

Supplementary Materials

Results of PROMETHEE-ranking. Generated in RStudio v. 2022.07.2 Build 576.

Preferred method for doing a PROMETHEE analysis using package promethee123

alternatives = studies
criteria = criteria
min-max = if the value preferred is a max or a min value
normalization function I equal for all criteria
q_indifference indicates when a difference so small that it is unimportant for a decision
p-preference indicates when a difference is large enough for making a difference between two alternatives
s-curve change is equal for all criteria
criteria weights can be changed but must sum to 1

Scenario 1 (S1):

```
alternatives <- c("S1", "S2", "S3", "S4", "S5", "S6", "S7", "S8", "S9", "S10", "S11", "S12", "S13")
criteria <- c("A", "B", "C", "D", "E", "F")
decision_matrix <- matrix(c(1,3,2,3,2,2,2,3,2,2,1,3,2,1,2,2,2,2,2,2,2,1,1,1,2,2,2,2,2,2,2,2,2,1,1,2,2,3,3,3,1,2,1,2,3,2,2,3,3,3,0,3,3,2,2,1,0,2,1,1,1,3,3,0,2,2,2,0,1,1,3,2,0,0,2,3),
ncol = length(alternatives), nrow = length(criteria), byrow = TRUE)
min_max <- c("max", "max", "max", "max", "max", "max")
normalization_function <- c( 1 , 1 , 1 , 1, 1, 1 )
q_indifference <- c(1, 1 , 1 , 1, 1, 1)
p_preference <- c(1 , 1 , 1 , 1, 1, 1)
s_curve_change <- c("", "", "", "", "", "")
criteria_weights <- c(0.16667 , 0.16667 , 0.16667 , 0.16667, 0.16667, 0.16667 )
)
promethee123(alternatives, criteria, decision_matrix, min_max, normalization_function,
q_indifference, p_preference, s_curve_change, criteria_weights)
```

```
[1] ""
[1] "===== Alternative Performances in Each Criterion ====="
[1] ""
[1] ""
[1] "Weighted Matrix relative to criterion A"
```

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11
S1	0.00000	0	0.00000	0	0.00000	0.00000	0.00000	0	0.00000	0.00000	0.00000
S2	0.16667	0	0.16667	0	0.16667	0.16667	0.16667	0	0.16667	0.16667	0.16667
S3	0.16667	0	0.00000	0	0.00000	0.00000	0.00000	0	0.00000	0.00000	0.16667
S4	0.16667	0	0.16667	0	0.16667	0.16667	0.16667	0	0.16667	0.16667	0.16667
S5	0.16667	0	0.00000	0	0.00000	0.00000	0.00000	0	0.00000	0.00000	0.16667

```

S6 0.16667 0 0.00000 0 0.00000 0.00000 0.00000 0 0.00000 0.00000 0.16667
S7 0.16667 0 0.00000 0 0.00000 0.00000 0.00000 0 0.00000 0.00000 0.16667
S8 0.16667 0 0.16667 0 0.16667 0.16667 0.16667 0 0.16667 0.16667 0.16667
S9 0.16667 0 0.00000 0 0.00000 0.00000 0.00000 0 0.00000 0.00000 0.16667
S10 0.16667 0 0.00000 0 0.00000 0.00000 0.00000 0 0.00000 0.00000 0.16667
S11 0.00000 0 0.00000 0 0.00000 0.00000 0.00000 0 0.00000 0.00000 0.00000
S12 0.16667 0 0.16667 0 0.16667 0.16667 0.16667 0 0.16667 0.16667 0.16667
S13 0.16667 0 0.00000 0 0.00000 0.00000 0.00000 0 0.00000 0.00000 0.16667

```

```

S12 S13
S1 0 0.00000
S2 0 0.16667
S3 0 0.00000
S4 0 0.16667
S5 0 0.00000
S6 0 0.00000
S7 0 0.00000
S8 0 0.16667
S9 0 0.00000
S10 0 0.00000
S11 0 0.00000
S12 0 0.16667
S13 0 0.00000

```

[1] ""

[1] "Weighted Matrix relative to criterion B"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0.00000	0	0	0	0	0	0	0	0	0.00000	0.00000	0.00000	0
S2	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S3	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S4	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S5	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S6	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S7	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S8	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S9	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0
S10	0.00000	0	0	0	0	0	0	0	0	0.00000	0.00000	0.00000	0
S11	0.00000	0	0	0	0	0	0	0	0	0.00000	0.00000	0.00000	0
S12	0.00000	0	0	0	0	0	0	0	0	0.00000	0.00000	0.00000	0
S13	0.16667	0	0	0	0	0	0	0	0	0.16667	0.16667	0.16667	0

[1] ""

[1] "Weighted Matrix relative to criterion C"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S2	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S3	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S4	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S5	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S6	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S7	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S8	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0
S9	0	0	0	0	0	0	0	0	0	0.16667	0.16667	0	0

```

S10 0 0 0 0 0 0 0 0 0 0.00000 0.00000 0 0
S11 0 0 0 0 0 0 0 0 0 0.00000 0.00000 0 0
S12 0 0 0 0 0 0 0 0 0 0.16667 0.16667 0 0
S13 0 0 0 0 0 0 0 0 0 0.16667 0.16667 0 0
[1] ""
[1] "Weighted Matrix relative to criterion D"
  S1 S2 S3 S4 S5 S6 S7 S8 S9 S10 S11 S12 S13
S1 0 0 0 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.16667 0 0 0
S2 0 0 0 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.16667 0 0 0
S3 0 0 0 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.16667 0 0 0
S4 0 0 0 0.00000 0.00000 0.00000 0.00000 0 0.00000 0.00000 0 0 0
S5 0 0 0 0.16667 0.00000 0.16667 0.00000 0 0.00000 0.00000 0 0 0
S6 0 0 0 0.00000 0.00000 0.00000 0.00000 0 0.00000 0.00000 0 0 0
S7 0 0 0 0.16667 0.00000 0.16667 0.00000 0 0.00000 0.00000 0 0 0
S8 0 0 0 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.16667 0 0 0
S9 0 0 0 0.16667 0.00000 0.16667 0.00000 0 0.00000 0.00000 0 0 0
S10 0 0 0 0.16667 0.00000 0.16667 0.00000 0 0.00000 0.00000 0 0 0
S11 0 0 0 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.16667 0 0 0
S12 0 0 0 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.16667 0 0 0
S13 0 0 0 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.16667 0 0 0
[1] ""
[1] "Weighted Matrix relative to criterion E"
  S1 S2 S3 S4 S5 S6 S7 S8 S9 S10
S1 0.00000 0 0 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000
S2 0.16667 0 0 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667
S3 0.16667 0 0 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667
S4 0.16667 0 0 0.00000 0.00000 0.16667 0.16667 0.00000 0.16667 0.16667
S5 0.16667 0 0 0.00000 0.00000 0.16667 0.16667 0.00000 0.16667 0.16667
S6 0.16667 0 0 0.00000 0.00000 0.00000 0.16667 0.00000 0.00000 0.00000
S7 0.00000 0 0 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000
S8 0.16667 0 0 0.00000 0.00000 0.16667 0.16667 0.00000 0.16667 0.16667
S9 0.16667 0 0 0.00000 0.00000 0.00000 0.16667 0.00000 0.00000 0.00000
S10 0.16667 0 0 0.00000 0.00000 0.00000 0.16667 0.00000 0.00000 0.00000
S11 0.16667 0 0 0.00000 0.00000 0.00000 0.16667 0.00000 0.00000 0.00000
S12 0.16667 0 0 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667
S13 0.16667 0 0 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667
  S11 S12 S13
S1 0.00000 0 0
S2 0.16667 0 0
S3 0.16667 0 0
S4 0.16667 0 0
S5 0.16667 0 0
S6 0.00000 0 0
S7 0.00000 0 0
S8 0.16667 0 0
S9 0.00000 0 0
S10 0.00000 0 0
S11 0.00000 0 0
S12 0.16667 0 0
S13 0.16667 0 0

```

```

[1] ""
[1] "Weighted Matrix relative to criterion F"
      S1      S2      S3      S4      S5      S6      S7 S8      S9      S
10
S1  0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0 0.00000 0.000
00
S2  0.16667 0.00000 0.00000 0.00000 0.16667 0.16667 0.16667 0 0.00000 0.166
67
S3  0.16667 0.00000 0.00000 0.00000 0.16667 0.16667 0.16667 0 0.00000 0.166
67
S4  0.16667 0.00000 0.00000 0.00000 0.16667 0.16667 0.16667 0 0.00000 0.166
67
S5  0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0 0.00000 0.000
00
S6  0.16667 0.00000 0.00000 0.00000 0.16667 0.00000 0.00000 0 0.00000 0.166
67
S7  0.16667 0.00000 0.00000 0.00000 0.16667 0.00000 0.00000 0 0.00000 0.166
67
S8  0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.166
67
S9  0.16667 0.00000 0.00000 0.00000 0.16667 0.16667 0.16667 0 0.00000 0.166
67
S10 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0 0.00000 0.000
00
S11 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0 0.00000 0.000
00
S12 0.16667 0.00000 0.00000 0.00000 0.16667 0.16667 0.16667 0 0.00000 0.166
67
S13 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0.16667 0 0.16667 0.166
67
      S11      S12 S13
S1  0.00000 0.00000 0
S2  0.16667 0.00000 0
S3  0.16667 0.00000 0
S4  0.16667 0.00000 0
S5  0.00000 0.00000 0
S6  0.16667 0.00000 0
S7  0.16667 0.00000 0
S8  0.16667 0.16667 0
S9  0.16667 0.00000 0
S10 0.00000 0.00000 0
S11 0.00000 0.00000 0
S12 0.16667 0.00000 0
S13 0.16667 0.16667 0
[1] "===== Global Index of Preference ====="
[1] ""
      S1      S2      S3      S4      S5      S6      S7      S8      S9      S10
S1  0.0000 0.0000 0.0000 0.0278 0.0278 0.0278 0.0278 0.0000 0.0278 0.0556
S2  0.1111 0.0000 0.0278 0.0556 0.1111 0.1111 0.1111 0.0278 0.0833 0.1667
S3  0.1111 0.0000 0.0000 0.0556 0.0833 0.0833 0.0833 0.0278 0.0556 0.1389

```

```

S4 0.1111 0.0000 0.0278 0.0000 0.0556 0.0833 0.0833 0.0000 0.0556 0.1389
S5 0.0833 0.0000 0.0000 0.0278 0.0000 0.0556 0.0278 0.0000 0.0278 0.0833
S6 0.1111 0.0000 0.0000 0.0000 0.0278 0.0000 0.0278 0.0000 0.0000 0.0833
S7 0.0833 0.0000 0.0000 0.0278 0.0278 0.0278 0.0000 0.0000 0.0000 0.0833
S8 0.1111 0.0278 0.0556 0.0556 0.0833 0.1111 0.1111 0.0000 0.1111 0.1667
S9 0.1111 0.0000 0.0000 0.0278 0.0278 0.0556 0.0556 0.0000 0.0000 0.0833
S10 0.0556 0.0000 0.0000 0.0278 0.0000 0.0278 0.0278 0.0000 0.0000 0.0000
S11 0.0278 0.0000 0.0000 0.0278 0.0278 0.0278 0.0556 0.0000 0.0278 0.0278
S12 0.0833 0.0000 0.0278 0.0556 0.1111 0.1111 0.1111 0.0278 0.0833 0.1389
S13 0.1111 0.0278 0.0278 0.0833 0.0833 0.0833 0.0833 0.0278 0.0833 0.1389

```

```

      S11      S12      S13
S1 0.0278 0.0000 0.0000
S2 0.1389 0.0278 0.0278
S3 0.1389 0.0278 0.0000
S4 0.1389 0.0278 0.0278
S5 0.1111 0.0278 0.0000
S6 0.1111 0.0278 0.0000
S7 0.1111 0.0278 0.0000
S8 0.1389 0.0556 0.0278
S9 0.1111 0.0278 0.0000
S10 0.0278 0.0000 0.0000
S11 0.0000 0.0000 0.0000
S12 0.1111 0.0000 0.0278
S13 0.1389 0.0556 0.0000

```

```

[1] ""
[1] ""
[1] "===== Outranking Flows ====="
[1] ""

```

	alternatives	positive_flows	negative_flows	net_flows
1	S1	0.2224	1.1110	-0.8886
2	S2	1.0001	0.0556	0.9445
3	S3	0.8056	0.1668	0.6388
4	S4	0.7501	0.4725	0.2776
5	S5	0.4445	0.6667	-0.2222
6	S6	0.3889	0.8056	-0.4167
7	S7	0.3889	0.8056	-0.4167
8	S8	1.0557	0.1112	0.9445
9	S9	0.5001	0.5556	-0.0555
10	S10	0.1668	1.3056	-1.1388
11	S11	0.2224	1.3056	-1.0832
12	S12	0.8889	0.3058	0.5831
13	S13	0.9444	0.1112	0.8332

```

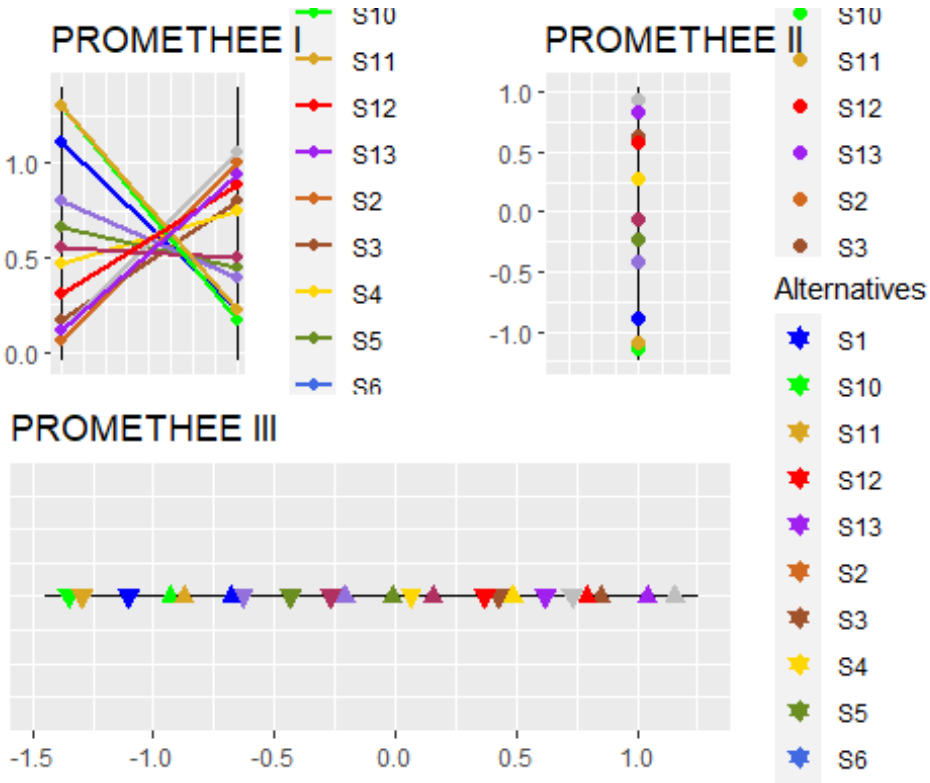
[1] "===== PROMETHEE II ====="
[1] "S8 = 0.9445"
[1] "S2 = 0.9445"
[1] "S13 = 0.8332"
[1] "S3 = 0.6388"
[1] "S12 = 0.5831"
[1] "S4 = 0.2776"

```

```

[1] "S9 = -0.0555"
[1] "S5 = -0.2222"
[1] "S7 = -0.4167"
[1] "S6 = -0.4167"
[1] "S1 = -0.8886"
[1] "S11 = -1.0832"
[1] "S10 = -1.1388"

```



Scenario 2 (S2):

```

alternatives <-
c("S1", "S2", "S3", "S4", "S5", "S6", "S7", "S8", "S9", "S10", "S11", "S12", "S13")
criteria <- c("A", "B", "C", "D", "E", "F")
decision_matrix <-
matrix(c(1,3,2,3,2,2,2,3,2,2,1,3,2,1,2,2,2,2,2,2,2,1,1,1,2,2,2,2,2,2,2,2,
2,1,1,2,2,3,3,3,1,2,1,2,3,2,2,3,3,3,0,3,3,2,2,1,0,2,1,1,1,3,3,0,2,2,2,0,1,1,3
,2,0,0,2,3),
ncol = length(alternatives), nrow = length(criteria), byrow = TRUE)
min_max <- c("max", "max", "max", "max", "max", "max")
normalization_function <- c( 1 , 1 , 1 , 1, 1, 1 )
q_indifference <- c(1, 1 , 1 , 1, 1, 1)
p_preference <- c(1 , 1 , 1 , 1, 1, 1)
s_curve_change <- c("", "", "", "", "", "")
criteria_weights <- c(0.15 , 0.15 , 0.15 , 0.15, 0.2, 0.2)

promethee123(alternatives, criteria, decision_matrix, min_max,
normalization_function,
q_indifference, p_preference, s_curve_change, criteria_weights)

```

```

[1] ""
[1] "===== Alternative Performances in Each Criterion ====="
[1] ""
[1] ""
[1] "Weighted Matrix relative to criterion A"
      S1 S2  S3 S4  S5  S6  S7 S8  S9  S10  S11 S12  S13
S1  0.00 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.00 0 0.00
S2  0.15 0 0.15 0 0.15 0.15 0.15 0 0.15 0.15 0.15 0 0.15
S3  0.15 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.15 0 0.00
S4  0.15 0 0.15 0 0.15 0.15 0.15 0 0.15 0.15 0.15 0 0.15
S5  0.15 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.15 0 0.00
S6  0.15 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.15 0 0.00
S7  0.15 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.15 0 0.00
S8  0.15 0 0.15 0 0.15 0.15 0.15 0 0.15 0.15 0.15 0 0.15
S9  0.15 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.15 0 0.00
S10 0.15 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.15 0 0.00
S11 0.00 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.00 0 0.00
S12 0.15 0 0.15 0 0.15 0.15 0.15 0 0.15 0.15 0.15 0 0.15
S13 0.15 0 0.00 0 0.00 0.00 0.00 0 0.00 0.00 0.15 0 0.00
[1] ""
[1] "Weighted Matrix relative to criterion B"
      S1 S2 S3 S4 S5 S6 S7 S8 S9  S10  S11  S12  S13
S1  0.00 0 0 0 0 0 0 0 0 0.00 0.00 0.00 0
S2  0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0
S3  0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0
S4  0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0
S5  0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0
S6  0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0
S7  0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0

```

```

S8 0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0
S9 0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0
S10 0.00 0 0 0 0 0 0 0 0 0.00 0.00 0.00 0
S11 0.00 0 0 0 0 0 0 0 0 0.00 0.00 0.00 0
S12 0.00 0 0 0 0 0 0 0 0 0.00 0.00 0.00 0
S13 0.15 0 0 0 0 0 0 0 0 0.15 0.15 0.15 0

```

[1] ""

[1] "Weighted Matrix relative to criterion C"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S2	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S3	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S4	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S5	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S6	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S7	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S8	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S9	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S10	0	0	0	0	0	0	0	0	0	0.00	0.00	0	0
S11	0	0	0	0	0	0	0	0	0	0.00	0.00	0	0
S12	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S13	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0

[1] ""

[1] "Weighted Matrix relative to criterion D"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S2	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S3	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S4	0	0	0	0.00	0.00	0.00	0.00	0	0.00	0.00	0	0	0
S5	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S6	0	0	0	0.00	0.00	0.00	0.00	0	0.00	0.00	0	0	0
S7	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S8	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S9	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S10	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S11	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S12	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S13	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0

[1] ""

[1] "Weighted Matrix relative to criterion E"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0.0	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0	0
S2	0.2	0	0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0	0
S3	0.2	0	0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0	0
S4	0.2	0	0	0.0	0.0	0.2	0.2	0.0	0.2	0.2	0.2	0	0
S5	0.2	0	0	0.0	0.0	0.2	0.2	0.0	0.2	0.2	0.2	0	0
S6	0.2	0	0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0	0
S7	0.0	0	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0	0
S8	0.2	0	0	0.0	0.0	0.2	0.2	0.0	0.2	0.2	0.2	0	0
S9	0.2	0	0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0	0


```

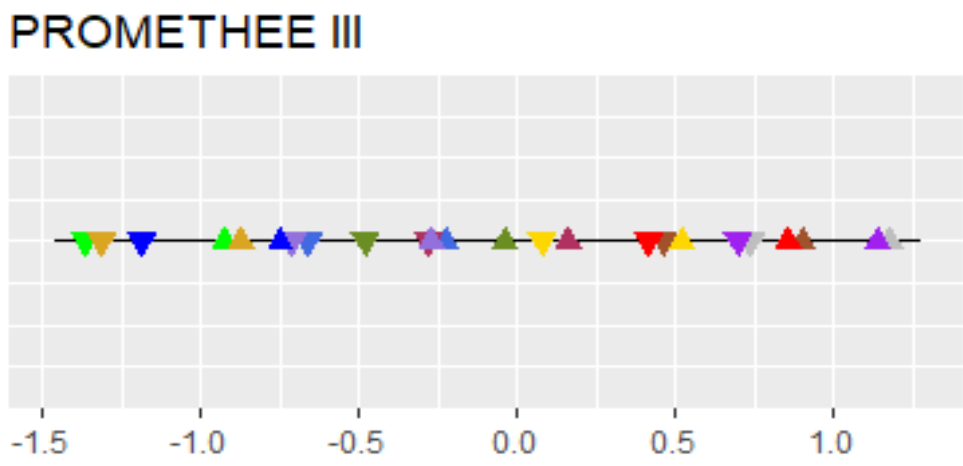
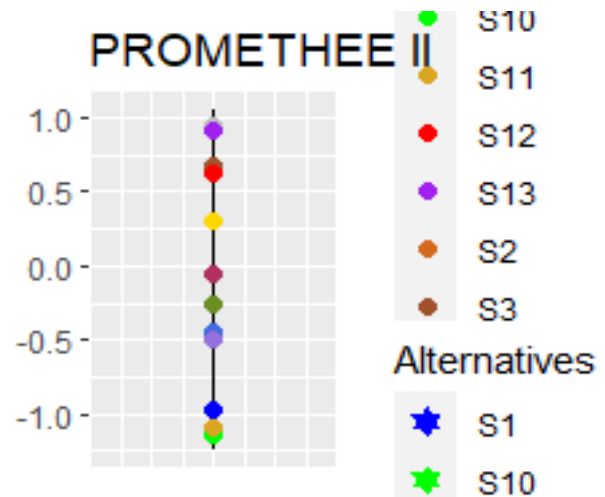
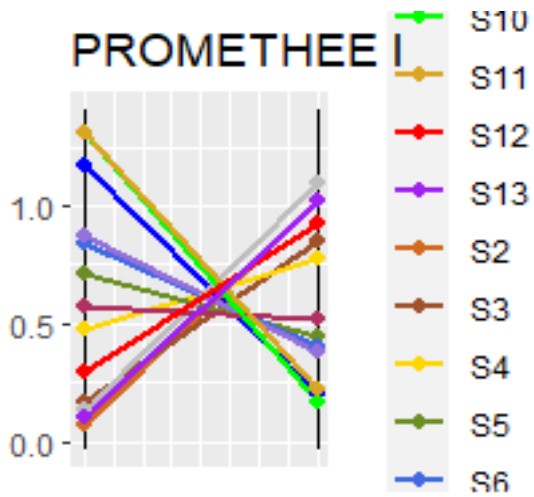
S10 0.2  0  0  0.0  0.0  0.0  0.2  0.0  0.0  0.0  0.0  0  0
S11 0.2  0  0  0.0  0.0  0.0  0.2  0.0  0.0  0.0  0.0  0  0
S12 0.2  0  0  0.2  0.2  0.2  0.2  0.2  0.2  0.2  0.2  0  0
S13 0.2  0  0  0.2  0.2  0.2  0.2  0.2  0.2  0.2  0.2  0  0
[1] ""
[1] "Weighted Matrix relative to criterion F"
      S1  S2  S3  S4  S5  S6  S7  S8  S9  S10  S11  S12  S13
S1  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0  0.0  0.0  0.0  0.0  0
S2  0.2  0.0  0.0  0.0  0.2  0.2  0.2  0  0.0  0.2  0.2  0.0  0
S3  0.2  0.0  0.0  0.0  0.2  0.2  0.2  0  0.0  0.2  0.2  0.0  0
S4  0.2  0.0  0.0  0.0  0.2  0.2  0.2  0  0.0  0.2  0.2  0.0  0
S5  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0  0.0  0.0  0.0  0.0  0
S6  0.2  0.0  0.0  0.0  0.2  0.0  0.0  0  0.0  0.2  0.2  0.0  0
S7  0.2  0.0  0.0  0.0  0.2  0.0  0.0  0  0.0  0.2  0.2  0.0  0
S8  0.2  0.2  0.2  0.2  0.2  0.2  0.2  0  0.2  0.2  0.2  0.2  0
S9  0.2  0.0  0.0  0.0  0.2  0.2  0.2  0  0.0  0.2  0.2  0.0  0
S10 0.0  0.0  0.0  0.0  0.0  0.0  0.0  0  0.0  0.0  0.0  0.0  0
S11 0.0  0.0  0.0  0.0  0.0  0.0  0.0  0  0.0  0.0  0.0  0.0  0
S12 0.2  0.0  0.0  0.0  0.2  0.2  0.2  0  0.0  0.2  0.2  0.0  0
S13 0.2  0.2  0.2  0.2  0.2  0.2  0.2  0  0.2  0.2  0.2  0.2  0
[1] "===== Global Index of Preference ====="
[1] ""
      S1      S2      S3      S4      S5      S6      S7      S8      S9      S10
S1  0.0000  0.0000  0.0000  0.0250  0.0250  0.0250  0.0250  0.0000  0.0250  0.0500
S2  0.1167  0.0000  0.0250  0.0583  0.1167  0.1167  0.1167  0.0333  0.0833  0.1667
S3  0.1167  0.0000  0.0000  0.0583  0.0917  0.0917  0.0917  0.0333  0.0583  0.1417
S4  0.1167  0.0000  0.0250  0.0000  0.0583  0.0917  0.0917  0.0000  0.0583  0.1417
S5  0.0833  0.0000  0.0000  0.0250  0.0000  0.0583  0.0333  0.0000  0.0333  0.0833
S6  0.1167  0.0000  0.0000  0.0000  0.0333  0.0000  0.0333  0.0000  0.0000  0.0833
S7  0.0833  0.0000  0.0000  0.0250  0.0333  0.0250  0.0000  0.0000  0.0000  0.0833
S8  0.1167  0.0333  0.0583  0.0583  0.0833  0.1167  0.1167  0.0000  0.1167  0.1667
S9  0.1167  0.0000  0.0000  0.0250  0.0333  0.0583  0.0667  0.0000  0.0000  0.0833
S10 0.0583  0.0000  0.0000  0.0250  0.0000  0.0250  0.0333  0.0000  0.0000  0.0000
S11 0.0333  0.0000  0.0000  0.0250  0.0250  0.0250  0.0583  0.0000  0.0250  0.0250
S12 0.0917  0.0000  0.0250  0.0583  0.1167  0.1167  0.1167  0.0333  0.0833  0.1417
S13 0.1167  0.0333  0.0333  0.0917  0.0917  0.0917  0.0917  0.0333  0.0917  0.1417
      S11      S12      S13
S1  0.0250  0.0000  0.000
S2  0.1417  0.0250  0.025
S3  0.1417  0.0250  0.000
S4  0.1417  0.0250  0.025
S5  0.1083  0.0250  0.000
S6  0.1083  0.0250  0.000
S7  0.1083  0.0250  0.000
S8  0.1417  0.0583  0.025
S9  0.1083  0.0250  0.000
S10 0.0250  0.0000  0.000
S11 0.0000  0.0000  0.000
S12 0.1167  0.0000  0.025
S13 0.1417  0.0583  0.000

```

```

[1] ""
[1] ""
[1] "===== Outranking Flows ====="
[1] ""
alternatives positive_flows negative_flows net_flows
1          S1          0.2000          1.1668         -0.9668
2          S2          1.0251          0.0666          0.9585
3          S3          0.8501          0.1666          0.6835
4          S4          0.7751          0.4749          0.3002
5          S5          0.4498          0.7083         -0.2585
6          S6          0.3999          0.8418         -0.4419
7          S7          0.3832          0.8751         -0.4919
8          S8          1.0917          0.1332          0.9585
9          S9          0.5166          0.5749         -0.0583
10         S10         0.1666          1.3084         -1.1418
11         S11         0.2166          1.3084         -1.0918
12         S12         0.9251          0.2916          0.6335
13         S13         1.0168          0.1000          0.9168
[1] "===== PROMETHEE II ====="
[1] "S8 = 0.9585"
[1] "S2 = 0.9585"
[1] "S13 = 0.9168"
[1] "S3 = 0.6835"
[1] "S12 = 0.6335"
[1] "S4 = 0.3002"
[1] "S9 = -0.0583"
[1] "S5 = -0.2585"
[1] "S6 = -0.4419"
[1] "S7 = -0.4919"
[1] "S1 = -0.9668"
[1] "S11 = -1.0918"
[1] "S10 = -1.1418"
[1] ""

```



- Alternatives
- S1
 - S10
 - S11
 - S12
 - S13
 - S2
 - S3
 - S4
 - S5
 - S6

Scenario 3 (S3):

```
alternatives <-  
c("S1", "S2", "S3", "S4", "S5", "S6", "S7", "S8", "S9", "S10", "S11", "S12", "S13")  
criteria <- c("A", "B", "C", "D", "E", "F")  
decision_matrix <-  
matrix(c(1,3,2,3,2,2,2,3,2,2,1,3,2,1,2,2,2,2,2,2,2,1,1,1,2,2,2,2,2,2,2,2,  
2,1,1,2,2,3,3,3,1,2,1,2,3,2,2,3,3,3,0,3,3,2,2,1,0,2,1,1,1,3,3,0,2,2,2,0,1,1,3,  
2,0,0,2,3),  
ncol = length(alternatives), nrow = length(criteria), byrow = TRUE)  
min_max <- c("max", "max", "max", "max", "max", "max")  
normalization_function <- c( 1 , 1 , 1 , 1, 1, 1 )  
q_indifference <- c(1, 1 , 1 , 1, 1, 1 )  
p_preference <- c(1 , 1 , 1 , 1, 1, 1 )  
s_curve_change <- c("", "", "", "", "", "")  
criteria_weights <- c(0.10 , 0.10 , 0.15 , 0.15, 0.25, 0.25)  
  
promethee123(alternatives, criteria, decision_matrix, min_max,  
normalization_function,  
q_indifference, p_preference, s_curve_change, criteria_weights)
```

```
[1] ""  
[1] "===== Alternative Performances in Each Criterion ====="  
[1] ""  
[1] ""  
[1] "Weighted Matrix relative to criterion A"  
   S1 S2 S3 S4 S5 S6 S7 S8 S9 S10 S11 S12 S13  
S1 0.0 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.0 0 0.0  
S2 0.1 0 0.1 0 0.1 0.1 0.1 0 0.1 0.1 0.1 0 0.1  
S3 0.1 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.1 0 0.0  
S4 0.1 0 0.1 0 0.1 0.1 0.1 0 0.1 0.1 0.1 0 0.1  
S5 0.1 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.1 0 0.0  
S6 0.1 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.1 0 0.0  
S7 0.1 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.1 0 0.0  
S8 0.1 0 0.1 0 0.1 0.1 0.1 0 0.1 0.1 0.1 0 0.1  
S9 0.1 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.1 0 0.0  
S10 0.1 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.1 0 0.0  
S11 0.0 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.0 0 0.0  
S12 0.1 0 0.1 0 0.1 0.1 0.1 0 0.1 0.1 0.1 0 0.1  
S13 0.1 0 0.0 0 0.0 0.0 0.0 0 0.0 0.0 0.1 0 0.0  
[1] ""  
[1] "Weighted Matrix relative to criterion B"  
   S1 S2 S3 S4 S5 S6 S7 S8 S9 S10 S11 S12 S13  
S1 0.0 0 0 0 0 0 0 0 0 0.0 0.0 0.0 0  
S2 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0  
S3 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0  
S4 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0  
S5 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0  
S6 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0  
S7 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0
```

```

S8 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0
S9 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0
S10 0.0 0 0 0 0 0 0 0 0 0.0 0.0 0.0 0
S11 0.0 0 0 0 0 0 0 0 0 0.0 0.0 0.0 0
S12 0.0 0 0 0 0 0 0 0 0 0.0 0.0 0.0 0
S13 0.1 0 0 0 0 0 0 0 0 0.1 0.1 0.1 0

```

[1] ""

[1] "Weighted Matrix relative to criterion C"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S2	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S3	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S4	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S5	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S6	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S7	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S8	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S9	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S10	0	0	0	0	0	0	0	0	0	0.00	0.00	0	0
S11	0	0	0	0	0	0	0	0	0	0.00	0.00	0	0
S12	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0
S13	0	0	0	0	0	0	0	0	0	0.15	0.15	0	0

[1] ""

[1] "Weighted Matrix relative to criterion D"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S2	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S3	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S4	0	0	0	0.00	0.00	0.00	0.00	0	0.00	0.00	0	0	0
S5	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S6	0	0	0	0.00	0.00	0.00	0.00	0	0.00	0.00	0	0	0
S7	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S8	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S9	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S10	0	0	0	0.15	0.00	0.15	0.00	0	0.00	0.00	0	0	0
S11	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S12	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0
S13	0	0	0	0.15	0.15	0.15	0.15	0	0.15	0.15	0	0	0

[1] ""

[1] "Weighted Matrix relative to criterion E"

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
S1	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0
S2	0.25	0	0	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0	0
S3	0.25	0	0	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0	0
S4	0.25	0	0	0.00	0.00	0.25	0.25	0.00	0.25	0.25	0.25	0	0
S5	0.25	0	0	0.00	0.00	0.25	0.25	0.00	0.25	0.25	0.25	0	0
S6	0.25	0	0	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0	0
S7	0.00	0	0	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0
S8	0.25	0	0	0.00	0.00	0.25	0.25	0.00	0.25	0.25	0.25	0	0
S9	0.25	0	0	0.00	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0	0

```

S10 0.25 0 0 0.00 0.00 0.00 0.25 0.00 0.00 0.00 0.00 0 0
S11 0.25 0 0 0.00 0.00 0.00 0.25 0.00 0.00 0.00 0.00 0 0
S12 0.25 0 0 0.25 0.25 0.25 0.25 0.25 0.25 0.25 0.25 0 0
S13 0.25 0 0 0.25 0.25 0.25 0.25 0.25 0.25 0.25 0.25 0 0
[1] ""
[1] "Weighted Matrix relative to criterion F"
      S1  S2  S3  S4  S5  S6  S7  S8  S9  S10  S11  S12  S13
S1  0.00 0.00 0.00 0.00 0.00 0.00 0.00 0 0.00 0.00 0.00 0.00 0
S2  0.25 0.00 0.00 0.00 0.25 0.25 0.25 0 0.00 0.25 0.25 0.00 0
S3  0.25 0.00 0.00 0.00 0.25 0.25 0.25 0 0.00 0.25 0.25 0.00 0
S4  0.25 0.00 0.00 0.00 0.25 0.25 0.25 0 0.00 0.25 0.25 0.00 0
S5  0.00 0.00 0.00 0.00 0.00 0.00 0.00 0 0.00 0.00 0.00 0.00 0
S6  0.25 0.00 0.00 0.00 0.25 0.00 0.00 0 0.00 0.25 0.25 0.00 0
S7  0.25 0.00 0.00 0.00 0.25 0.00 0.00 0 0.00 0.25 0.25 0.00 0
S8  0.25 0.25 0.25 0.25 0.25 0.25 0.25 0 0.25 0.25 0.25 0.25 0
S9  0.25 0.00 0.00 0.00 0.25 0.25 0.25 0 0.00 0.25 0.25 0.00 0
S10 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0 0.00 0.00 0.00 0.00 0
S11 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0 0.00 0.00 0.00 0.00 0
S12 0.25 0.00 0.00 0.00 0.25 0.25 0.25 0 0.00 0.25 0.25 0.00 0
S13 0.25 0.25 0.25 0.25 0.25 0.25 0.25 0 0.25 0.25 0.25 0.25 0
[1] "===== Global Index of Preference ====="
[1] ""
      S1  S2  S3  S4  S5  S6  S7  S8  S9  S10
S1  0.0000 0.0000 0.0000 0.0250 0.0250 0.0250 0.0250 0.0000 0.0250 0.0500
S2  0.1167 0.0000 0.0167 0.0667 0.1250 0.1250 0.1250 0.0417 0.0833 0.1667
S3  0.1167 0.0000 0.0000 0.0667 0.1083 0.1083 0.1083 0.0417 0.0667 0.1500
S4  0.1167 0.0000 0.0167 0.0000 0.0583 0.1000 0.1000 0.0000 0.0583 0.1417
S5  0.0750 0.0000 0.0000 0.0250 0.0000 0.0667 0.0417 0.0000 0.0417 0.0833
S6  0.1167 0.0000 0.0000 0.0000 0.0417 0.0000 0.0417 0.0000 0.0000 0.0833
S7  0.0750 0.0000 0.0000 0.0250 0.0417 0.0250 0.0000 0.0000 0.0000 0.0833
S8  0.1167 0.0417 0.0583 0.0667 0.0833 0.1250 0.1250 0.0000 0.1250 0.1667
S9  0.1167 0.0000 0.0000 0.0250 0.0417 0.0667 0.0833 0.0000 0.0000 0.0833
S10 0.0583 0.0000 0.0000 0.0250 0.0000 0.0250 0.0417 0.0000 0.0000 0.0000
S11 0.0417 0.0000 0.0000 0.0250 0.0250 0.0250 0.0667 0.0000 0.0250 0.0250
S12 0.1000 0.0000 0.0167 0.0667 0.1250 0.1250 0.1250 0.0417 0.0833 0.1500
S13 0.1167 0.0417 0.0417 0.1083 0.1083 0.1083 0.1083 0.0417 0.1083 0.1500
      S11  S12  S13
S1  0.0250 0.0000 0.0000
S2  0.1417 0.0167 0.0167
S3  0.1417 0.0167 0.0000
S4  0.1417 0.0167 0.0167
S5  0.1000 0.0167 0.0000
S6  0.1000 0.0167 0.0000
S7  0.1000 0.0167 0.0000
S8  0.1417 0.0583 0.0167
S9  0.1000 0.0167 0.0000
S10 0.0167 0.0000 0.0000
S11 0.0000 0.0000 0.0000
S12 0.1250 0.0000 0.0167
S13 0.1417 0.0583 0.0000

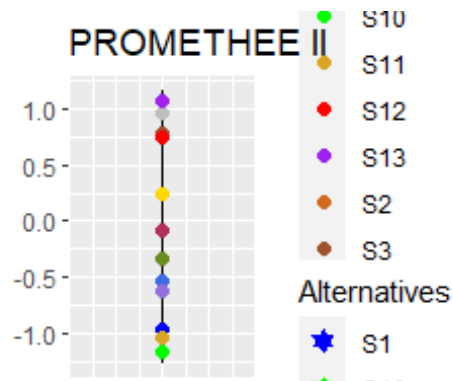
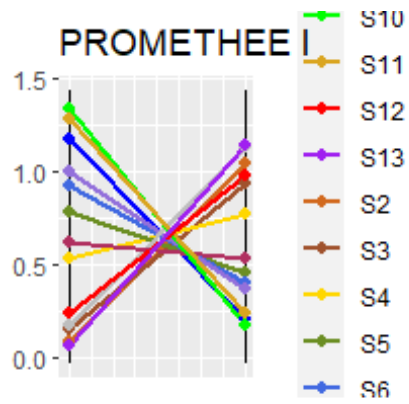
```

```

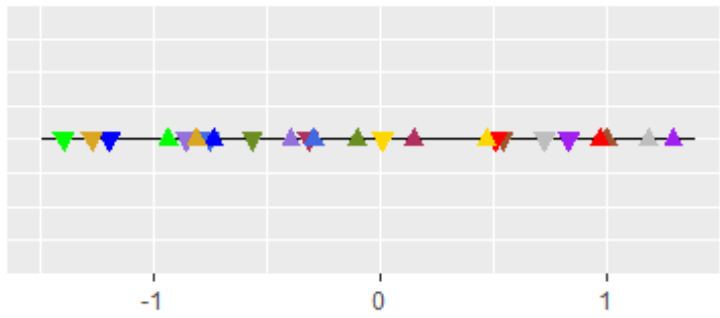
[1] ""
[1] ""
[1] "===== Outranking Flows ====="
[1] ""
alternatives positive_flows negative_flows net_flows
1          S1          0.2000          1.1669         -0.9669
2          S2          1.0419          0.0834          0.9585
3          S3          0.9251          0.1501          0.7750
4          S4          0.7668          0.5251          0.2417
5          S5          0.4501          0.7833         -0.3332
6          S6          0.4001          0.9250         -0.5249
7          S7          0.3667          0.9917         -0.6250
8          S8          1.1251          0.1668          0.9583
9          S9          0.5334          0.6166         -0.0832
10         S10         0.1667          1.3333         -1.1666
11         S11         0.2334          1.2752         -1.0418
12         S12         0.9751          0.2335          0.7416
13         S13         1.1333          0.0668          1.0665

[1] "===== PROMETHEE II ====="
[1] "S13 = 1.0665"
[1] "S2 = 0.9585"
[1] "S8 = 0.9583"
[1] "S3 = 0.775"
[1] "S12 = 0.7416"
[1] "S4 = 0.2417"
[1] "S9 = -0.08319999999999999"
[1] "S5 = -0.3332"
[1] "S6 = -0.5249"
[1] "S7 = -0.625"
[1] "S1 = -0.9669"
[1] "S11 = -1.0418"
[1] "S10 = -1.1666"

```



PROMETHEE III



- Alternatives
- S1 (Blue star)
 - S10 (Green star)
 - S11 (Orange star)
 - S12 (Red star)
 - S13 (Purple star)
 - S2 (Brown star)
 - S3 (Dark brown star)
 - S4 (Yellow star)
 - S5 (Olive star)
 - S6 (Blue star)

Table S1. Summary of methods and results related to spatial aspects of 13 articles included in the systematic review on spatial analysis of AMR in the environment, published between 2012-2022.

Authors (year)	Summary	Spatial Methods	Results
(Agga <i>et al.</i>, 2019)	The effect of cessation of a beef cattle backgrounding operation comparing the intensively used feeding area with the more extensively used grazing area on the persistence and distribution of antibiotic resistance genes (ARGs).	26 sampling sites were georeferenced and used for interpolation maps. The spatial distribution of bacteria and ARGs. Was compared with the spatial patterns of feeding and grazing areas. The temporal changes of the spatial patterns were monitored for two years.	Higher concentrations of bacteria and ARGs were found in the feeding area as well as along the fence between the feeding and grazing area, compared to the grazing area. Comparison of interpolation maps over time showed a significant decline of bacteria and ARGs in the feeding area. However, the levels were still significantly higher in the feeding area compared the grazing area after two years. Manure had a positive effect on antibiotic resistant bacteria occurrence.
(Bueno <i>et al.</i>, 2021)	Quantification and prediction of antimicrobial and ARG-occurrence in waterbodies. Sampling aided by spatial analysis at both macro and micro-scale. Animal and human density served as a proxy to predict release of antimicrobials.	Overlay analysis was used to find hot spots for antimicrobial occurrence. Factors included landscape features, e.g. livestock density, human population density and pollution point-sources like hospitals and water treatment plants. Kernel interpolation was used to create predictive maps. Micro-scale was limited to a maximum of 2 km from the effluent point source.	Clusters of antimicrobial concentrations were identified by mapping sampling sites with higher occurrence of antimicrobials and ARGs. Results were described by the authors as descriptive due to the low number of data points at a state-wide level, and the results were considered less precise. At macro-level the authors point out areas of possible occurrence of AMR. There was no statistical association between sample values at micro-level and human activity.
(Bueno <i>et al.</i>, 2022)	Risk assessment of spatial and temporal vulnerability of soils to antimicrobial contamination.	Maps on soil vulnerability were created with kernel density interpolation, raster calculations were calculated with data on livestock density, estimated soil contamination potential and other influencing factors. Maps were created for each month of the year to illustrate seasonal differences.	The study identifies sources and pathways for antimicrobials to enter soils. Most prominent sources were wastewater treatment plants, hospitals, ethanol plants and livestock farms. The southwest region of the state has the highest density of livestock and had the highest vulnerability scores for all antimicrobials. Practices of when manure is applied to soils could be guided by the results as temporal vulnerability varied with highest values in the months of April and October.
(Chique <i>et al.</i>, 2019)	Exploratory study aimed at exemplifying the use of GIS to identify transmission routes and sources of antimicrobial resistant organisms.	Clip, union, merge, table join, and dissolve were used to collate data sets. Combinations of data sets on maps to visually identify areas of specific	The main outcome was a presentation of how thematic maps can be used to identify clusters of areas exhibiting high risk for occurrence of AMR. The authors show that GIS together with expert

		<p>interest. Maps created at macro- and micro-level. Standardisation and harmonisation of data sets for comparability, estimation of livestock intensity based on literature indices. Used data categories were agriculture, demography, groundwater, healthcare, hydrology, marine environments, water supply, wastewater and waste management.</p>	<p>knowledge of AMR creates a useful tool for guiding efficient sampling strategies for monitoring of, and interventions against AMR.</p>
(Czekalski <i>et al.</i>, 2014)	<p>Spatial distribution of ARGs in relation to an underwater wastewater discharge point in a lake.</p>	<p>Interpolation maps were created to visualise abundance and concentration of ARGs from the sampling sites in relation to the wastewater discharge point.</p>	<p>Results indicated a directionality of pollution by hydrodynamic transport of water in the lake that was complex and not possible to predict. Distance was not only weakly associated to occurrence levels of antibiotics tested. Spatial distribution analysis showed that discharge of antibiotic resistance genes can be linked to wastewater discharge. But there was no linear function between wastewater pipes and the detection of pathogens. Higher values surrounded the point source, especially within 350 metres. The authors found that pollution occurred over considerable distances.</p>
(de la Torre <i>et al.</i>, 2012)	<p>Risk analysis of soil vulnerability to antibiotic contamination in the entire European Union.</p>	<p>Choropleth maps were created through weighted overlay analysis to define areas of high risk for visual inspection and qualitative assessment. Quantities of antimicrobial pollution were based on estimated animal population sizes. Ecological conditions were approximated through annual mean temperature and the proportion of organic carbon. Ten kilometres distance to animal farms was chosen as the estimated extent of manure spreading. Hot spots were identified using spatial statistics.</p>	<p>Socioeconomic factors and land use, as well as livestock density were identified as factors correlated to soil vulnerability. Concentrations of high soil vulnerability were found in parts of western Europe, but to a varying degree for different antibiotics. Soil vulnerability maps, based on bacteria binding potential and persistence, were considered a starting point for further predictive modelling.</p>
(Ginn <i>et al.</i>, 2021)	<p>Aerosol sampling testing for ARGs and mobile integrons. The aim was to analyse possible point sources of</p>	<p>Estimation of the distance between open wastewater canals and aerosols containing ARGs. Lateral distance was measured two-dimensionally.</p>	<p>The authors managed to identify both aerosolized faecal material and ARGs in the aerosol samples. There were no significant associations between the occurrence of resistance genes and distances from</p>

	pollution in urban settings with open wastewater systems.	Topography was included to consider effects of elevation. Sampling sites were within a maximum distance of 200 metres from the mid-point of the point source, control sites were at >1km from the point source.	the point sources. Still, bioaerosols may pose a risk for environmental pollution in cities with sewage in open wastewater canals.
(Kucukdogan et al., 2015)	GIS-based multi criteria decision analyses used for mapping antibiotic contamination from pasture surface water in north-western Turkey.	GIS was used for identifying catchments and sub-catchments with a flow direction map. The catchment map was used in a hydrological storm water management model to estimate percent imperviousness values for each sub-catchment. Pasture polygons size was used to estimate animal population size. Data on precipitation, topographical, and hydrodynamical characteristics, cattle and poultry, manure production, and estimations of antibiotic transportation, were used in a multi criteria decision analysis used to map the environmental risk.	GIS-based multi criteria decision analyses appear to be a useful tool for mapping environmental risks. Validation of the models used showed some inconsistencies between modelling results and empirical measurements. However, the inconsistency was not alarming. The environmental Risk map showed moderate levels for antibiotic pollution in large parts of the investigated region. Only a few specific areas with high pasture density showed high risk, mainly due to large populations of poultry.
(Miller et al., 2020)	Analysis of spatial distribution of AMR gene distribution sampled from wild owl fecal material in the midwestern United States.	Spatial cluster analysis was used to analyze presence of spatial clusters of AMR genes within the owl populations. Risk factor analyses were performed with multiple logistic regressions using spatial covariates measured with GIS at two different spatial scales: potential home range and water catchment.	Agricultural land cover significantly increased the presence of ARGs. ARGs were more likely to be present in Owls recovered from water catchments containing a high density of hay, pasture, or row crops. Other anthropogenic point sources included in the analyses did not show any significant associations with presence of ARGs. This may have been affected by low sample size in combination with low prevalence of resistance genes in the faecal samples
(Sacristán et al., 2020)	Analysis of the effect of anthropisation on wildlife using a wild feline as sentinel for the presence of ARGs in anthropized and pristine areas in Chile.	The study involved guignas <i>Leopardus guigna</i> trapped or killed at 51 different sites throughout the entire guigna range in Chile. GIS was used to estimate the degree of anthropisation at each site, based on six different landscape variables: vegetation cover, presence and quantity of houses, distance to capture location, landscape use, and administrative region.	There were significant positive associations between ARGs and fragmented landscapes. None of the other landscape variables affected the distribution of antibiotic resistance among the sampled guignas. Still, the result indicates a clear effect from human activities on wildlife in the form of antibiotic resistance pollution.

(Xiang <i>et al.</i>, 2018)	Investigation of anthropogenic influence on the temporal and spatial distribution of ARGs.	Characterisation of ARGs in soil samples from 32 peri-urban sites along a gradient of land use intensity at the watershed scale. Sites were classified as forest or arable. GIS was used to create interpolation maps of total antibiotic resistance gene distribution in soil.	There was a significant positive correlation between the abundance of antibiotic resistance genes and mobile genetic elements, suggesting potential mobility of ARGs in peri-urban areas. The authors conclude that anthropogenic activities are driving the spatial and temporal distribution of antibiotic pollution.
(Yopasa-Arenas and Fostier, 2018)	Estimation of the exposure risk of soil and groundwater to pollution by growth promoters and anticoccidial additives originating from animal husbandry by GIS.	To identify the areas vulnerable to pollution of coccidiostats and growth promoters a qualitative additive model of GIS layers including release, exposure and consequences was created. Exposure risk was estimated with qualitative multi-criteria decision analysis, using the release, exposure, and consequence data in weighted overlay GIS mapping.	Higher risks were found for the mid-west, southeast and south regions of Brazil. Groundwater was more vulnerable to contamination than soil. The method described showed to be a useful tool to analyse compounds of interest that are likely to pollute the environment. The main limitation was the access to good data to establish reliable GIS layers for the risk estimation.
(Zhao <i>et al.</i>, 2020)	Linking land use patterns to the distribution of antibiotic pollution based on soil samples.	Remote sensing was used to identify land use types and roads from satellite images. Different buffer zones around sampling sites were created to make possible a comparison depending on distance to different land use types, and the proportions of the different land use types. The buffers were between 50 m and 1 km. Overlay maps were created. Land use types were grouped into cropland, orchard, village, forestland, and main roads.	Land use patterns significantly influenced the presence and concentration of antibiotics in buffer zones with a radius of 350 metres. There were also significant seasonal variations in antibiotic distributions in the soil. Cropland had the highest antibiotic soil contamination, and agriculture and road networks were suggested as important risk factors.