

# Stokes Radius Analysis by Gel Filtration

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```
require(ggplot2)
```

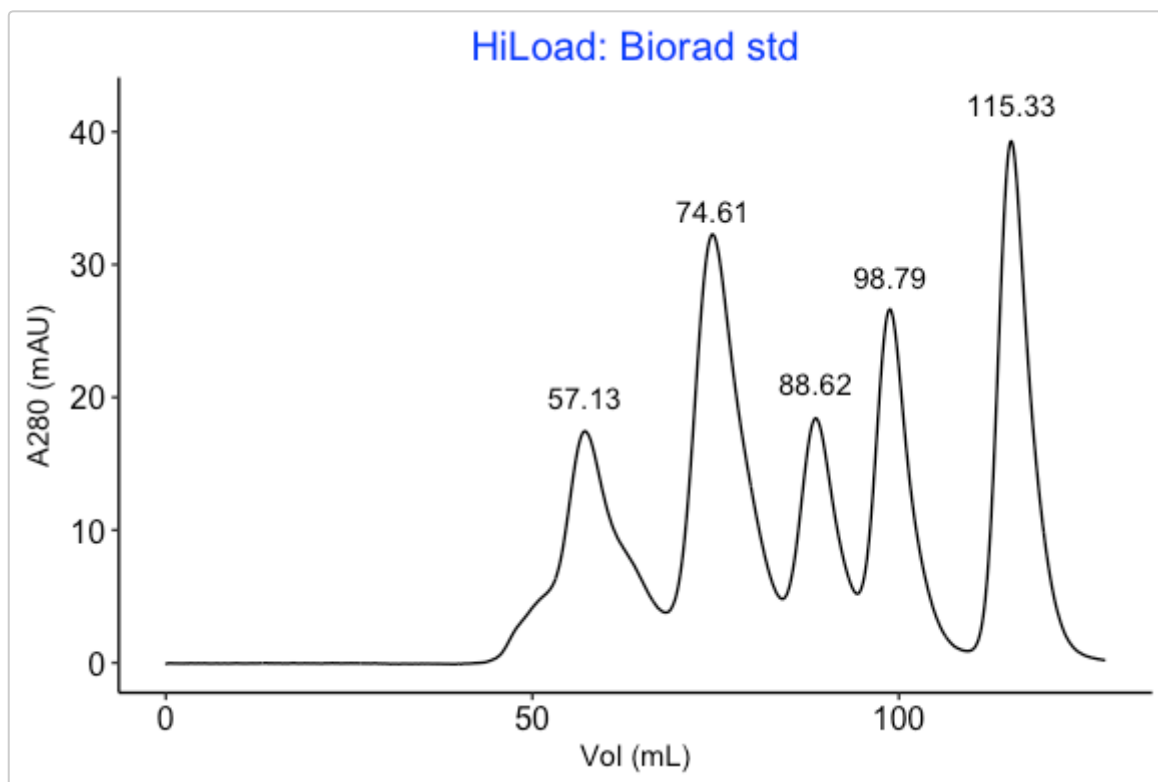
```
## Loading required package: ggplot2
```

```
##  
## Attaching package: 'ggplot2'
```

```
## The following object is masked from 'package:radii':  
##  
##      ggplot
```

```
require(radii)
```

```
# Load the data: the gel filtration elution profile  
file <- system.file("extdata", "160826bioradstdpH74EDTA_HiLoad.asc", package="radii")  
HiLoad_std <- read.csv(file, header = TRUE, skip=2, sep = "\t");  
HiLoad_std <- na.omit(HiLoad_std[, 1:2])  
  
# plot the data: gel filtration profile  
# with(HiLoad_std, plot(mAU ~ mL, type = "l", main = "HiLoad: Biorad STD"))  
#  
g <- radii::ggplot()  
g <- g + ggplot2::geom_line(aes(mL, mAU), data=HiLoad_std)  
g <- g + ggtitle("HiLoad: Biorad std") + xlab("Vol (mL)") + ylab("A280 (mAU)")  
label=as.character(radii::protein_std_HiLoad$ve)  
pos <- data.frame(x= as.numeric(label), y = c(42, 29, 21, 34, 20))  
g <- g + annotate("text", label=label, x=pos$x, y=pos$y)  
print(g)
```



```
# superdex 200 HiLoad 16/60
vt = mean(c(122.31,122.93))
vo = mean(c(47.26,46.59))

protein_std_HiLoad$sigma <- radii::partition_coef(protein_std_HiLoad$ve, vo=vo, vt=vt)
protein_std_HiLoad$erfcinv <- radii::erfcinv(protein_std_HiLoad$sigma)
#
knitr::kable(protein_std_HiLoad, format = "markdown")
```

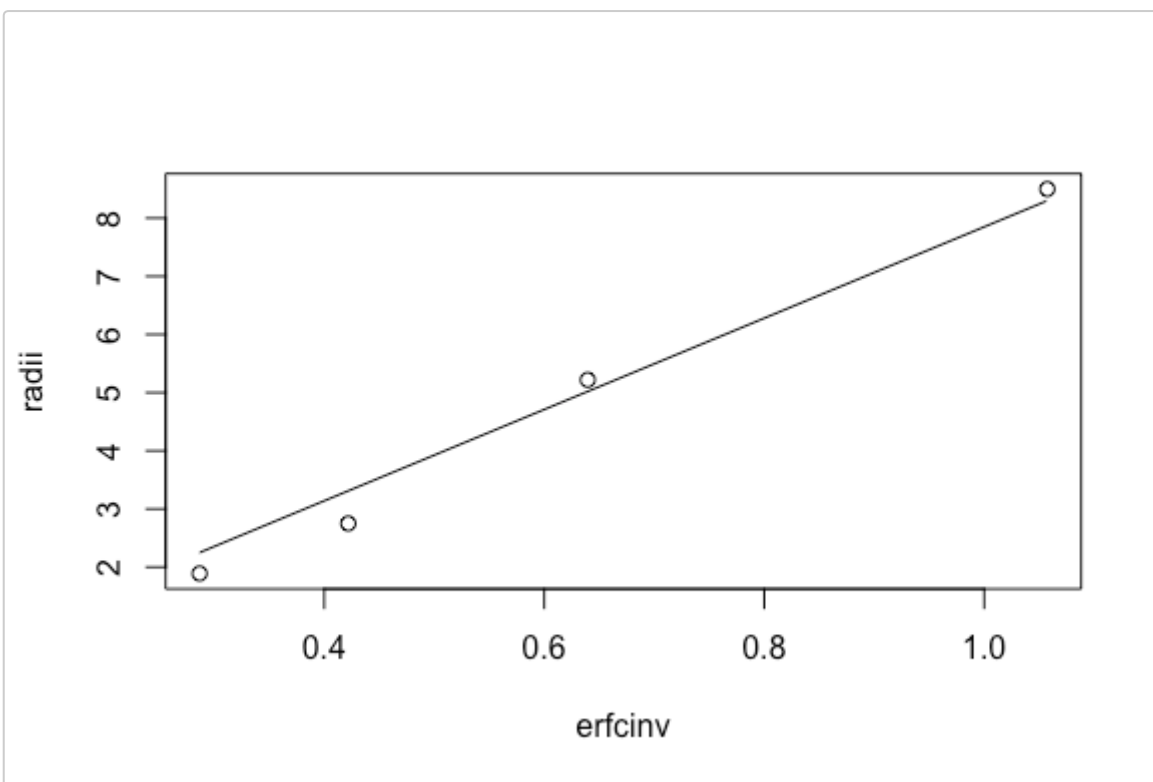
name	mw	radii	ve	sigma	erfcinv
vitamin B12	1350	NA	115.33	0.9036924	0.0855587
horse myoglobin	17000	1.89	98.79	0.6851840	0.2866607
chicken ovalbumin	44000	2.75	88.62	0.5508290	0.4218022
bovine gamma-globulin	158000	5.22	74.61	0.3657441	0.6395597
bovine thyroglobulin	670000	8.50	57.13	0.1348174	1.0573877

```
protein_std_HiLoad <- na.omit(protein_std_HiLoad)
with(protein_std_HiLoad, plot(erfcinv, radii))
fit <- lm (radii~erfcinv-1, data = protein_std_HiLoad)
summary(fit)
```

```
##
## Call:
```

```
## lm(formula = radii ~ erfcinv - 1, data = protein_std_HiLoad)
##
## Residuals:
##      2      3      4      5
## -0.3601 -0.5608  0.2000  0.2004
##
## Coefficients:
##      Estimate Std. Error t value Pr(>|t|)
## erfcinv    7.8492     0.3127   25.1 0.000139 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.418 on 3 degrees of freedom
## Multiple R-squared:  0.9953, Adjusted R-squared:  0.9937
## F-statistic: 630.1 on 1 and 3 DF, p-value: 0.0001387
```

```
xdat <- seq(min(protein_std_HiLoad$erfcinv), max(protein_std_HiLoad$erfcinv), by = 0.01 )
pred <- predict(fit, newdata = data.frame(erfcinv=xdat))
lines(xdat,pred)
```



```
p <- ggplot() + geom_point(mtcars, aes(wt, mpg))
p + annotate("text", x=2:3, y=20, label=c("label1", "label2"))
```