

## **Dilation of fusion pores by crowding of SNARE proteins**

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Fig.5—source data 1

Summary of Matlab analysis of fusion rate statistics for different NLP v-SNARE copy  
numbers

Perform a 1-way ANOVA to test if the means of groups (different SNARE copy numbers) are different

Then use the ANOVA results to do pairwise comparisons using 'multcompare'

```
% copy pores/min data (one value per cell) from excel to matlab. Name PperMinvNLP00, etc. These are  
vectors of different lengths (different numbers of cells), so fill with NaNs to 40 elements each (the longest  
vector, vNLP30 has 40 observations).
```

```
>> PperMinvNLP15(24:40)=NaN;  
>> PperMinvNLP08(27:40)=NaN;  
>> PperMinvNLP04(21:40)=NaN;  
>> PperMinvNLP01(33:40)=NaN;  
>> PperMinvNLP00(27:40)=NaN;
```

```
% combine into a matrix. Each column is a different group.
```

```
>> Frates = [PperMinvNLP00, PperMinvNLP01, PperMinvNLP04, PperMinvNLP08, PperMinvNLP15,  
PperMinvNLP30];
```

```
% give meaningful names the groups ("levels")
```

```
>> groups={'eNLP', 'vNLP1', 'vNLP4', 'vNLP8', 'vNLP15', 'vNLP30'};
```

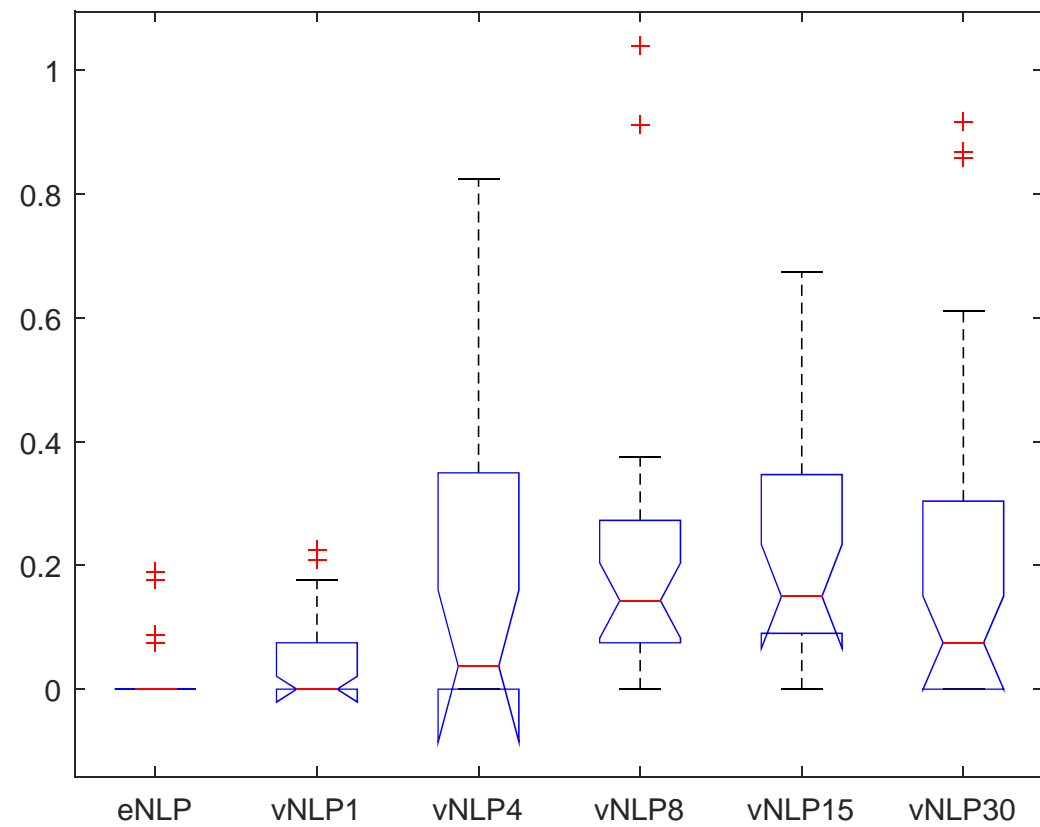
```
% Perform 1-way ANOVA
```

```
>> [p,tbl,stats] = anova1(Frates, groups);
```

**ANOVA Table**

Source	SS	df	MS	F	Prob>F
Groups	1.10873	5	0.22175	5.38	0.0001
Error	6.63163	161	0.04119		
Total	7.74036	166			

rejects the null hypothesis that  
all group means are equal.



% we saved the statistics in the structure stats

```
>> stats
```

```
stats =
```

```
  gnames: {6x1 cell}
```

```
    n: [26 32 20 26 23 40]
```

```
 source: 'anova1'
```

```
 means: [0.0232 6.6936e-04 0.1700 0.2058 0.2324 0.1921]
```

```
   df: 161
```

```
    s: 0.2009
```

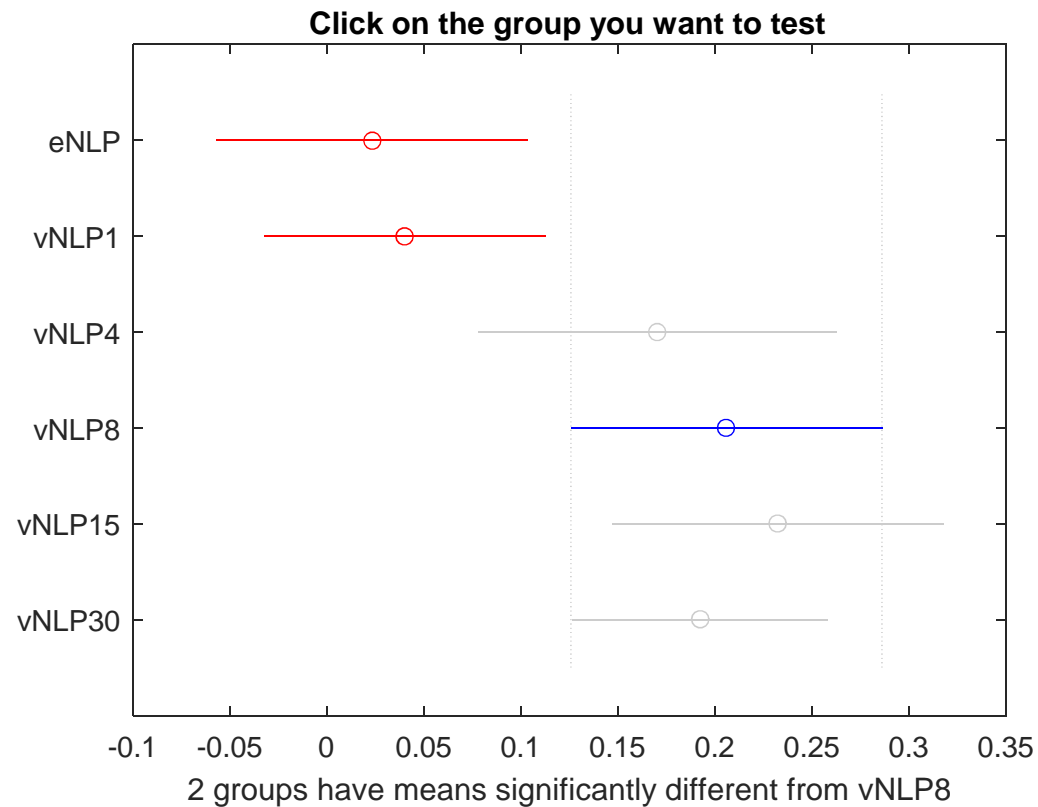
% Perform a multiple comparison test to determine which groups are different than the others in terms of mean fusion rate. Use the function multcompare, which accepts stats as an input argument.

```
>> multcompare(stats)
```

```
ans =
```

1.0000	2.0000	-0.1696	-0.0169	0.1358	0.9996
1.0000	3.0000	-0.3188	-0.1468	0.0252	0.1451
1.0000	4.0000	-0.3430	-0.1826	-0.0222	0.0149
1.0000	5.0000	-0.3747	-0.2092	-0.0436	0.0043
1.0000	6.0000	-0.3146	-0.1689	-0.0232	0.0123
2.0000	3.0000	-0.2947	-0.1299	0.0350	0.2171
2.0000	4.0000	-0.3184	-0.1657	-0.0130	0.0244
2.0000	5.0000	-0.3503	-0.1922	-0.0341	0.0070
2.0000	6.0000	-0.2891	-0.1519	-0.0148	0.0199
3.0000	4.0000	-0.2078	-0.0358	0.1362	0.9915
3.0000	5.0000	-0.2392	-0.0624	0.1145	0.9165
3.0000	6.0000	-0.1804	-0.0220	0.1363	0.9987
4.0000	5.0000	-0.1921	-0.0266	0.1390	0.9975
4.0000	6.0000	-0.1320	0.0137	0.1594	0.9998
5.0000	6.0000	-0.1110	0.0403	0.1917	0.9742

Each row of the matrix contains the result of one paired comparison test. Columns 1 and 2 contain the indices of the two samples being compared. Column 3 contains the lower confidence interval, column 4 contains the estimate, and column 5 contains the upper confidence interval. Column 6 contains the p-value for the hypothesis test that the corresponding mean difference is not equal to 0.



We also get an interactive plot.

There are no significant differences in the means among the groups vNLP4, vNLP8, vNLP15, and vNLP30.

In this example, clicking on vNLP8 (turns blue), we see pairwise comparisons with the other groups. Only eNLP and vNLP1 have different means.(red).

eNLP is not different than vNLP1 and vNLP4.  
vNLP1 is not different than eNLP and vNLP4  
vNLP4 is not different from any other.  
vNLP8, 15, 30 are not different from one another, but different than eNLP and vNLP1