Oh the pHs you will see

Document setup options

```
knitr::opts_chunk$set(echo = TRUE)
library(knitr)
opts_chunk$set(tidy.opts=list(width.cutoff=55),tidy=TRUE)
shh <- suppressPackageStartupMessages
shh(require(sensorOverlord))
shh(require(ggplot2))
shh(require(cowplot))
```

```
## Warning: package 'cowplot' was built under R version 3.5.3
```

```
shh(require(stringr))
shh(require(ggalt))
```

```
## Warning: package 'ggalt' was built under R version 3.5.3
```

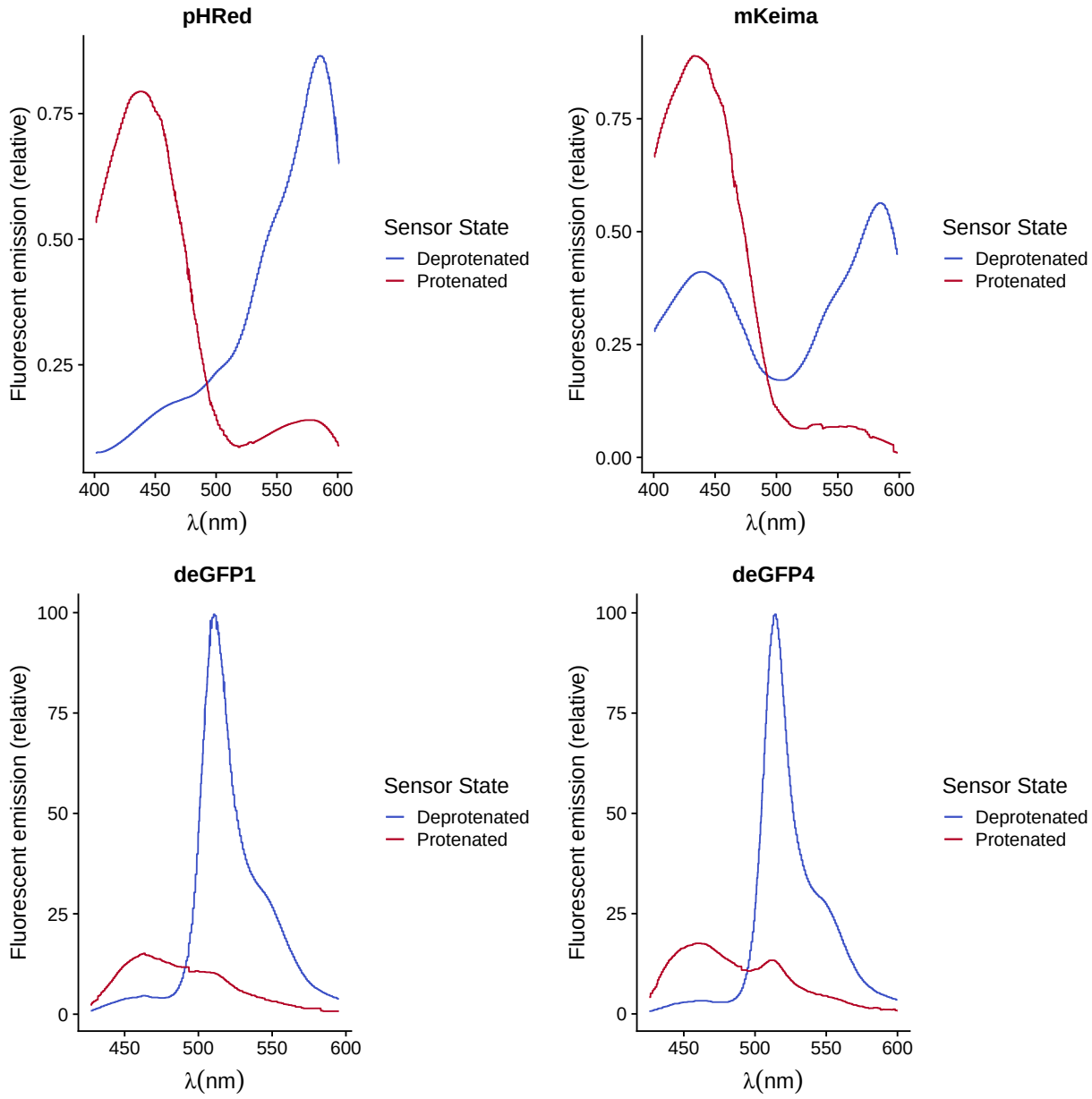
Initalize Sensors

```
sensor_repo <- ""

# phRed
phRed_data <- read.csv(paste(sensor_repo, "spectra_phred.csv",
    sep = ""), header = FALSE)
phred_spectra <- spectraMatrixFromValues(lambdas_minimum = phRed_data$V3,
    values_minimum = phRed_data$V4, lambdas_maximum = phRed_data$V1,
    values_maximum = phRed_data$V2)
phred_sensor <- new("pHSensor", newSensorFromSpectra(phred_spectra,
    lambda_1 = c(400, 420), lambda_2 = c(575, 585)), pKa = 7.8)

# mkeima
mkeima_data <- read.csv(paste(sensor_repo, "spectra_mkeima.csv",
    sep = ""), header = FALSE)
mkeima_spectra <- spectraMatrixFromValues(lambdas_minimum = mkeima_data$V3,
    values_minimum = mkeima_data$V4, lambdas_maximum = mkeima_data$V1,
    values_maximum = mkeima_data$V2)
mkeima_sensor <- new("pHSensor", newSensorFromSpectra(mkeima_spectra,
    lambda_1 = c(400, 420), lambda_2 = c(575, 585)), pKa = 6.6)

# deGFP1
degfp1_data <- read.csv(paste(sensor_repo, "spectra_deGFP1.csv",
    sep = ""), header = FALSE)
degfp1_spectra <- spectraMatrixFromValues(lambdas_minimum = degfp1_data$V3,
    values_minimum = degfp1_data$V4, lambdas_maximum = degfp1_data$V1,
    values_maximum = degfp1_data$V2)
degfp1_sensor <- new("pHSensor", newSensorFromSpectra(degfp1_spectra,
    lambda_1 = c(450, 470), lambda_2 = c(500, 520)), pKa = 8.02)

# deGFP4
```

```
degfp4_data <- read.csv(paste(sensor_repo, "spectra_deGFP4.csv",
    sep = ""), header = FALSE)
degfp4_spectra <- spectraMatrixFromValues(lambdas_minimum = degfp4_data$V3,
    values_minimum = degfp4_data$V4, lambdas_maximum = degfp4_data$V1,
    values_maximum = degfp4_data$V2)
degfp4_sensor <- new("pHSensor", newSensorFromSpectra(degfp4_spectra,
    lambda_1 = c(450, 470), lambda_2 = c(500, 520)), pKa = 7.34)
```

All

```
phRed_spectraPlot <- plotSpectra(phred_spectra, "Deprotenated",
    "Protenated") + ggtitle("pHRed")
mkeima_spectraPlot <- plotSpectra(mkeima_spectra, "Deprotenated",
    "Protenated") + ggtitle("mKeima")
degfp1_spectraPlot <- plotSpectra(degfp1_spectra, "Deprotenated",
    "Protenated") + ggtitle("deGFP1")
degfp4_spectraPlot <- plotSpectra(degfp4_spectra, "Deprotenated",
    "Protenated") + ggtitle("deGFP4")


plot_grid(phRed_spectraPlot, mkeima_spectraPlot, degfp1_spectraPlot,
    degfp4_spectraPlot, ncol = 2)
```

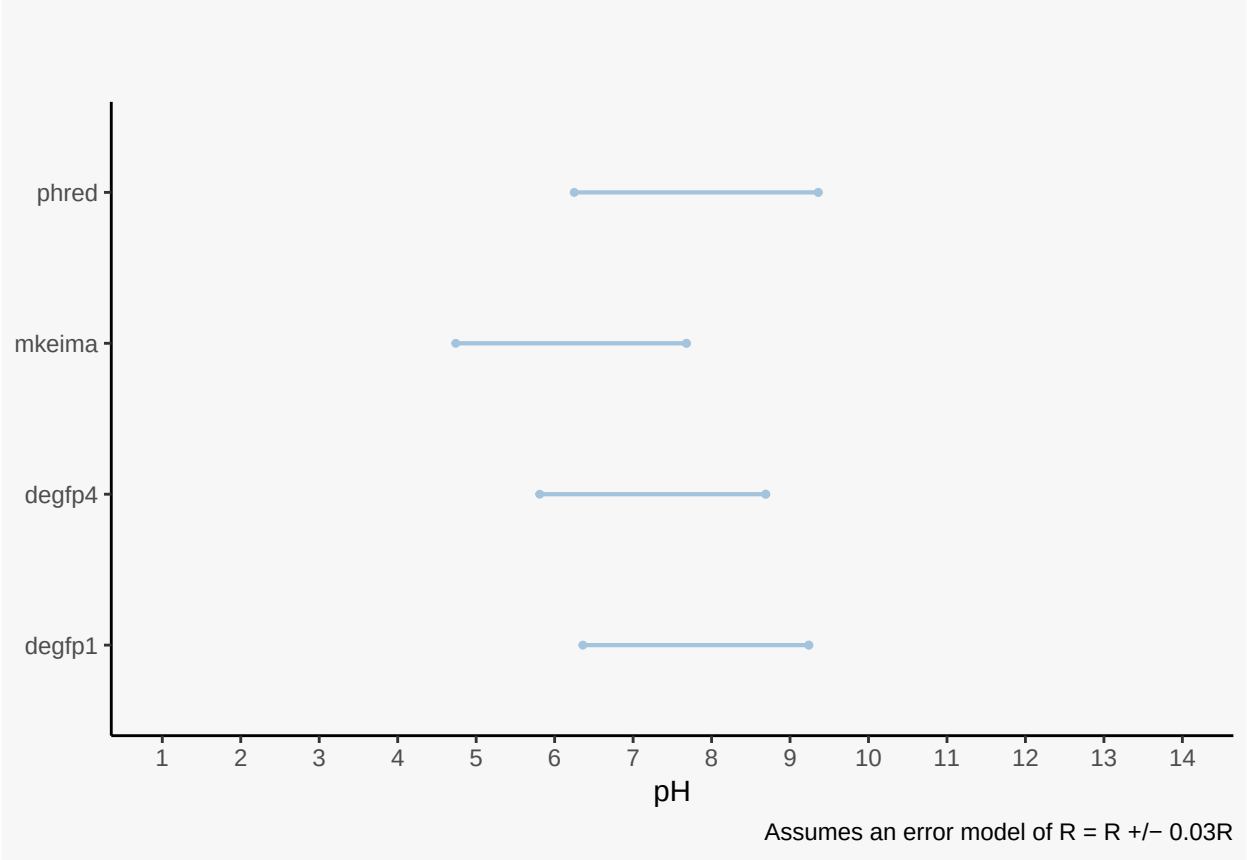



```
q <- function(...) {
    sapply(match.call()[-1], deparse)
}

sensorList <- q(degfp1_sensor, degfp4_sensor, mkeima_sensor,
    phred_sensor)
```

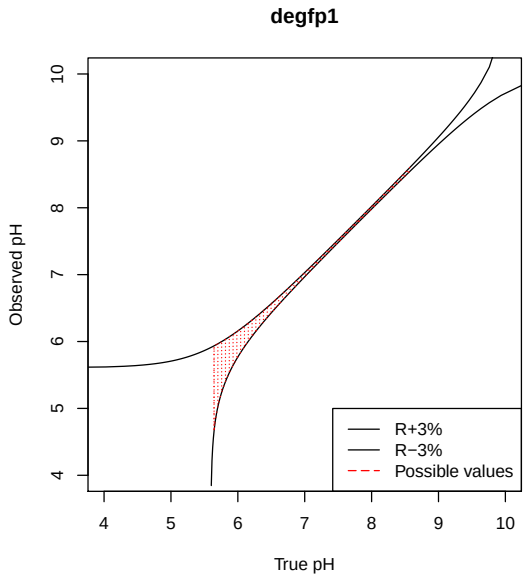
```
acceptable_error <- 0.1
error_model <- function(x) {
    return(0.03 * x)
}

minMaxMatrix <- c()
sensors <- c()
```

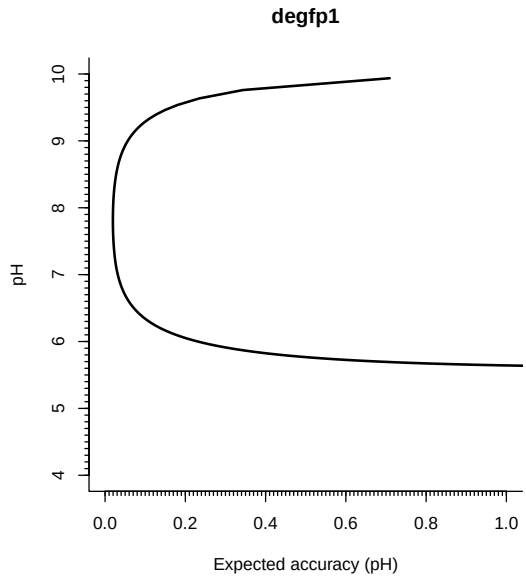
```r
for (sensorName in sensorList) {
    sensor <- get(sensorName)
    sensorName <- str_replace(sensorName, "_sensor", "")
    sensors <- c(sensors, sensorName)
    error_data <- getErrorTable(sensor, R = getR(sensor),
        FUN = getpH, Error_Model = error_model)

    error_filter <- subset(error_data, error_data$max_abs_error <
        acceptable_error)

    minimum <- ifelse(test = length(error_filter$FUN_true) ==
        0, yes = NaN, no = min(error_filter$FUN_true))

    maximum <- ifelse(test = length(error_filter$FUN_true) ==
        0, yes = NaN, no = max(error_filter$FUN_true))

    minMaxMatrix <- rbind(minMaxMatrix, c(round(minimum,
        2), round(maximum, 2)))
}
ranges <- data.frame(minMaxMatrix)
ranges$Sensor_Name <- sensors
colnames(ranges) <- c("Minimum", "Maximum", "Sensor_Name")
```

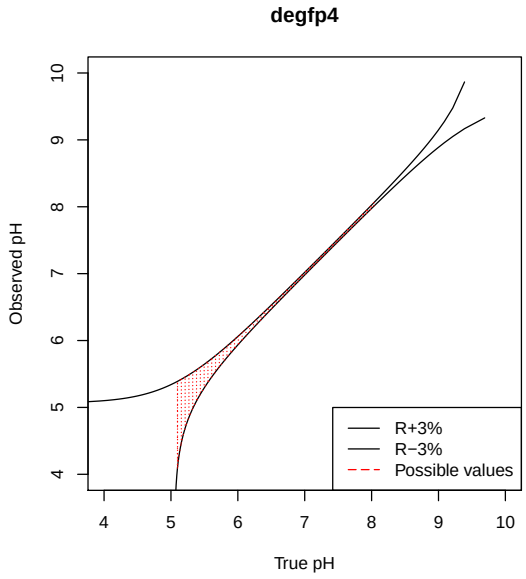
```r
theme_set(theme_classic())

ranges$Sensor_Name <- factor(ranges$Sensor_Name, levels = as.character(ranges$Sensor_Name))

gg <- ggplot(ranges, aes(x = Minimum, xend = Maximum, y = Sensor_Name,
    group = Sensor_Name)) + geom_dumbbell(color = "#a3c4dc",
    size = 0.75) + labs(y = NULL, title = "", caption = "Assumes an error model of R = R +/- 0.03R",
    subtitle = "") + scale_x_continuous("pH", limits = c(1,
    14), breaks = 1:14) + theme(plot.title = element_text(hjust = 0.5,
    face = "bold"), plot.background = element_rect(fill = "#f7f7f7"),
    panel.background = element_rect(fill = "#f7f7f7"), panel.grid.minor = element_blank(),
    panel.grid.major.y = element_blank(), legend.position = "top",
    panel.border = element_blank())
# axis.text.x = element_text(angle = 90, hjust = 1))
plot(gg)
```

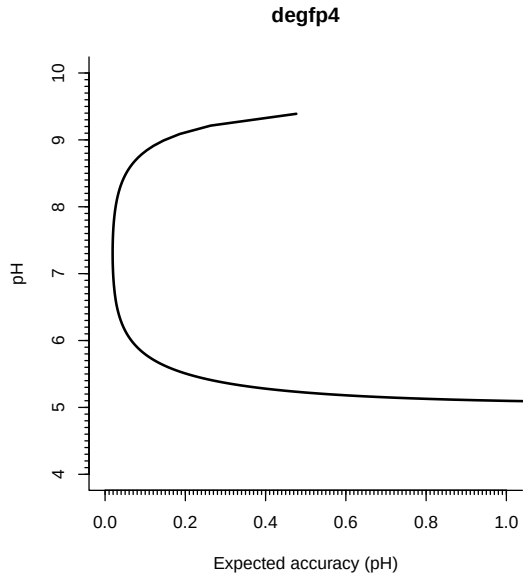



```
## [1] "degfp1"
## [1] "degfp4"
```

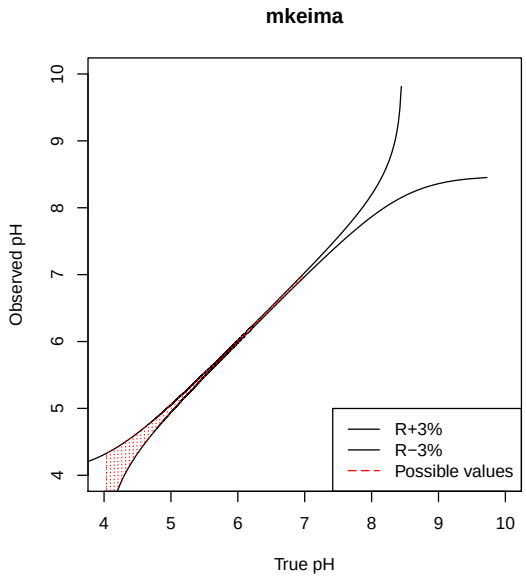


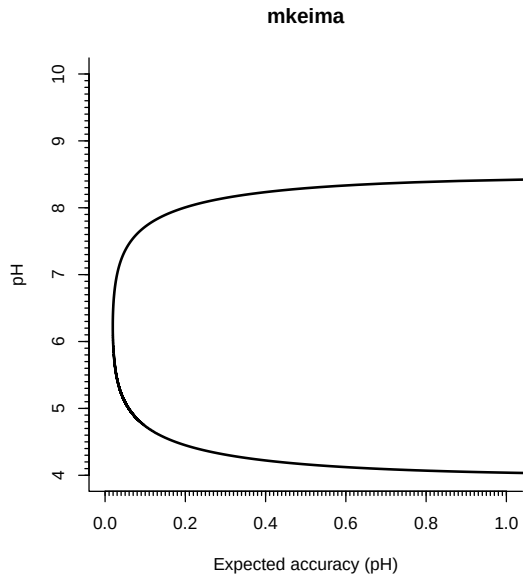


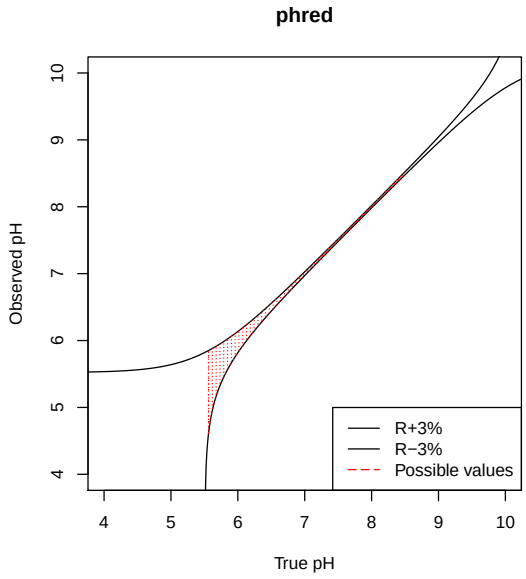


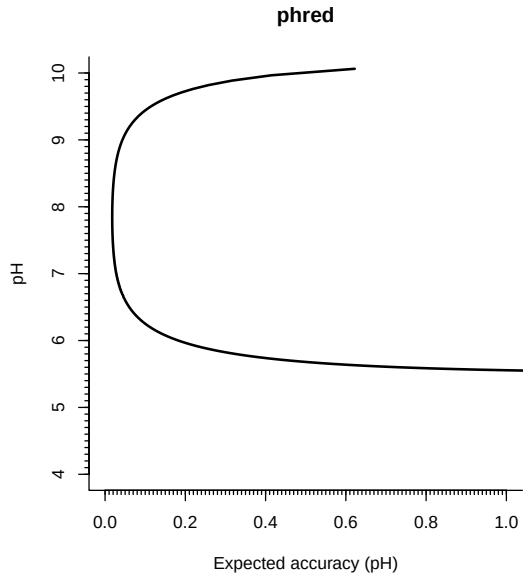



```
## [1] "mkeima"
## [1] "phred"
```


mkeima
Observed pH
True pH
R+3%
R−3%
Possible values


mkeima
pH
Expected accuracy (pH)


phred
Observed pH
True pH
R+3%
R−3%
Possible values


phred
pH
Expected accuracy (pH)