

1. Summary of Analysis

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> #Ho: the discriminant analysis scores of nuclear localization signals of both nuclear and non-nuclear proteins does not vary with class type
> #H1: the discriminant analysis scores of nuclear localization signals of both nuclear and non-nuclear proteins vary with class type
> levels(yeast_data$class)
[1] "CYT" "ERL" "EXC" "ME1" "ME2" "ME3" "MIT" "NUC" "POX" "VAC"
> mean(x = yeast_data$nuc)
[1] 0.2762374
> res.aov <- aov(nuc ~ class, data = yeast_data)
> # Summary of the analysis
> summary(res.aov)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
class	9	1.99	0.22110	21.97	<2e-16 ***
Residuals	1473	14.82	0.01006		

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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> |
```

2. Histogram distribution for nuc wrt class

