Solution Sheet 02

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4/15/2022

```
library(Iso)
```

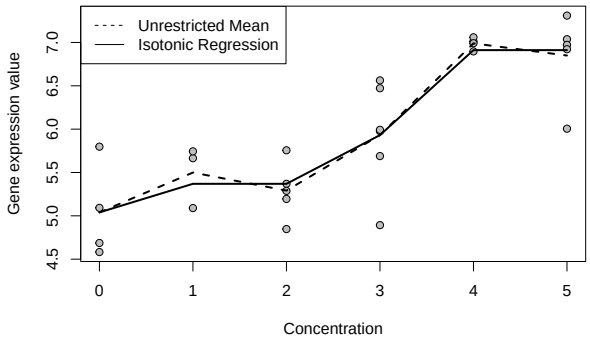
```
## Iso 0.0-18.1
```

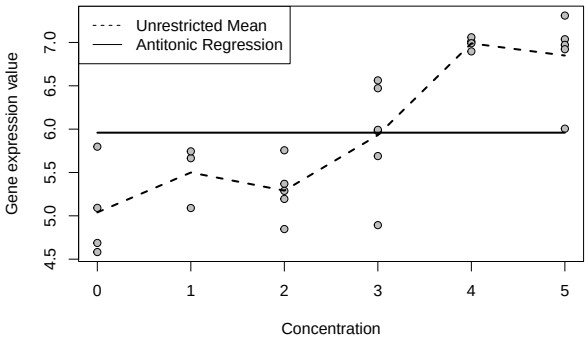
```
load("E:/TUD/04.Semester/toxicology-I/assignments/2/Simulated-Isotonic.RData")
conc <-  c(rep(0, 4), rep(1, 3), rep(2, 5), rep(3, 6), rep(4, 4), rep(5, 5))
```

Gene 1

```
plot(
  conc,
  Simulated.Isotonic[, "ExprGene1"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  unique(conc),
  tapply(Simulated.Isotonic[, "ExprGene1"], conc, mean),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  unique(conc),
  pava(tapply(Simulated.Isotonic[, "ExprGene1"], conc, mean), c(4, 3, 5, 6, 4, 5)),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topleft",
  legend = c("Unrestricted Mean", "Isotonic Regression"),
  lty = c(2, 1)
)
plot(
```

```
  conc,
  Simulated.Isotonic[, "ExprGene1"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  unique(conc),
  tapply(Simulated.Isotonic[, "ExprGene1"], conc, mean),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  unique(conc),
  pava(
    tapply(Simulated.Isotonic[, "ExprGene1"], conc, mean),
    c(4, 3, 5, 6, 4, 5),
    decreasing = TRUE
  ),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topleft",
  legend = c("Unrestricted Mean", "Antitonic Regression"),
  lty = c(2, 1)
)
```



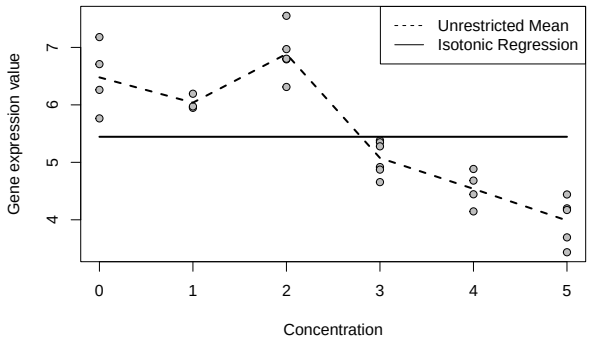


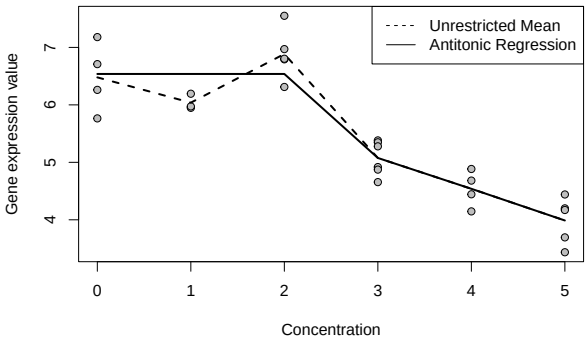
Gene 2

```
plot(
  conc,
  Simulated.Isotonic[, "ExprGene2"],
```

```
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  unique(conc),
  tapply(Simulated.Isotonic[, "ExprGene2"], conc, mean),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  unique(conc),
  pava(tapply(Simulated.Isotonic[, "ExprGene2"], conc, mean), c(4, 3, 5, 6, 4, 5)),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topright",
  legend = c("Unrestricted Mean", "Isotonic Regression"),
  lty = c(2, 1)
)
plot(
  conc,
  Simulated.Isotonic[, "ExprGene2"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  unique(conc),
  tapply(Simulated.Isotonic[, "ExprGene2"], conc, mean),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  unique(conc),
  pava(
    tapply(Simulated.Isotonic[, "ExprGene2"], conc, mean),
    c(4, 3, 5, 6, 4, 5),
    decreasing = TRUE
  ),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topright",
  legend = c("Unrestricted Mean", "Antitonic Regression"),
```

```
  lty = c(2, 1)
)
```

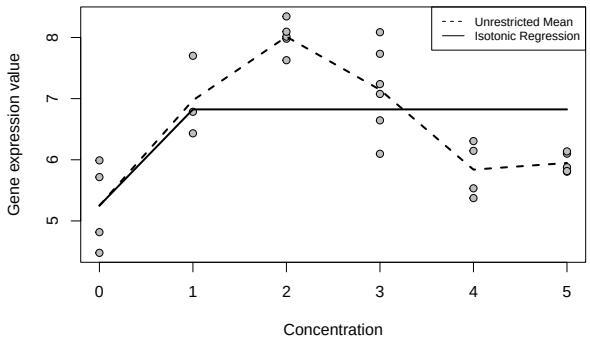


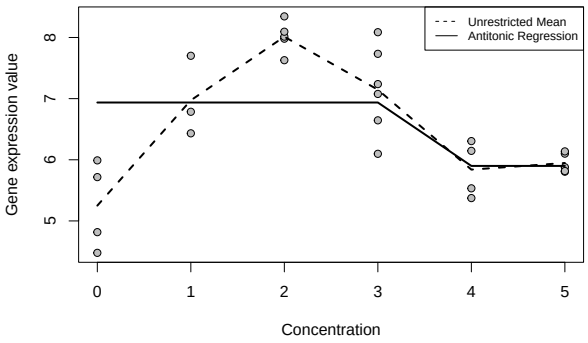


Gene 3

```
plot(
  conc,
  Simulated.Isotonic[, "ExprGene3"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  unique(conc),
  tapply(Simulated.Isotonic[, "ExprGene3"], conc, mean),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  unique(conc),
  pava(tapply(Simulated.Isotonic[, "ExprGene3"], conc, mean), c(4, 3, 5, 6, 4, 5)),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topright",
  legend = c("Unrestricted Mean", "Isotonic Regression"),
  lty = c(2, 1),
  cex = 0.75
)
plot(
  conc,
  Simulated.Isotonic[, "ExprGene3"],
```

```
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  unique(conc),
  tapply(Simulated.Isotonic[, "ExprGene3"], conc, mean),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  unique(conc),
  pava(
    tapply(Simulated.Isotonic[, "ExprGene3"], conc, mean),
    c(4, 3, 5, 6, 4, 5),
    decreasing = TRUE
  ),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topright",
  legend = c("Unrestricted Mean", "Antitonic Regression"),
  lty = c(2, 1),
  cex = 0.75
)
```





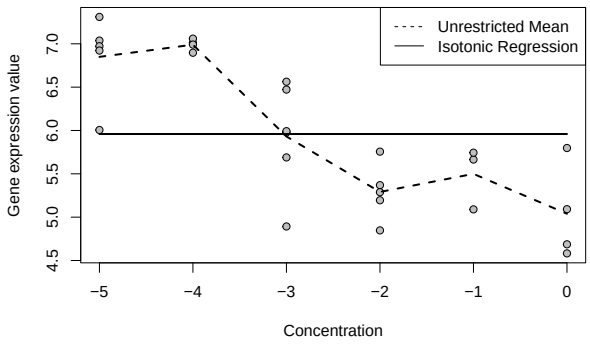
Reverse of each genes

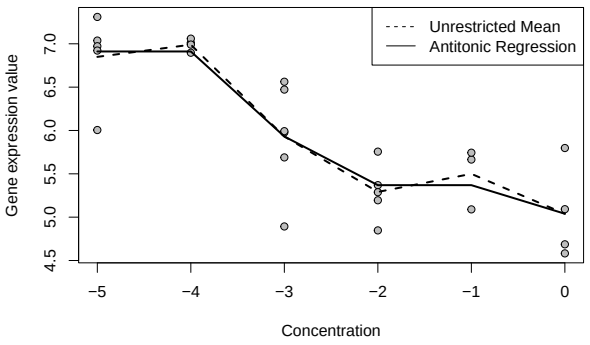
Gene 1

```
plot(
  -conc,
```

```
  Simulated.Isotonic[, "ExprGene1"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  rev(-unique(conc)),
  rev(tapply(Simulated.Isotonic[, "ExprGene1"], conc, mean)),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  rev(-unique(conc)),
  pava(rev(tapply(
    Simulated.Isotonic[, "ExprGene1"], conc, mean
  )), rev(c(4, 3, 5, 6, 4, 5))),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topright",
  legend = c("Unrestricted Mean", "Isotonic Regression"),
  lty = c(2, 1)
)
plot(
  -conc,
  Simulated.Isotonic[, "ExprGene1"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  rev(-unique(conc)),
  rev(tapply(Simulated.Isotonic[, "ExprGene1"], conc, mean)),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  rev(-unique(conc)),
  pava(rev(tapply(
    Simulated.Isotonic[, "ExprGene1"], conc, mean
  )), rev(c(4, 3, 5, 6, 4, 5)),
  decreasing = TRUE),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
```

```
  "topright",
  legend = c("Unrestricted Mean", "Antitonic Regression"),
  lty = c(2, 1)
)
```

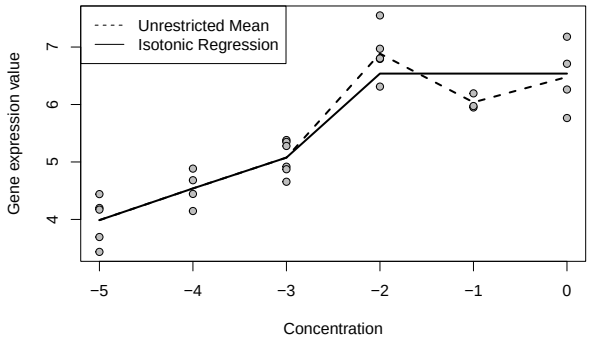


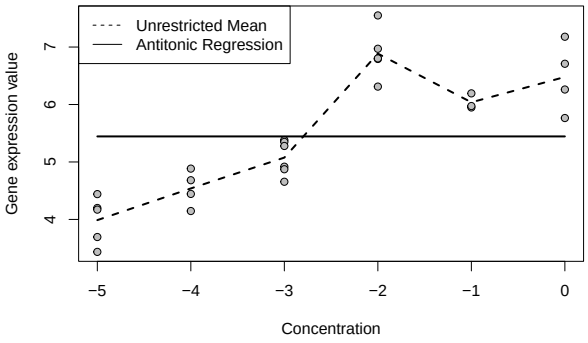


Gene 2

```
plot(
  -conc,
  Simulated.Isotonic[, "ExprGene2"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  rev(-unique(conc)),
  rev(tapply(Simulated.Isotonic[, "ExprGene2"], conc, mean)),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  rev(-unique(conc)),
  pava(rev(tapply(
    Simulated.Isotonic[, "ExprGene2"], conc, mean
  )), rev(c(4, 3, 5, 6, 4, 5))),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topleft",
  legend = c("Unrestricted Mean", "Isotonic Regression"),
  lty = c(2, 1)
)
plot(
```

```
  -conc,
  Simulated.Isotonic[, "ExprGene2"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  rev(-unique(conc)),
  rev(tapply(Simulated.Isotonic[, "ExprGene2"], conc, mean)),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  rev(-unique(conc)),
  pava(rev(tapply(
    Simulated.Isotonic[, "ExprGene2"], conc, mean
  )), rev(c(4, 3, 5, 6, 4, 5)),
  decreasing = TRUE),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topleft",
  legend = c("Unrestricted Mean", "Antitonic Regression"),
  lty = c(2, 1)
)
```





Gene 3

```
plot(
  -conc,
  Simulated.Isotonic[, "ExprGene3"],
  pch = 21,
  bg = "grey",
```

```
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  rev(-unique(conc)),
  rev(tapply(Simulated.Isotonic[, "ExprGene3"], conc, mean)),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  rev(-unique(conc)),
  pava(rev(tapply(
    Simulated.Isotonic[, "ExprGene3"], conc, mean
  )), rev(c(4, 3, 5, 6, 4, 5))),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topleft",
  legend = c("Unrestricted Mean", "Isotonic Regression"),
  lty = c(2, 1),
  cex = 0.75
)
plot(
  -conc,
  Simulated.Isotonic[, "ExprGene3"],
  pch = 21,
  bg = "grey",
  xlab = "Concentration",
  ylab = "Gene expression value"
)
points(
  rev(-unique(conc)),
  rev(tapply(Simulated.Isotonic[, "ExprGene3"], conc, mean)),
  type = "l",
  lty = 2,
  lwd = 2
)
points(
  rev(-unique(conc)),
  pava(rev(tapply(
    Simulated.Isotonic[, "ExprGene3"], conc, mean
  )), rev(c(4, 3, 5, 6, 4, 5)),
  decreasing = TRUE),
  type = "l",
  lty = 1,
  lwd = 2
)
legend(
  "topleft",
  legend = c("Unrestricted Mean", "Antitonic Regression"),
```

```
  lty = c(2, 1),
  cex = 0.75
)
```