------------|-------------|
| 0.9337741 | -0.0046118 | 1 | 1/R | 3.9 | tbuooh | medial_axis |
| 0.9395289 | 0.0036138 | 1 | 1/R | 3.9 | tbuooh | medial_axis |
| 0.9128210 | -0.0160148 | 1 | 1/R | 3.9 | tbuooh | medial_axis |
| 0.9582169 | 0.0189314 | 1 | 1/R | 3.9 | tbuooh | medial_axis |
| 0.9547130 | 0.0078177 | 1 | 1/R | 3.9 | tbuooh | medial_axis |
| 0.9120921 | -0.0000264 | 1 | 1/R | 3.9 | tbuooh | medial_axis |

Combine the data into one dataframe



Import pm3 data from the same experiment, unaltered.

```
## [1] TRUE
```

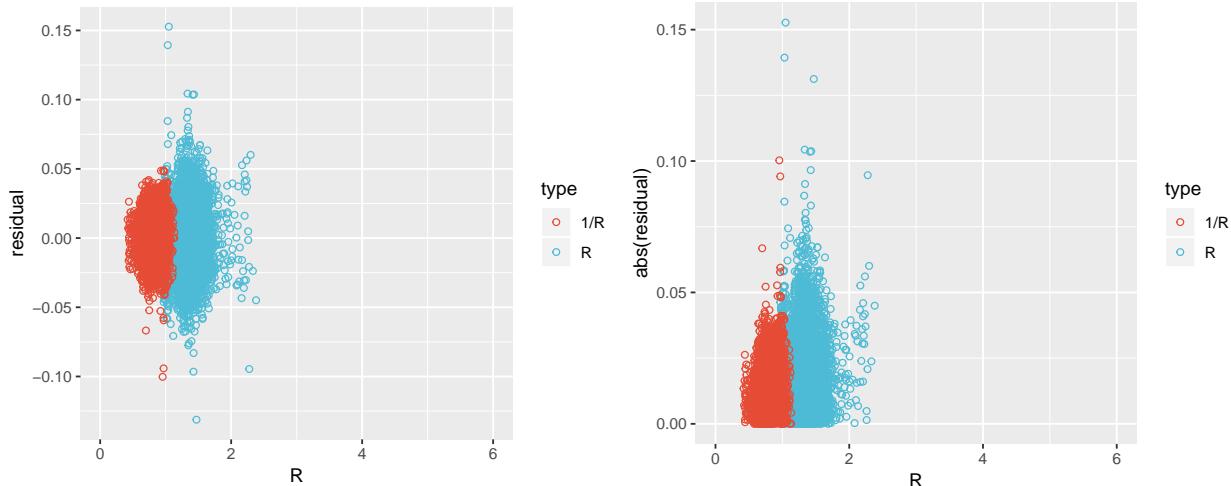
| | R | residual | individual | type | lambda | experiment | location |
|----------|------------|----------|------------|------|--------|------------|----------|
| 1.051199 | 0.0110215 | 1 | | R | 3.9 | tbuoooh | pm3 |
| 1.027513 | -0.0059460 | 1 | | R | 3.9 | tbuoooh | pm3 |
| 1.068549 | 0.0265750 | 1 | | R | 3.9 | tbuoooh | pm3 |
| 1.048825 | -0.0378065 | 1 | | R | 3.9 | tbuoooh | pm3 |
| 1.029389 | -0.0134021 | 1 | | R | 3.9 | tbuoooh | pm3 |
| 1.093999 | -0.0189916 | 1 | | R | 3.9 | tbuoooh | pm3 |

Import pm3 data from the same experiment, inverse.

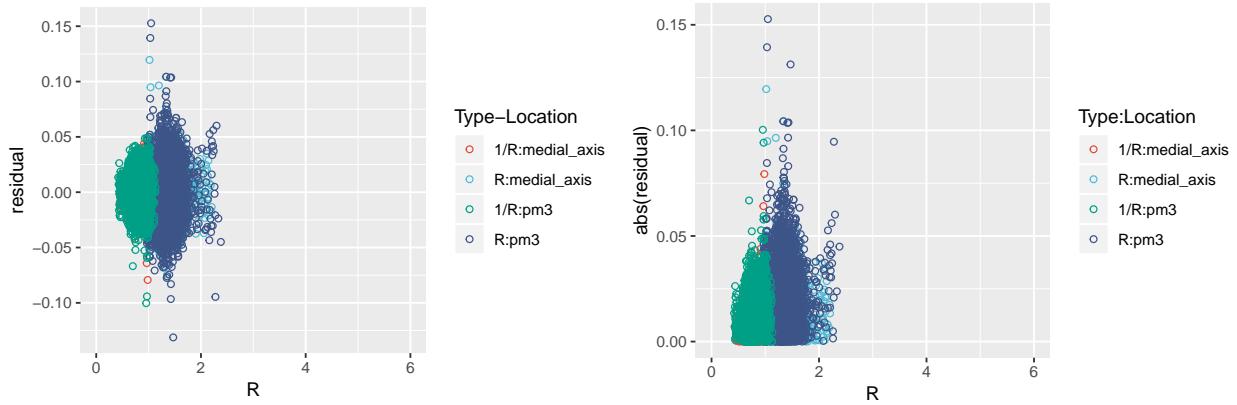
```
## [1] TRUE
```

| R | residual | individual | type | lambda | experiment | location |
|-----------|------------|------------|------|--------|------------|----------|
| 0.9512950 | -0.0074415 | 1 | 1/R | 3.9 | tbuooh | pm3 |
| 0.9732235 | 0.0037841 | 1 | 1/R | 3.9 | tbuooh | pm3 |
| 0.9358485 | -0.0180500 | 1 | 1/R | 3.9 | tbuooh | pm3 |
| 0.9534477 | 0.0261412 | 1 | 1/R | 3.9 | tbuooh | pm3 |
| 0.9714496 | 0.0088599 | 1 | 1/R | 3.9 | tbuooh | pm3 |
| 0.9140774 | 0.0129719 | 1 | 1/R | 3.9 | tbuooh | pm3 |

Put the pm3 data into one dataframe.



Put the medial axis and pm3 data into one dataframe.



Import pm3 data from the diamide recovery experiment, unaltered.

```
## [1] TRUE
```

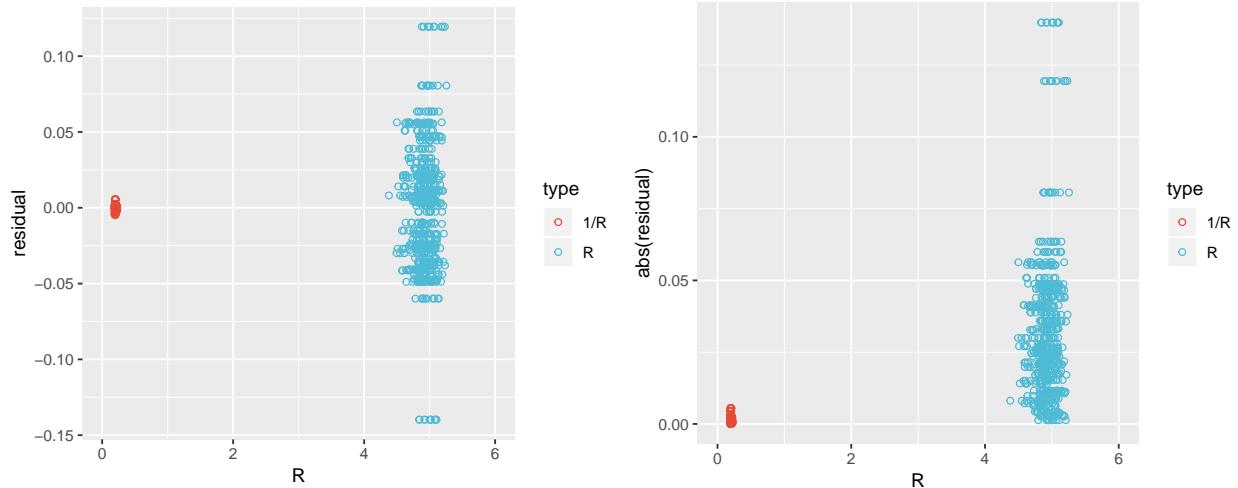
| R | residual | individual | type | lambda | experiment | location |
|----------|------------|------------|------|--------|------------------|----------|
| 4.803131 | 0.0563131 | 0.0179271 | R | 1 | diamide_recovery | pm3 |
| 4.823183 | -0.0413889 | 0.0531677 | R | 1 | diamide_recovery | pm3 |
| 4.740862 | -0.0299442 | -0.1036459 | R | 1 | diamide_recovery | pm3 |
| 4.777698 | 0.0081014 | 0.0411288 | R | 1 | diamide_recovery | pm3 |
| 4.834791 | -0.0270949 | -0.0227222 | R | 1 | diamide_recovery | pm3 |
| 4.757147 | 0.0140736 | -0.0289367 | R | 1 | diamide_recovery | pm3 |

Import pm3 data from the diamide recovery experiment, inverse.

```
## [1] TRUE
```

| R | residual | individual | type | lambda | experiment | location |
|-----------|------------|------------|------|--------|------------------|----------|
| 0.2081975 | -0.0023012 | -0.0007544 | 1/R | 1 | diamide_recovery | pm3 |
| 0.2073319 | 0.0017625 | -0.0024441 | 1/R | 1 | diamide_recovery | pm3 |
| 0.2109321 | 0.0012307 | 0.0048090 | 1/R | 1 | diamide_recovery | pm3 |
| 0.2093058 | -0.0004113 | -0.0020008 | 1/R | 1 | diamide_recovery | pm3 |
| 0.2068342 | 0.0011124 | 0.0009526 | 1/R | 1 | diamide_recovery | pm3 |
| 0.2102100 | -0.0006249 | 0.0012739 | 1/R | 1 | diamide_recovery | pm3 |

Put the pm3 diamide recovery data into one dataframe.

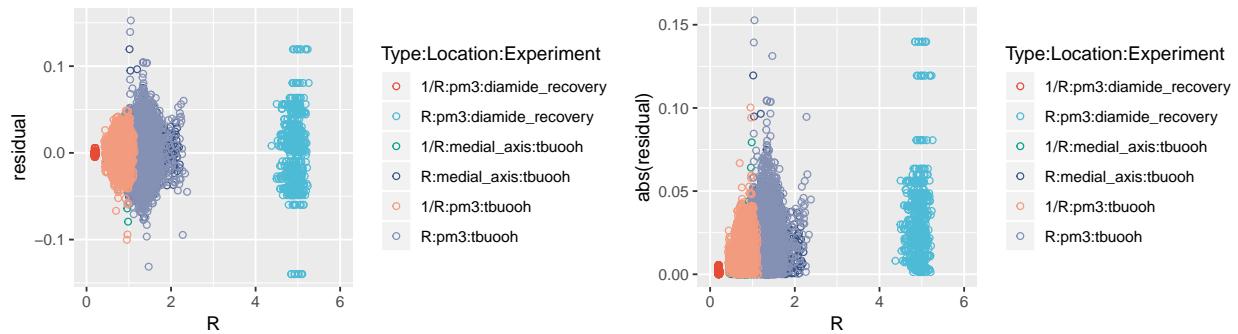


Add this experiment to the growing big dataframe

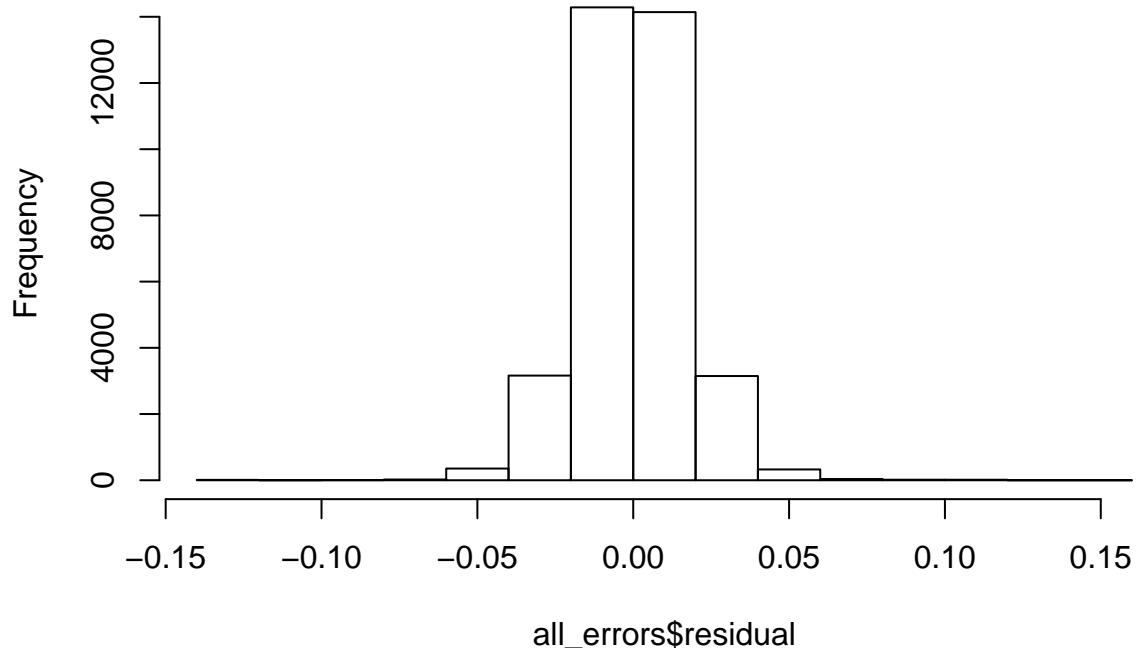
```

## Warning in `[<-.factor`(`*tmp*`, ri, value = c(0.017927098605277,
## 0.053167729078034, : invalid factor level, NA generated

```

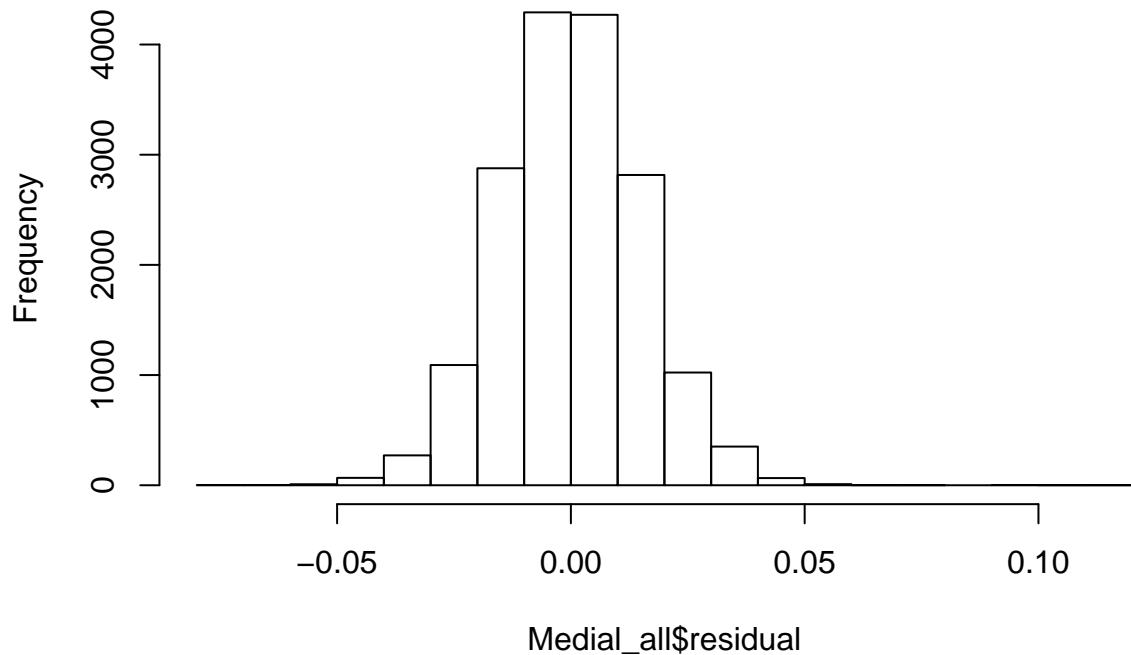


All Residuals



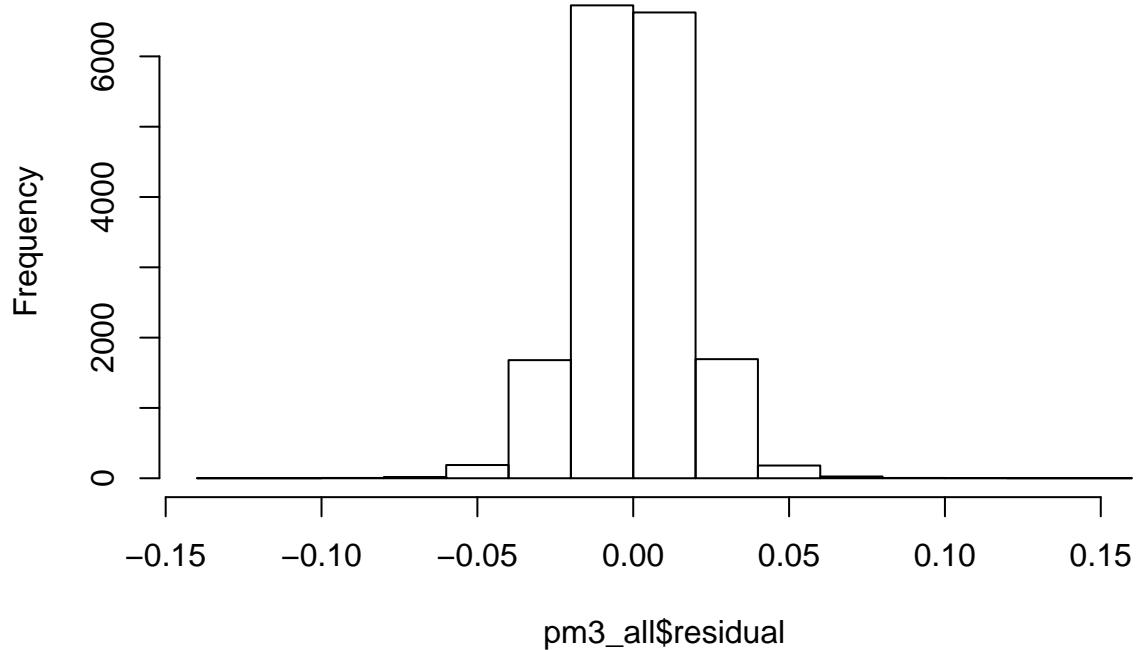
```
##      2.5%      97.5%
## -0.02789713  0.02777684
```

Residuals from Medial Axis tubooth



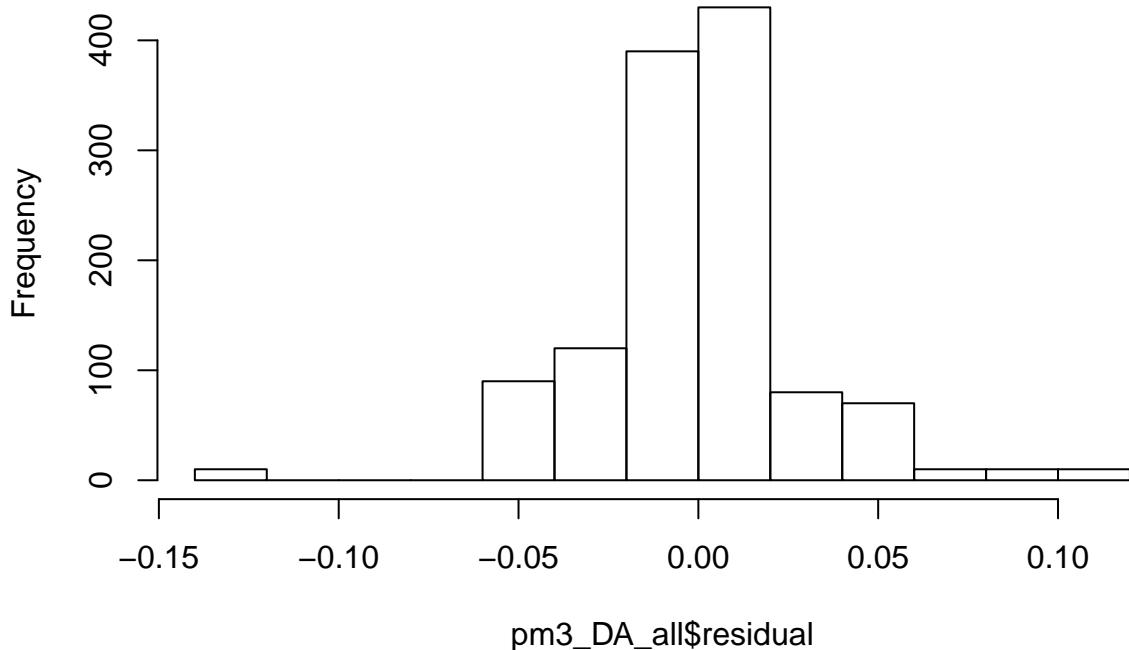
```
##      2.5%      97.5%
## -0.02581250  0.02545579
```

Residuals from pm3 tubooth



```
##      2.5%      97.5%
## -0.03031707  0.03014992
```

Residuals from pm3 diamide recovery



```
##      2.5%      97.5%
## -0.01301606  0.01317427
```