

```

> medi <- data.frame(MEDICINE=rep(c("M1", "M2", "M3"),times=1,each=5),
+                     SUBJECT=rep(c("S1", "S2", "S3", "S4", "S5"),times=3,each=1),
+                     EFFECT=c(0.62,0.77,0.33,0.27,0.84,0.15,0.13,0.29,0.18,0.62,0.72,0.13,0.09,0.57,0.44),
+                     PROBLEM=c(0.11,0.05,0.16,0.89,0.77,0.13,0.77,0.22,0.10,0.21,0.33,0.31,0.42,0.55,0.66))
>
> #약물 별 평균 효과 발생률
> tapply(medi$EFFECT,medi$MEDICINE,function(x) {mean(x)})
  M1    M2    M3
0.566 0.274 0.390
> #약물 별 평균 문제 발생률
> tapply(medi$PROBLEM,medi$MEDICINE,function(x) {mean(x)})
  M1    M2    M3
0.396 0.286 0.454
> #평균 문제 발생률이 높은 약물부터 순서대로 출력
> sort(tapply(medi$PROBLEM,medi$MEDICINE,function(x) {mean(x)}),T)
  M3    M1    M2
0.454 0.396 0.286

```