

Sample size calculation for estrogen and urine microbiome study

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```
foo <- apply.labels(aids[,c("death", "CD4", "drug", "gender", "prevOI", "AZT")],  
                   c("Died", "CD4", "Group", "Gender", "Previous OI", "AZT"))  
  
tex.tableone(tidy.tableone(df = foo,  
                           grpvar="drug",  
                           testTypes = rep("t", 6),  
                           caption = "Clinical characteristics."))
```

Table 1: Clinical characteristics.

	n	ddC (n=717)	ddI (n=688)	Combined (n=1405)	p
Died	1405	0.3 ± 0.4	0.3 ± 0.5	0.3 ± 0.5	0.23 ^a
CD4	1405	6.7 ± 4.9	7.3 ± 5	7 ± 5	0.027 ^a
Gender	1405				0.729 ^b
- female		9% (62)	8% (55)	8% (117)	
- male		91% (655)	92% (633)	92% (1288)	
Previous OI	1405				0.577 ^b
- noAIDS		38% (271)	39% (271)	39% (542)	
- AIDS		62% (446)	61% (417)	61% (863)	
AZT	1405				0.182 ^b
- intolerance		63% (454)	67% (460)	65% (914)	
- failure		37% (263)	33% (228)	35% (491)	

x ± x indicates mean ± standard deviation.

^a Student's *t*-test (two-sided)

^b Pearson's chi-squared test