

HW solutions

Md Rasheduzzaman

2025-05-03

dataframe, matrices, list, factor, vector, etc.

Table of contents

1	L3	2
1.1	Task 1: Protein Concentration in Samples	2
1.1.1	Total Protein per Sample	2
1.1.2	Total Protein per Protein Type	2
1.1.3	Heatmap of Protein Concentrations	3
1.1.4	Interpretation	3
1.2	Task 2: Gene-to-Protein Translation	3
1.2.1	Protein Output	4
1.2.2	Barplot of Output	4
1.2.3	Heatmap of Expression	5
1.2.4	Interpretation	5
1.3	Task 3: Animal Breeding – Bull Ranking by Economic Traits	6
1.3.1	Economic Score	6
1.3.2	Rank Bulls	7
1.3.3	Barplot	7
1.3.4	Interpretation	7
1.4	Task 4: Plant Breeding – Trait Contributions from Parental Lines	8
1.4.1	Hybrid Traits	8
1.4.2	Identity Matrix	9
1.4.3	Subset to T1 and T2	9
1.4.4	Interpretation	9
1.5	Task 5: Managing Tasks Using Lists	9
1.5.1	Access & Operate	10
1.5.2	Interpretation	10

1 L3

1.1 Task 1: Protein Concentration in Samples

We measured the concentration (in $\mu\text{g}/\mu\text{L}$) of three proteins (P1, P2, P3) in four samples (S1–S4):

```
ProteinMatrix <- matrix(c(  
  12, 18, 5,  
  9, 15, 8,  
  14, 12, 6,  
  10, 20, 7  
) , nrow = 4, byrow = TRUE)  
rownames(ProteinMatrix) <- c("S1", "S2", "S3", "S4")  
colnames(ProteinMatrix) <- c("P1", "P2", "P3")  
ProteinMatrix
```

	P1	P2	P3
S1	12	18	5
S2	9	15	8
S3	14	12	6
S4	10	20	7

1.1.1 Total Protein per Sample

```
rowSums(ProteinMatrix)
```

S1	S2	S3	S4
35	32	32	37

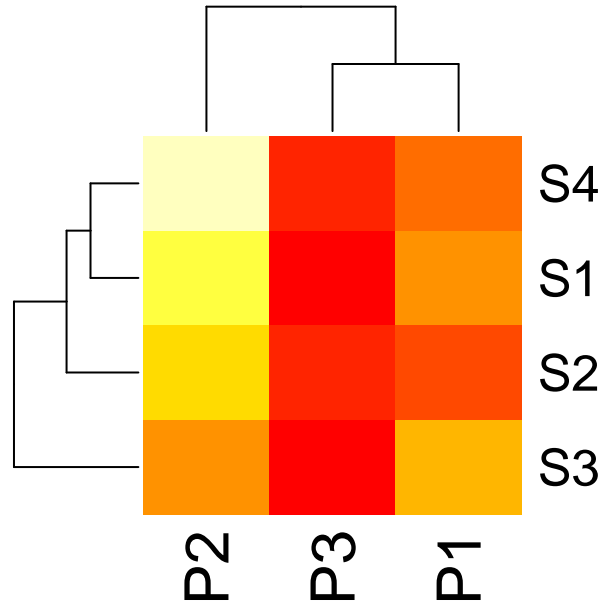
1.1.2 Total Protein per Protein Type

```
colSums(ProteinMatrix)
```

P1	P2	P3
45	65	26

1.1.3 Heatmap of Protein Concentrations

```
heatmap(ProteinMatrix, scale = "none", col = heat.colors(10))
```



1.1.4 Interpretation

- Sample S4 has the highest P2.
 - Heatmap reveals P2 is most abundant across all samples.
-

1.2 Task 2: Gene-to-Protein Translation

Gene expression (G1–G3) measured in tissues (Liver, Heart, Brain):

```
GeneExpression <- matrix(c(  
  8, 5, 7,  
  6, 4, 5,  
  9, 7, 6  
) , nrow = 3, byrow = TRUE)  
rownames(GeneExpression) <- c("Liver", "Heart", "Brain")  
colnames(GeneExpression) <- c("G1", "G2", "G3")
```

GeneExpression

	G1	G2	G3
Liver	8	5	7
Heart	6	4	5
Brain	9	7	6

Translation efficiency:

```
TranslationEfficiency <- matrix(c(0.8, 0.6, 0.9), ncol = 1)
rownames(TranslationEfficiency) <- c("G1", "G2", "G3")
TranslationEfficiency
```

	[,1]
G1	0.8
G2	0.6
G3	0.9

1.2.1 Protein Output

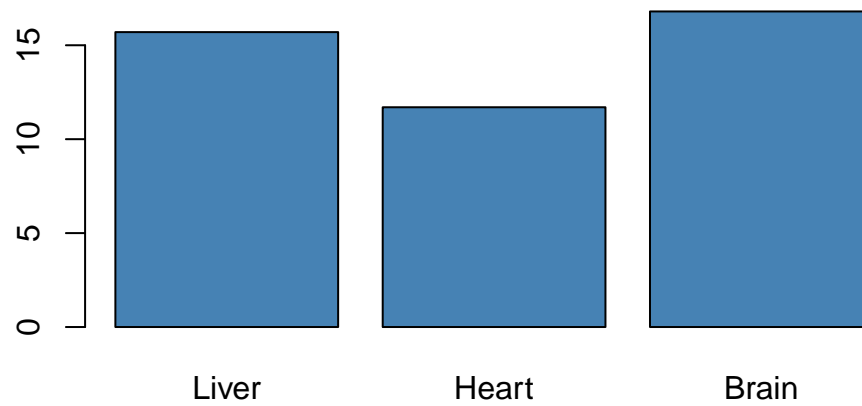
```
ProteinOutput <- GeneExpression %*% TranslationEfficiency
rownames(ProteinOutput) <- rownames(GeneExpression)
colnames(ProteinOutput) <- "TotalProtein"
ProteinOutput
```

	TotalProtein
Liver	15.7
Heart	11.7
Brain	16.8

1.2.2 Barplot of Output

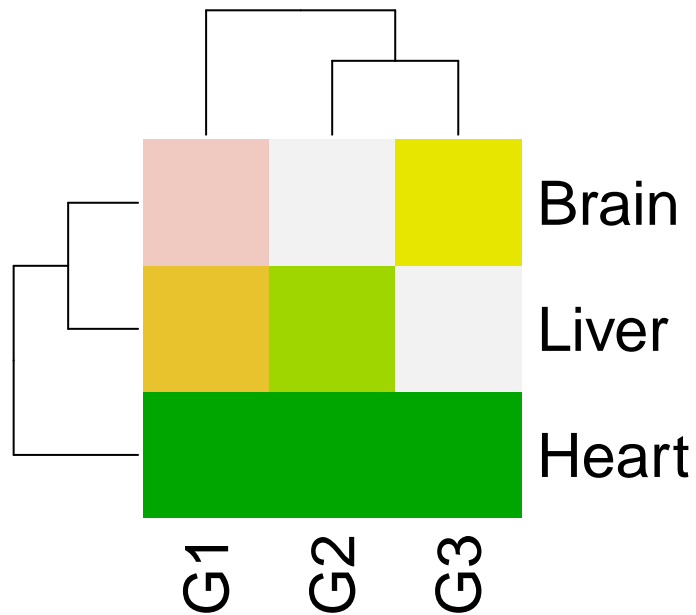
```
barplot(ProteinOutput[,1], main = "Protein Output per Tissue", col = "steelblue")
```

Protein Output per Tissue



1.2.3 Heatmap of Expression

```
heatmap(GeneExpression, col = terrain.colors(10), scale = "column")
```



1.2.4 Interpretation

- Brain has highest protein output.
- Heatmap shows relative expression.

1.3 Task 3: Animal Breeding – Bull Ranking by Economic Traits

Bull trait scores:

```
BullTraits <- matrix(c(
  80, 3.5, 1.2,
  90, 3.2, 1.5,
  70, 3.8, 1.1,
  85, 3.0, 1.4
), nrow = 4, byrow = TRUE)
rownames(BullTraits) <- c("B1", "B2", "B3", "B4")
colnames(BullTraits) <- c("Milk", "Fat%", "Growth")
BullTraits
```

	Milk	Fat%	Growth
B1	80	3.5	1.2
B2	90	3.2	1.5
B3	70	3.8	1.1
B4	85	3.0	1.4

Weights:

```
EconomicWeights <- matrix(c(0.5, 0.3, 0.2), ncol = 1)
rownames(EconomicWeights) <- c("Milk", "Fat%", "Growth")
EconomicWeights
```

	[,1]
Milk	0.5
Fat%	0.3
Growth	0.2

1.3.1 Economic Score

```
BullScore <- BullTraits %*% EconomicWeights
colnames(BullScore) <- "EconomicScore"
BullScore
```

	EconomicScore
B1	41.29
B2	46.26
B3	36.36
B4	43.68

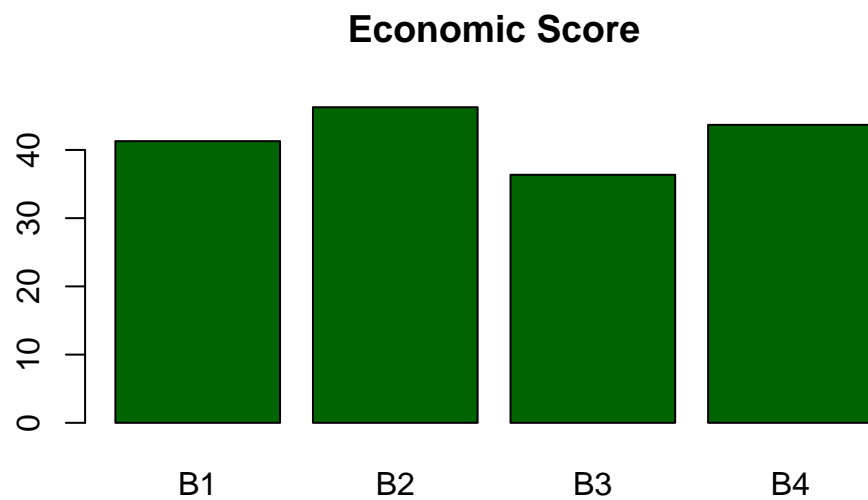
1.3.2 Rank Bulls

```
BullScore[order(-BullScore), , drop=FALSE]
```

	EconomicScore
B2	46.26
B4	43.68
B1	41.29
B3	36.36

1.3.3 Barplot

```
barplot(BullScore[,1], names.arg = rownames(BullScore), col = "darkgreen", main = "Economic Score")
```



1.3.4 Interpretation

- B2 ranked highest.
- Weighted sum allows multi-trait selection.

1.4 Task 4: Plant Breeding – Trait Contributions from Parental Lines

Parent trait matrix:

```
ParentTraits <- matrix(c(
  7, 5, 3,
  6, 8, 4,
  5, 6, 6
), nrow = 3, byrow = TRUE)
rownames(ParentTraits) <- c("P1", "P2", "P3")
colnames(ParentTraits) <- c("T1_Drought", "T2_Yield", "T3_Maturation")
ParentTraits
```

	T1_Drought	T2_Yield	T3_Maturation
P1	7	5	3
P2	6	8	4
P3	5	6	6

Hybrid weights:

```
HybridWeights <- matrix(c(0.5, 0.3, 0.2), ncol = 1)
rownames(HybridWeights) <- c("P1", "P2", "P3")
HybridWeights
```

	[,1]
P1	0.5
P2	0.3
P3	0.2

1.4.1 Hybrid Traits

```
HybridTraits <- t(HybridWeights) %*% ParentTraits
colnames(HybridTraits) <- colnames(ParentTraits)
HybridTraits
```

	T1_Drought	T2_Yield	T3_Maturation
[1,]	6.3	6.1	3.9

1.4.2 Identity Matrix

```
I3 <- diag(3)
I3 %*% ParentTraits
```

```
      T1_Drought T2_Yield T3_Maturation
[1,]          7         5             3
[2,]          6         8             4
[3,]          5         6             6
```

1.4.3 Subset to T1 and T2

```
HybridTraits_sub <- t(HybridWeights) %*% ParentTraits[, c("T1_Drought", "T2_Yield")]
HybridTraits_sub
```

```
      T1_Drought T2_Yield
[1,]          6.3         6.1
```

1.4.4 Interpretation

- Trait values represent weighted parental influence.
- Identity matrix preserves values.
- Subsetting traits removes T3 influence.

1.5 Task 5: Managing Tasks Using Lists

```
TaskList <- list(
  Task1 = list(
    M = ProteinMatrix
  ),
  Task2 = list(
    M = GeneExpression,
    W = TranslationEfficiency
  ),
  Task3 = list(
```

```

    M = BullTraits,
    W = EconomicWeights
  ),
  Task4 = list(
    M = ParentTraits,
    W = HybridWeights
  )
)

```

1.5.1 Access & Operate

```
TaskList$Task2$M
```

```

      G1 G2 G3
Liver  8  5  7
Heart  6  4  5
Brain  9  7  6

```

```
TaskList$Task2$M %*% TaskList$Task2$W
```

```

      [,1]
Liver 15.7
Heart 11.7
Brain 16.8

```

1.5.2 Interpretation

Using lists helps manage and operate on structured data across tasks.