Customizable Tables with Stata

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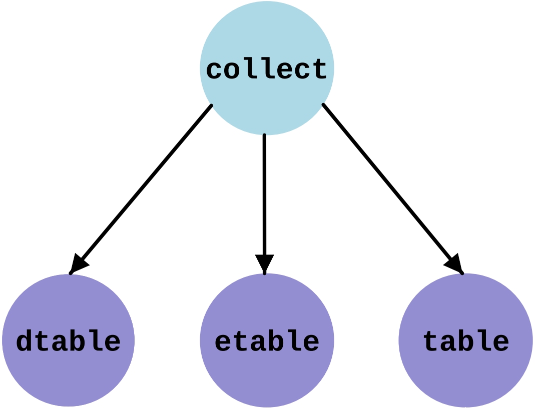
German Stata Conference

- Creating customized tables
  - Motivating examples
  - Creating tables of summary statistics with `dtable`
  - Creating tables of regression results with `etable`
  - Creating cross-tabulations and more with `table`
  - Creating fully customized tables using the `collect` suite
- Incorporating tables in complete reports


collect
dtable
etable
table

You can create a table of summary statistics,

Table 1: Summary statistics

	Hypertension		
	No	Yes	Total
Age (years)	42.2 (16.8)	55.0 (14.9)	47.6 (17.2)
Body mass index (BMI)	24.2 (4.1)	27.4 (5.3)	25.5 (4.9)
Sex			
Male	2,611 (43.7%)	2,304 (52.7%)	4,915 (47.5%)
Female	3,364 (56.3%)	2,072 (47.3%)	5,436 (52.5%)
Race			
White	5,317 (89.0%)	3,748 (85.6%)	9,065 (87.6%)
Black	545 (9.1%)	541 (12.4%)	1,086 (10.5%)
Other	113 (1.9%)	87 (2.0%)	200 (1.9%)
Health status			
Excellent	1,649 (27.7%)	758 (17.3%)	2,407 (23.3%)
Very good	1,666 (27.9%)	925 (21.2%)	2,591 (25.1%)
Good	1,572 (26.4%)	1,366 (31.2%)	2,938 (28.4%)
Fair	766 (12.8%)	904 (20.7%)	1,670 (16.2%)
Poor	310 (5.2%)	419 (9.6%)	729 (7.1%)
Serum cholesterol (mg/dL)	208.7 (47.3)	229.9 (49.6)	217.7 (49.4)
Serum triglycerides (mg/dL)	129.2 (83.9)	166.0 (109.2)	143.9 (96.5)
High density lipids (mg/dL)	49.9 (14.1)	49.2 (14.5)	49.6 (14.3)

Mean and standard deviation reported for continuous variables.

And export your table to a Word document,

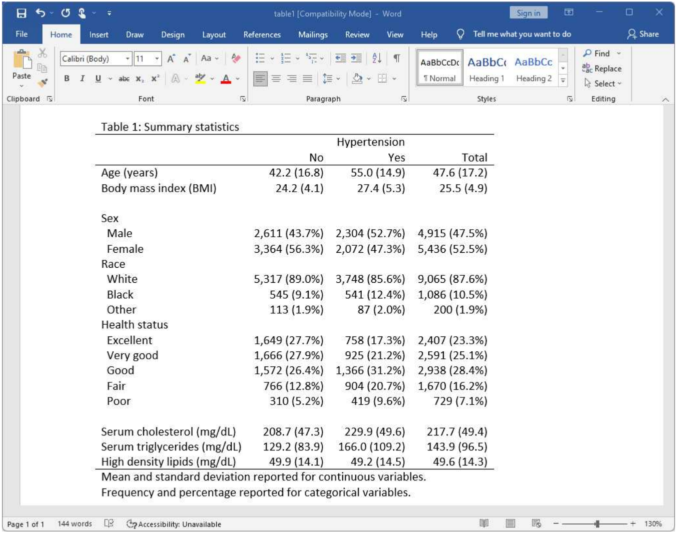


Table 1: Summary statistics

	Hypertension		
	No	Yes	Total
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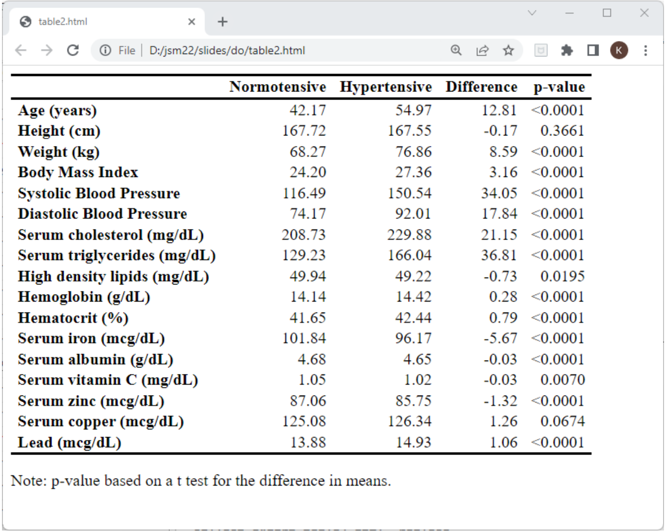
Serum cholesterol (mg/dL)	208.7 (47.3)	229.9 (49.6)	217.7 (49.4)
Serum triglycerides (mg/dL)	129.2 (83.9)	166.0 (109.2)	143.9 (96.5)
High density lipids (mg/dL)	49.9 (14.1)	49.2 (14.5)	49.6 (14.3)

Mean and standard deviation reported for continuous variables.
Frequency and percentage reported for categorical variables.

You can create a table of means and *t* tests of differences,

```
-------------------------------------------------------------------------------
                             Normotensive   Hypertensive   Difference   p-value
-------------------------------------------------------------------------------
Age (years)                         42.17          54.97        12.81   <0.0001
Height (cm)                        167.72         167.55        -0.17    0.3661
Weight (kg)                         68.27          76.86         8.59   <0.0001
Body Mass Index                     24.20          27.36         3.16   <0.0001
Systolic Blood Pressure            116.49         150.54        34.05   <0.0001
Diastolic Blood Pressure            74.17          92.01        17.84   <0.0001
Serum cholesterol (mg/dL)          208.73         229.88        21.15   <0.0001
Serum triglycerides (mg/dL)        129.23         166.04        36.81   <0.0001
High density lipids (mg/dL)         49.94          49.22        -0.73    0.0195
Hemoglobin (g/dL)                   14.14          14.42         0.28   <0.0001
Hematocrit (%)                      41.65          42.44         0.79   <0.0001
Serum iron (mcg/dL)                101.84          96.17        -5.67   <0.0001
Serum albumin (g/dL)                 4.68           4.65        -0.03   <0.0001
Serum vitamin C (mg/dL)              1.05           1.02        -0.03    0.0070
Serum zinc (mcg/dL)                 87.06          85.75        -1.32   <0.0001
Serum copper (mcg/dL)              125.08         126.34         1.26    0.0674
Lead (mcg/dL)                       13.88          14.93         1.06   <0.0001
-------------------------------------------------------------------------------
Note: p-value based on a t test for the difference in means.
```

And export your table to HTML,



	Normotensive	Hypertensive	Difference	p-value
Age (years)	42.17	54.97	12.81	<0.0001
Height (cm)	167.72	167.55	-0.17	0.3661
Weight (kg)	68.27	76.86	8.59	<0.0001
Body Mass Index	24.20	27.36	3.16	<0.0001
Systolic Blood Pressure	116.49	150.54	34.05	<0.0001
Diastolic Blood Pressure	74.17	92.01	17.84	<0.0001
Serum cholesterol (mg/dL)	208.73	229.88	21.15	<0.0001
Serum triglycerides (mg/dL)	129.23	166.04	36.81	<0.0001
High density lipids (mg/dL)	49.94	49.22	-0.73	0.0195
Hemoglobin (g/dL)	14.14	14.42	0.28	<0.0001
Hematocrit (%)	41.65	42.44	0.79	<0.0001
Serum iron (mcg/dL)	101.84	96.17	-5.67	<0.0001
Serum albumin (g/dL)	4.68	4.65	-0.03	<0.0001
Serum vitamin C (mg/dL)	1.05	1.02	-0.03	0.0070
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Lead (mcg/dL)	13.88	14.93	1.06	<0.0001

Note: p-value based on a t test for the difference in means.

You can create a table of regression results,

Table 3: Logistic regression results

	1	2	3
Body mass index (BMI)	1.145	1.147	1.148
	(0.006)	(0.006)	(0.006)
Age (years)	1.046	1.047	1.034
	(0.001)	(0.001)	(0.002)
Female		0.617	0.152
		(0.028)	(0.023)
Female x Age (years)			1.028
			(0.003)
Intercept	0.002	0.003	0.005
	(0.000)	(0.000)	(0.001)
AIC	11812.48	11698.99	11605.77
BIC	11834.21	11727.97	11642.00

Odds ratio (Std. Err.)

And export your table to a PDF,

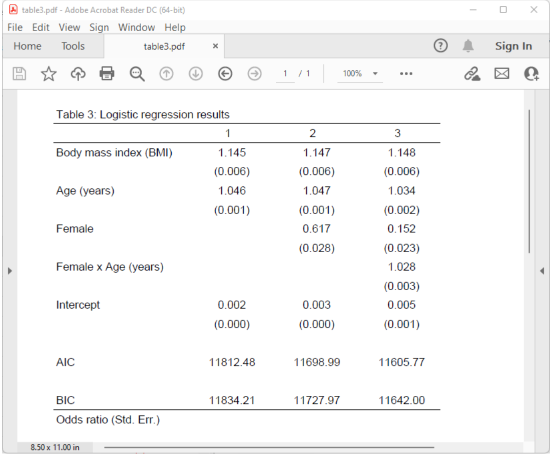
table3.pdf - Adobe Acrobat Reader DC (64-bit)
File Edit View Sign Window Help
Home Tools table3.pdf ×
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Table 3: Logistic regression results

	1	2	3
Body mass index (BMI)	1.145	1.147	1.148
	(0.006)	(0.006)	(0.006)
Age (years)	1.046	1.047	1.034
	(0.001)	(0.001)	(0.002)
Female		0.617	0.152
		(0.028)	(0.023)
Female x Age (years)			1.028
			(0.003)
Intercept	0.002	0.003	0.005
	(0.000)	(0.000)	(0.001)
AIC	11812.48	11698.99	11605.77
BIC	11834.21	11727.97	11642.00

Odds ratio (Std. Err.)

We can use the `dtable`, `etable`, `table`, and `collect` commands to create tables of

- Summary statistics, including a classic Table 1
- Results of classical hypothesis tests
- Cross-tabulations
- Regression results
- Postestimation tests
- Combinations of the above
- Results returned by any Stata commands

We can customize tables by changing

- Table layout
- Numeric formats
- Labels appearing on rows and columns
- Stars and other added text
- Font type, size, and color
- Shading, borders, margins, alignment, and more

We can export the customized tables to

- Word
- Excel
- LaTeX
- PDF
- Markdown
- HTML
- SMCL
- Plain text

dtable

The `dtable` command produces tables of summary statistics.

It can report separate summary statistics for groups and perform tests comparing groups.

To demonstrate, we will use NHANES II data.

```
. webuse nhanes2l, clear
(Second National Health and Nutrition Examination Survey)

. describe age sex race height weight bmi highbp
>          bpsystol bpdiast tcresult hdresult

Variable      Storage   Display    Value
    name         type    format    label      Variable label
──────────────────────────────────────────────────────────────────────────────────

age             byte    %9.0g                 Age (years)
sex             byte    %9.0g      sex        Sex
race            byte    %9.0g      race       Race
height          float   %9.0g                 Height (cm)
weight          float   %9.0g                 Weight (kg)
bmi             float   %9.0g                 Body mass index (BMI)
highbp          byte    %8.0g               * High blood pressure
bpsystol        int     %9.0g                 Systolic blood pressure
bpdiast         int     %9.0g                 Diastolic blood pressure
tcresult        int     %9.0g                 Serum cholesterol (mg/dL)
hdresult        int     %9.0g                 High-density lipids (mg/dL)
```

The most basic syntax for `dtable` is

```
. dtable [varlist]
```

where *varlist* includes both continuous and factor variables, specified in the order we would like to see them in the table.

```
. dtable age bmi i.sex i.hlthstat tcresult tgresult
────────────────────────────────────────────
                                 Summary
────────────────────────────────────────────
N                                     10,351
Age (years)                  47.580 (17.215)
Body mass index (BMI)         25.538 (4.915)
Sex
  Male                         4,915 (47.5%)
  Female                       5,436 (52.5%)
Health status
  Excellent                    2,407 (23.3%)
  Very good                    2,591 (25.1%)
  Good                         2,938 (28.4%)
  Fair                         1,670 (16.2%)
  Poor                            729 (7.1%)
Serum cholesterol (mg/dL)   217.670 (49.387)
Serum triglycerides (mg/dL) 143.896 (96.496)
────────────────────────────────────────────
```

We specify the by() option to request summary statistics for multiple groups.

```
. dtable age bmi i.sex i.hlthstat tcresult tgresult,
> by(highbp)
────────────────────────────────────────────────────────────────────────────────
                                            High blood pressure
                                     0                1               Total
────────────────────────────────────────────────────────────────────────────────
N                              5,975 (57.7%)     4,376 (42.3%)  10,351 (100.0%)
Age (years)                  42.165 (16.772)   54.973 (14.909)  47.580 (17.215)
Body mass index (BMI)         24.202 (4.100)    27.361 (5.332)   25.538 (4.915)
Sex
  Male                         2,611 (43.7%)     2,304 (52.7%)    4,915 (47.5%)
  Female                       3,364 (56.3%)     2,072 (47.3%)    5,436 (52.5%)
Health status
  Excellent                    1,649 (27.7%)       758 (17.3%)    2,407 (23.3%)
  Very good                    1,666 (27.9%)       925 (21.2%)    2,591 (25.1%)
  Good                         1,572 (26.4%)     1,366 (31.2%)    2,938 (28.4%)
  Fair                           766 (12.8%)       904 (20.7%)    1,670 (16.2%)
  Poor                            310 (5.2%)        419 (9.6%)       729 (7.1%)
Serum cholesterol (mg/dL)   208.727 (47.287)  229.880 (49.583) 217.670 (49.387)
Serum triglycerides (mg/dL) 129.228 (83.930) 166.043 (109.200) 143.896 (96.496)
────────────────────────────────────────────────────────────────────────────────
```

The by() option allows suboptions for customizing the table:

- nototals suppresses the column of summary statistics for the full dataset.
- tests requests that tests be reported comparing summary statistics across groups.

```
. dtable age bmi i.sex i.hlthstat tcresult tgresult,
> by(highbp, nototals tests)
note: using test regress across levels of highbp for age, bmi, tcresult, and
      tgresult.
note: using test pearson across levels of highbp for sex and hlthstat.
─────────────────────────────────────────────────────────────────────
                                       High blood pressure
                                    0                1          Test
─────────────────────────────────────────────────────────────────────
N                              5,975 (57.7%)     4,376 (42.3%)
Age (years)                  42.165 (16.772)   54.973 (14.909) <0.001
Body mass index (BMI)         24.202 (4.100)    27.361 (5.332) <0.001
Sex
  Male                         2,611 (43.7%)     2,304 (52.7%) <0.001
  Female                       3,364 (56.3%)     2,072 (47.3%)
Health status
  Excellent                    1,649 (27.7%)       758 (17.3%) <0.001
  Very good                    1,666 (27.9%)       925 (21.2%)
  Good                         1,572 (26.4%)     1,366 (31.2%)
  Fair                           766 (12.8%)       904 (20.7%)
  Poor                            310 (5.2%)        419 (9.6%)
Serum cholesterol (mg/dL)   208.727 (47.287)  229.880 (49.583) <0.001
Serum triglycerides (mg/dL) 129.228 (83.930) 166.043 (109.200) <0.001
─────────────────────────────────────────────────────────────────────
```

The first line of the table provides the frequency and percentage of the sample size in each group.

The `sample()` option allows us to specify the title for this first row, which sample statistics to report, and where to place the statistics.

- The `statistics()` suboption specifies whether frequencies, percentages, or proportions are reported.
- The `place()` suboption specifies where the sample statistics are reported.

The `nformat()` and `sformat()` options specify the numeric and string formats for the sample statistics.

```
. dtable age bmi i.sex i.hlthstat tcresult tgresult,
> by(highbp, nototals tests)
> sample(, place(seplabels)) sformat("N=%s" frequency)
note: using test regress across levels of highbp for age, bmi, tcresult, and
      tgresult.
note: using test pearson across levels of highbp for sex and hlthstat.
─────────────────────────────────────────────────────────────────────
                                    High blood pressure
                                     0                 1          Test
                              N=5,975 (57.7%)  N=4,376 (42.3%)
─────────────────────────────────────────────────────────────────────
Age (years)                   42.165 (16.772)   54.973 (14.909) <0.001
Body mass index (BMI)          24.202 (4.100)    27.361 (5.332) <0.001
Sex
  Male                         2,611 (43.7%)     2,304 (52.7%) <0.001
  Female                       3,364 (56.3%)     2,072 (47.3%)
Health status
  Excellent                    1,649 (27.7%)       758 (17.3%) <0.001
  Very good                    1,666 (27.9%)       925 (21.2%)
  Good                         1,572 (26.4%)     1,366 (31.2%)
  Fair                           766 (12.8%)       904 (20.7%)
  Poor                            310 (5.2%)        419 (9.6%)
Serum cholesterol (mg/dL)    208.727 (47.287) 229.880 (49.583) <0.001
Serum triglycerides (mg/dL) 129.228 (83.930) 166.043 (109.200) <0.001
─────────────────────────────────────────────────────────────────────
```

By default, the frequency and percentage are reported for each factor variables while the mean and standard deviation are reported for each continuous variable.

Pearson's chi-squared tests are reported by default for factor variables, and linear-regression-based tests are reported for continuous variables.

The `factor()` and `continuous()` options allow you to change these defaults for individual variables or for all variables of one type.

- The `statistics()` suboption specifies the statistics to be reported.
- The `test()` suboption specifies the test to be reported.

The `nformat()` and `sformat()` options specify the numeric and string formats for the selected statistics.

```
. dtable age bmi i.sex i.hlthstat tcresult tgresult,
> by(highbp, nototals tests)
> sample(, place(seplabels)) sformat("N=%s" frequency)
> continuous(, statistics(median iqr) test(kwallis)) sformat("(%s)" iqr)
note: using test kwallis across levels of highbp for age, bmi, tcresult, and
      tgresult.
note: using test pearson across levels of highbp for sex and hlthstat.
─────────────────────────────────────────────────────────────────────
                                       High blood pressure
                                    0                1          Test
                             N=5,975 (57.7%)  N=4,376 (42.3%)
─────────────────────────────────────────────────────────────────────
Age (years)                  38.000 (33.000)   60.000 (22.000) <0.001
Body mass index (BMI)         23.690 (5.002)    26.528 (6.364) <0.001
Sex
  Male                         2,611 (43.7%)     2,304 (52.7%) <0.001
  Female                       3,364 (56.3%)     2,072 (47.3%)
Health status
  Excellent                    1,649 (27.7%)       758 (17.3%) <0.001
  Very good                    1,666 (27.9%)       925 (21.2%)
  Good                         1,572 (26.4%)     1,366 (31.2%)
  Fair                           766 (12.8%)       904 (20.7%)
  Poor                            310 (5.2%)        419 (9.6%)
Serum cholesterol (mg/dL)   203.000 (63.000)  226.000 (64.000) <0.001
Serum triglycerides (mg/dL) 108.000 (77.000) 142.000 (103.000) <0.001
─────────────────────────────────────────────────────────────────────
```

We can make the table publication ready by adding a title and notes explaining the tests.

- `title()` adds a title to the top of the table.
- `note()` adds a note below the table. This option may be repeated to add multiple notes on separate lines.

```
. dtable age bmi i.sex i.hlthstat tcresult tgresult,
> by(highbp, nototals tests notestnotes)
> sample(, place(seplabels)) sformat("N=%s" frequency)
> continuous(, statistics(median iqr) test(kwallis)) sformat("(%s)" iqr)
> title("Table 1: Descriptive statistics")
> note("Frequency, percentage, and Pearson´s chi-squared test reported for factor
> variables.")
> note("Median, IQR, and Kruskal-Wallis test reported for continuous variables.")
```

```
Table 1: Descriptive statistics
---------------------------------------------------------------------
                                     High blood pressure
                                    0                 1          Test
                             N=5,975 (57.7%)  N=4,376 (42.3%)
---------------------------------------------------------------------
Age (years)                  38.000 (33.000)   60.000 (22.000) <0.001
Body mass index (BMI)         23.690 (5.002)    26.528 (6.364) <0.001
Sex
  Male                         2,611 (43.7%)     2,304 (52.7%) <0.001
  Female                       3,364 (56.3%)     2,072 (47.3%)
Health status
  Excellent                    1,649 (27.7%)       758 (17.3%) <0.001
  Very good                    1,666 (27.9%)       925 (21.2%)
  Good                         1,572 (26.4%)     1,366 (31.2%)
  Fair                           766 (12.8%)       904 (20.7%)
  Poor                            310 (5.2%)        419 (9.6%)
Serum cholesterol (mg/dL)   203.000 (63.000)  226.000 (64.000) <0.001
Serum triglycerides (mg/dL) 108.000 (77.000) 142.000 (103.000) <0.001
---------------------------------------------------------------------
Frequency, percentage, and Pearson´s chi-squared test reported for factor
variables.
Median, IQR, and Kruskal-Wallis test reported for continuous variables.
```

Finally, we can use the export() option to export our table to a variety of formats.

```
. dtable age bmi i.sex i.hlthstat tcresult tgresult,
> by(highbp, nototals tests notestnotes)
> sample(, place(seplabels)) sformat("N=%s" frequency)
> continuous(, statistics(median iqr) test(kwallis)) sformat("(%s)" iqr)
> title("Table 1: Descriptive statistics")
> note("Frequency, percentage, and Pearson´s chi-squared test reported for factor
> variables.")
> note("Median, IQR, and Kruskal-Wallis test reported for continuous variables.")
> export(sumtable.docx)
```

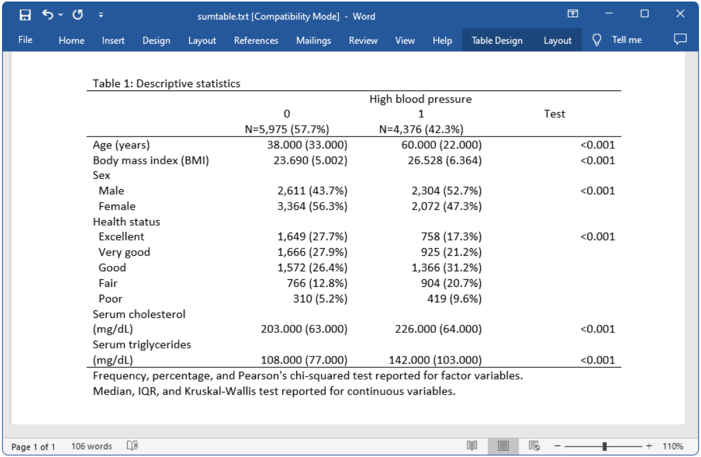


Table 1: Descriptive statistics

	High blood pressure		
	0	1	Test
	N=5,975 (57.7%)	N=4,376 (42.3%)	
Age (years)	38.000 (33.000)	60.000 (22.000)	<0.001
Body mass index (BMI)	23.690 (5.002)	26.528 (6.364)	<0.001
Sex			
Male	2,611 (43.7%)	2,304 (52.7%)	<0.001
Female	3,364 (56.3%)	2,072 (47.3%)	
Health status			
Excellent	1,649 (27.7%)	758 (17.3%)	<0.001
Very good	1,666 (27.9%)	925 (21.2%)	
Good	1,572 (26.4%)	1,366 (31.2%)	
Fair	766 (12.8%)	904 (20.7%)	
Poor	310 (5.2%)	419 (9.6%)	
Serum cholesterol (mg/dL)	203.000 (63.000)	226.000 (64.000)	<0.001
Serum triglycerides (mg/dL)	108.000 (77.000)	142.000 (103.000)	<0.001

Frequency, percentage, and Pearson's chi-squared test reported for factor variables.
Median, IQR, and Kruskal-Wallis test reported for continuous variables.

Tables created by `dtable` can be customized in many additional ways. Type

```
. help dtable
```

in Stata to see the full syntax of this command.

etable

After fitting any regression model—whether a linear regression, logistic regression, Cox proportional hazards model, multilevel model, or any other regression model available in Stata—we can use the `etable` command to create a table of regression results.

We can also use `etable` to create a table comparing results from multiple models.

To create a table, we simply type `etable` after fitting a model to create the default table. To demonstrate, we first fit a logistic regression model.

```
. logistic highbp bmi age
Logistic regression                                    Number of obs =  10,351
                                                       LR chi2(2)    = 2295.05
                                                       Prob > chi2   =  0.0000
Log likelihood = -5903.2393                            Pseudo R2     =  0.1628
------------------------------------------------------------------------------
      highbp | Odds ratio   Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
         bmi |   1.145469   .0058173    26.74   0.000     1.134124    1.156928
         age |   1.046239   .0014489    32.64   0.000     1.043403    1.049083
       _cons |    .002455    .000372   -39.66   0.000     .0018242    .0033038
------------------------------------------------------------------------------
Note: _cons estimates baseline odds.
```

Then we create our table of results.

```
. etable
──────────────────────────────
                        highbp
──────────────────────────────
Body mass index (BMI)    1.145
                       (0.006)
Age (years)              1.046
                       (0.001)
Intercept                0.002
                       (0.000)
Number of observations   10351
──────────────────────────────
```

By default, `etable` reports the coefficients or related statistics reported by the regression command (odds ratios in this case). The corresponding standard errors are reported in parentheses.

We can request that different statistics related to each coefficient be reported by specifying the cstat() option.

Instead of reporting odds ratios and standard errors, perhaps we want to report odds ratios and confidence intervals. We type

```
. etable, cstat(_r_b) cstat(_r_ci)
----------------------------------------
                             highbp
----------------------------------------
Body mass index (BMI)                1.145
                       [1.134      1.157]
Age (years)                          1.046
                       [1.043      1.049]
Intercept                            0.002
                       [0.002      0.003]
Number of observations               10351
----------------------------------------
```

Each result is specified separately to allow different formatting options. Similar to `table`, we can specify an `nformat()` and `sformat()` for each result. We can also specify the delimiter to be used between the upper and lower bound of the confidence interval with `cidelimiter()`.

```
. etable, cstat(_r_b) cstat(_r_ci, cidelimiter(", ") nformat(%4.2f))
────────────────────────────────────
                          highbp    
────────────────────────────────────
Body mass index (BMI)          1.145
                        [1.13, 1.16]
Age (years)                    1.046
                        [1.04, 1.05]
Intercept                      0.002
                        [0.00, 0.00]
Number of observations         10351
────────────────────────────────────
```

We could request that the *p*-value be displayed alongside each odds ratio. However, another alternative is to request that stars corresponding to specific *p*-value levels be displayed.

```
. etable, showstars showstarsnote
---------------------------------
                           highbp
---------------------------------
Body mass index (BMI)    1.145 **
                       (0.006)
Age (years)              1.046 **
                       (0.001)
Intercept                0.002 **
                       (0.000)
Number of observations   10351
---------------------------------
** p<.01, * p<.05
```

We can also request a variety of overall model statistics by specifying the mstat() option.

Rather than the number of observations, we request that AIC and BIC be reported so that we can later compare this model to others.

```
. etable, mstat(aic) mstat(bic)
------------------------------
                        highbp
------------------------------
Body mass index (BMI)    1.145
                       (0.006)
Age (years)              1.046
                       (0.001)
Intercept                0.002
                       (0.000)
AIC                   11812.48
BIC                   11834.21
------------------------------
```

Suppose we want to compare the model we fit above to two other models. We can build our table in two ways. The first is to use the `append` option with `etable` after fitting the second and third models.

We begin by fitting the first model and using `etable` just as we did previously.

```
. logistic highbp bmi age
Logistic regression                                     Number of obs =  10,351
                                                        LR chi2(2)    = 2295.05
                                                        Prob > chi2   =  0.0000
Log likelihood = -5903.2393                             Pseudo R2     =  0.1628
─────────────┬────────────────────────────────────────────────────────────────
      highbp │ Odds ratio   Std. err.      z    P>|z|     [95% conf. interval]
─────────────┼────────────────────────────────────────────────────────────────
         bmi │   1.145469   .0058173    26.74   0.000     1.134124    1.156928
         age │   1.046239   .0014489    32.64   0.000     1.043403    1.049083
       _cons │    .002455    .000372   -39.66   0.000     .0018242    .0033038
─────────────┴────────────────────────────────────────────────────────────────
Note: _cons estimates baseline odds.
```

```
. etable, mstat(aic) mstat(bic)
──────────────────────────────
                        highbp
──────────────────────────────
Body mass index (BMI)    1.145
                       (0.006)
Age (years)              1.046
                       (0.001)
Intercept                0.002
                       (0.000)
AIC                   11812.48
BIC                   11834.21
──────────────────────────────
```

Next, we fit our second model, which includes sex as a regressor, and then specify the append option with etable.

```
. logistic highbp bmi age i.sex

Logistic regression                                     Number of obs =  10,351
                                                        LR chi2(3)    = 2410.54
                                                        Prob > chi2   =  0.0000
Log likelihood = -5845.4948                             Pseudo R2     =  0.1709

------------------------------------------------------------------------------
      highbp | Odds ratio   Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
         bmi |   1.147006    .005827    27.00   0.000     1.135642    1.158484
         age |   1.047058   .0014632    32.91   0.000     1.044194     1.04993
             |
         sex |
     Female  |   .6172715   .0278625   -10.69   0.000     .5650079    .6743695
       _cons |   .0029059   .0004428   -38.33   0.000     .0021556    .0039174
------------------------------------------------------------------------------
Note: _cons estimates baseline odds.
```

```
. etable, append
───────────────────────────────────────
                       highbp   highbp 
───────────────────────────────────────
Body mass index (BMI)    1.145    1.147
                       (0.006)  (0.006)
Age (years)              1.046    1.047
                       (0.001)  (0.001)
Sex
  Female                          0.617
                                (0.028)
Intercept                0.002    0.003
                       (0.000)  (0.000)
AIC                   11812.48 11698.99
BIC                   11834.21 11727.97
───────────────────────────────────────
```

Similarly, we fit our third model, which includes an interaction between age and sex, and again specify append with etable.

```
. logistic highbp bmi c.age##i.sex

Logistic regression                                    Number of obs =  10,351
                                                       LR chi2(4)    = 2505.76
                                                       Prob > chi2   =  0.0000
Log likelihood = -5797.8856                            Pseudo R2     =  0.1777

------------------------------------------------------------------------------
      highbp | Odds ratio   Std. err.      z    P>|z|     [95% conf. interval]
-------------+----------------------------------------------------------------
         bmi |   1.147615   .0058948    26.80   0.000     1.136119    1.159226
         age |   1.034097   .0019132    18.12   0.000     1.030354    1.037854
             |
         sex |
     Female  |   .1522122   .0232902   -12.30   0.000     .1127732    .2054439
             |
   sex#c.age |
     Female  |      1.028   .0029402     9.66   0.000     1.022253    1.033779
             |
       _cons |   .0052605   .0008567   -32.22   0.000      .003823    .0072384
------------------------------------------------------------------------------
Note: _cons estimates baseline odds.
```

```
. etable, append
────────────────────────────────────────────────
                       highbp   highbp   highbp 
────────────────────────────────────────────────
Body mass index (BMI)    1.145    1.147    1.148
                       (0.006)  (0.006)  (0.006)
Age (years)              1.046    1.047    1.034
                       (0.001)  (0.001)  (0.002)
Sex
  Female                          0.617    0.152
                                (0.028)  (0.023)
Sex # Age (years)
  Female                                   1.028
                                         (0.003)
Intercept                0.002    0.003    0.005
                       (0.000)  (0.000)  (0.001)
AIC                   11812.48 11698.99 11605.77
BIC                   11834.21 11727.97 11642.00
────────────────────────────────────────────────
```

Finally, we modify our table by adding a title, notes, and numbers for the column headings. We specify the `replay` option to make these modifications to the existing table.

```
. etable, replay column(index)
>   title("Table 2: Logistic regression results")
>   notes("Odds ratio (Std. Err.)")
Table 2: Logistic regression results
------------------------------------------------
                             1        2        3
------------------------------------------------
Body mass index (BMI)    1.145    1.147    1.148
                       (0.006)  (0.006)  (0.006)
Age (years)              1.046    1.047    1.034
                       (0.001)  (0.001)  (0.002)
Sex
  Female                          0.617    0.152
                                (0.028)  (0.023)
Sex # Age (years)
  Female                                   1.028
                                         (0.003)
Intercept                0.002    0.003    0.005
                       (0.000)  (0.000)  (0.001)
AIC                   11812.48 11698.99 11605.77
BIC                   11834.21 11727.97 11642.00
------------------------------------------------
Odds ratio (Std. Err.)
```

We could have fit all three models and then created the same table with a single etable command as follows:

```
. logistic highbp bmi age
. estimates store M1
. logistic highbp bmi age i.sex
. estimates store M2
. logistic highbp bmi c.age##i.age
. estimates store M3
. etable, estimates(M1 M2 M3) mstat(aic) mstat(bic)
          title("Table 2: Logistic regression results")
          notes("Odds ratio (Std. Err.)")
```

The `etable` command also allows us to create tables of marginal means and marginal effects produced by `margins` and more. Type

```
. help etable
```

in Stata to see the full syntax of this command.

`table`

The `table` command is a flexible command that can produce cross-tabulations; one-way, two-way, and multiway tables of summary statistics; and tables or results from other Stata commands.

A simplified syntax for the `table` command is

. `table` (*row variables*) (*column variables*)

To create a one-way tabulation, we can specify a single row variable in the first set of parenthesis or a single column variable in the second set of parentheses.

```
. table (highbp) ()

--------------------------------
                    |  Frequency
--------------------+-----------
High blood pressure |
  0                 |      5,975
  1                 |      4,376
  Total             |     10,351
--------------------------------

. table () (highbp)

------------------------------------
          |  High blood pressure
          |       0       1    Total
----------+-------------------------
Frequency |   5,975   4,376   10,351
------------------------------------
```

To create a two-way tabulation, we specify both a row and a column variable.

```
. table (sex) (highbp)

-----------------------------------
         |   High blood pressure
         |        0        1   Total
---------+-------------------------
Sex      |
  Male   |    2,611    2,304    4,915
  Female |    3,364    2,072    5,436
  Total  |    5,975    4,376   10,351
-----------------------------------
```

We can add the `nototals` option to remove the row frequencies, column frequencies, and overall frequencies from the tabulation.

```
. table (sex) (highbp), nototals

─────────┬──────────────────────
         │ High blood pressure
         │          0          1
─────────┼──────────────────────
Sex      │
  Male   │      2,611      2,304
  Female │      3,364      2,072
─────────┴──────────────────────
```

Alternatively, we could request totals only for columns (`highbp`) or only for rows (`sex`).

```
. table (sex) (highbp), totals(highbp)

---------------------------------
         |   High blood pressure
         |          0           1
---------+-----------------------
Sex      |
  Male   |      2,611       2,304
  Female |      3,364       2,072
  Total  |      5,975       4,376
---------------------------------

. table (sex) (highbp), totals(sex)

-----------------------------------
         |   High blood pressure
         |        0         1  Total
---------+-------------------------
Sex      |
  Male   |    2,611     2,304  4,915
  Female |    3,364     2,072  5,436
-----------------------------------
```

By default, the `table` command reports frequencies. Many additional summary statistics can be specified using the `statistic()` option.

```
. table ( row variables ) ( column variables ),
          statistic( statspec )
```

We can specify the statistic() option repeatedly to display multiple statistics in a table. For example, we can request both frequencies and percentages for highbp.

```
. table () (highbp),
>       statistic(frequency)
>       statistic(percent)
────────────────────────────────────
          │
          │   High blood pressure
          │       0        1   Total
──────────┼─────────────────────────
Frequency │   5,975    4,376  10,351
Percent   │   57.72    42.28  100.00
────────────────────────────────────
```

We can also request multiple statistics for our two-way table. This time, we omit the totals.

```
. table (sex) (highbp),
>       statistic(frequency)
>       statistic(percent)
>       nototals

-----------------------------------------------
                 |     High blood pressure
                 |            0            1
-----------------+-----------------------------
Sex              |
  Male           |
    Frequency    |        2,611        2,304
    Percent      |        25.22        22.26
  Female         |
    Frequency    |        3,364        2,072
    Percent      |        32.50        20.02
-----------------------------------------------
```

We might instead want to compare the means and standard deviations of some continuous variables, here age and `bmi`, across the levels of `highbp`.

```
. table () (highbp),
>       statistic(mean age bmi)
>       statistic(sd age bmi)

----------------------------------------------------------
                        |      High blood pressure
                        |          0           1     Total
------------------------+---------------------------------
Mean                    |
  Age (years)           |   42.16502    54.97281  47.57965
  Body mass index (BMI) |   24.20231    27.36081   25.5376
Standard deviation      |
  Age (years)           |   16.77157    14.90897  17.21483
  Body mass index (BMI) |   4.100279    5.332119  4.914969
----------------------------------------------------------
```

We can request different statistics for different variables. In addition to the means and standard deviations of continuous variables, we can compare the frequencies and percentages of the factor variable `sex` across the levels of `highbp`.

```
. table () (highbp),
>       statistic(mean age bmi)
>       statistic(sd age bmi)
>       statistic(fvfrequency sex)
>       statistic(fvpercent sex)

----------------------------------------------------------
                          |      High blood pressure
                          |         0          1     Total
--------------------------+-------------------------------
Mean                      |
  Age (years)             |  42.16502   54.97281  47.57965
  Body mass index (BMI)   |  24.20231   27.36081   25.5376
Standard deviation        |
  Age (years)             |  16.77157   14.90897  17.21483
  Body mass index (BMI)   |  4.100279   5.332119  4.914969
Factor-variable frequency |
  Sex=Male                |     2,611      2,304     4,915
  Sex=Female              |     3,364      2,072     5,436
Factor-variable percent   |
  Sex=Male                |     43.70      52.65     47.48
  Sex=Female              |     56.30      47.35     52.52
----------------------------------------------------------
```

We can change the numeric format and the string format of the results in our table by using the `nformat()` and `sformat()` options.

```
. table ( row variables ) ( column variables ),
        nformat() sformat()
```

We can modify the numeric and string formats of the reported statistics by specifying the nformat() and sformat() options.

```
. table () (highbp),
        statistic(mean age bmi)
        statistic(sd age bmi)
        statistic(fvfrequency sex)
        statistic(fvpercent sex)
        nformat(%5.2f mean sd)
        sformat("(%s%%)" fvpercent)
        sformat("(%s)" sd)
```

```
--------------------------------------------------------------------------
                                  |       High blood pressure
                                  |         0           1       Total
----------------------------------+---------------------------------------
Mean                              |
  Age (years)                     |     42.17       54.97       47.58
  Body mass index (BMI)           |     24.20       27.36       25.54
Standard deviation                |
  Age (years)                     |   (16.77)     (14.91)     (17.21)
  Body mass index (BMI)           |    (4.10)      (5.33)      (4.91)
Factor variable frequency         |
  Sex=Male                        |     2,611       2,304       4,915
  Sex=Female                      |     3,364       2,072       5,436
Factor variable percent           |
  Sex=Male                        |  (43.70%)    (52.65%)    (47.48%)
  Sex=Female                      |  (56.30%)    (47.35%)    (52.52%)
--------------------------------------------------------------------------
```

The `table` command also allows us to specify keywords in the row and column specifications to further control the layout of the table.

`. table (`*rowspec*`) (`*colspec*`),` *options*

`result`	requested statistics
`var`	variables from statistic() option
`across`	index across() specifications
`colname`	column names for matrix statistics
`rowname`	row names for matrix statistics
`coleq`	column equation names for matrix statistics
`roweq`	row equation names for matrix statistics
`command`	index option command()
`statcmd`	index options statistic() and command()

We modify our table so that the rows to are organized by variables (var) and then statistics (result) nested within variables.

```
. table (var result) (highbp),
        statistic(mean age bmi)
        statistic(sd age bmi)
        statistic(fvfrequency sex)
        statistic(fvpercent sex)
        nformat(%5.2f mean sd)
        sformat("(%s%%)" fvpercent)
        sformat("(%s)" sd)
```

```
----------------------------------------------------------------
                             |       High blood pressure
                             |          0           1      Total
-----------------------------+----------------------------------
Age (years)                  |
  Mean                       |      42.17       54.97      47.58
  Standard deviation         |    (16.77)     (14.91)    (17.21)
Body mass index (BMI)        |
  Mean                       |      24.20       27.36      25.54
  Standard deviation         |     (4.10)      (5.33)     (4.91)
Sex=Male                     |
  Factor variable frequency  |      2,611       2,304      4,915
  Factor variable percent    |   (43.70%)    (52.65%)   (47.48%)
Sex=Female                   |
  Factor variable frequency  |      3,364       2,072      5,436
  Factor variable percent    |   (56.30%)    (47.35%)   (52.52%)
----------------------------------------------------------------
```

The table command also allows us to create three-way and higher-way tables, include results from other Stata commands, add titles and notes, and more. Type

```
. help table
```

in Stata to see the full syntax of this command.

collect

collect is a suite of commands designed to collect results from various Stata commands; place the selected results into a table; customize the labels, formats, and style; and export the final table to Word, Excel, LaTeX, PDF, Markdown, HTML, and more.

Because the dtable, etable, and table commands are based on the collect system, we can also use the collect commands to further modify tables originally created by one of these commands.

The basic workflow for collecting results and building tables is

- Collect results from Stata commands—`collect` command, `collect:` prefix, `dtable`, `etable`, or `table`
- Explore the collection—`collect dims`, `collect levelsof`, and `collect label list`
- Define the rows and columns of the table—`collect layout`, `dtable`, `etable`, or `table`
- Modify items within the collection—`collect composite`, `collect recode`, `collect remap`, and `collect addtags`

- Customize the table, specifying formats, labels, font, shading, and more—`collect label`, `collect style`, `collect stars`, ...
- Export the table to Word, Excel, LaTeX, PDF, Markdown, HTML, SMCL, or plain text—`collect export`
- Save the style, labels, and collection to use and modify later—`collect label save`, `collect style save`, and `collect save`

Suppose we want to create a table that displays the results from *t* tests performed using the `ttest` command. We first take a look at the results that this command returns by typing `return list`.

```
. ttest age, by(highbp)
Two-sample t test with equal variances
------------------------------------------------------------------------------
   Group |     Obs        Mean    Std. err.   Std. dev.   [95% conf. interval]
---------+--------------------------------------------------------------------
       0 |   5,975    42.16502    .2169725    16.77157    41.73968    42.59037
       1 |   4,376    54.97281    .2253767    14.90897    54.53095    55.41466
---------+--------------------------------------------------------------------
Combined |  10,351    47.57965    .1692044    17.21483    47.24798    47.91133
---------+--------------------------------------------------------------------
    diff |           -12.80779    .3185604               -13.43223   -12.18335
------------------------------------------------------------------------------
    diff = mean(0) - mean(1)                                      t = -40.2052
H0: diff = 0                                     Degrees of freedom =    10349

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

```
. return list

scalars:
              r(level) =  95
                 r(sd) =  17.21482923023818
               r(sd_2) =  14.9089715191102
               r(sd_1) =  16.77156676799842
                 r(se) =  .3185603831285
                r(p_u) =  1
                r(p_l) =  0
                  r(p) =  0
                  r(t) =  -40.20520433030012
               r(df_t) =  10349
               r(mu_2) =  54.97280621572212
                r(N_2) =  4376
               r(mu_1) =  42.16502092050209
                r(N_1) =  5975
```

Before collecting results, we use `collect clear` to make sure any previous results are cleared from the default collection. Then we are ready to store results in the collection. We do this with the `collect` prefix. We want our table to include the mean of each group (stored in `r(mu_1)` and `r(mu_2)`) as well as the *p*-value (stored in `r(p)`).

```
. collect clear

. collect r(mu_1) r(mu_2) r(p): ttest age, by(highbp)

Two-sample t test with equal variances
------------------------------------------------------------------------------
   Group |     Obs        Mean    Std. err.   Std. dev.   [95% conf. interval]
---------+--------------------------------------------------------------------
       0 |   5,975    42.16502    .2169725    16.77157    41.73968    42.59037
       1 |   4,376    54.97281    .2253767    14.90897    54.53095    55.41466
---------+--------------------------------------------------------------------
Combined |  10,351    47.57965    .1692044    17.21483    47.24798    47.91133
---------+--------------------------------------------------------------------
    diff |           -12.80779    .3185604               -13.43223   -12.18335
------------------------------------------------------------------------------
    diff = mean(0) - mean(1)                                      t = -40.2052
H0: diff = 0                                     Degrees of freedom =    10349

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

```
. collect r(mu_1) r(mu_2) r(p): ttest weight, by(highbp)
Two-sample t test with equal variances
------------------------------------------------------------------------------
   Group |     Obs        Mean    Std. err.   Std. dev.   [95% conf. interval]
---------+--------------------------------------------------------------------
       0 |   5,975    68.26626    .1755737    13.57152    67.92207    68.61045
       1 |   4,376    76.85565    .2455179    16.24134    76.37431    77.33699
---------+--------------------------------------------------------------------
Combined |  10,351    71.89752    .1509381    15.35642    71.60165    72.19339
---------+--------------------------------------------------------------------
    diff |           -8.589386    .2936615               -9.165019   -8.013753
------------------------------------------------------------------------------
    diff = mean(0) - mean(1)                                      t = -29.2493
H0: diff = 0                                     Degrees of freedom =    10349

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

```
. collect r(mu_1) r(mu_2) r(p): ttest bmi, by(highbp)
Two-sample t test with equal variances
------------------------------------------------------------------------------
   Group |     Obs        Mean    Std. err.   Std. dev.   [95% conf. interval]
---------+--------------------------------------------------------------------
       0 |   5,975    24.20231     .053045    4.100279    24.09832    24.30629
       1 |   4,376    27.36081    .0806049    5.332119    27.20279    27.51884
---------+--------------------------------------------------------------------
Combined |  10,351     25.5376    .0483092    4.914969     25.4429    25.63229
---------+--------------------------------------------------------------------
    diff |           -3.158506    .0927376                -3.34029   -2.976723
------------------------------------------------------------------------------
    diff = mean(0) - mean(1)                                      t = -34.0585
H0: diff = 0                                     Degrees of freedom =    10349
    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

Values in a collection are organized according to their *tags*. A tag consists of a *dimension* and a *level* within the dimension. A tag is written as `dimension[level]`. Consider the means and *p*-value from the previous `ttest` command.

Value	Tag 1	Tag 2
24.202	`cmdset[3]`	`result[mu_1]`
27.361	`cmdset[3]`	`result[mu_2]`
0.000	`cmdset[3]`	`result[p]`

Our collection includes dimensions `cmdset` and `result`, among others. These results all come from the third `ttest` command, so they have level 3 of dimension `cmdset`. The level of dimension `result` corresponds to the name in the `r()` result.

How do we find out what is in the collection? We can use `collect dims` to see a list of the dimensions.

```
. collect dims

Collection dimensions
Collection: default
-----------------------------------------
                   Dimension   No. levels
-----------------------------------------
Layout, style, header, label
                      cmdset   3
               program_class   1
                      result   14
                 result_type   1
Style only
                border_block   4
                   cell_type   4
-----------------------------------------
```

We can see the levels of a specified dimension with `collect levelsof` or `collect label list`. We add option `all` to see the levels that are not labeled in addition to those that are.

```
. collect label list result, all

  Collection: default
   Dimension: result
       Label: Result
Level labels:
         N_1  Sample size n1
         N_2  Sample size n2
        df_t  Degrees of freedom
       level  Confidence level
        mu_1  x1 mean for population 1
        mu_2  x2 mean for population 2
           p  Two-sided p-value
         p_l  Lower one-sided p-value
         p_u  Upper one-sided p-value
          sd  Combined std. dev.
        sd_1  Standard deviation for first variable
        sd_2  Standard deviation for second variable
          se  Std. error
           t  t statistic
```

```
. collect label list cmdset, all

  Collection: default
   Dimension: cmdset
       Label: Command results index
Level labels:
           1
           2
           3
```

The levels of the cmdset dimension correspond to our three ttest commands. The levels of the result dimension correspond to the statistics. We use the dimension names to specify a table layout with commands on the rows and statistics on the columns by typing

```
. collect layout (cmdset) (result)
Collection: default
      Rows: cmdset
   Columns: result
   Table 1: 3 x 3
──┬────────────────────────────────────────────────────────────────────
  │ x1 mean for population 1 x1 mean for population 2 Two-sided p-value
──┼────────────────────────────────────────────────────────────────────
1 │                 42.16502                 54.97281                 0
2 │                 68.26626                 76.85565          9.1e-181
3 │                 24.20231                 27.36081          4.5e-241
──┴────────────────────────────────────────────────────────────────────
```

We could label the values of cmdset to give more information about the rows. Another option is to create meaningful tags when we collect results.

Here, we use the tags() option with the collect prefix to create a new dimension named varname. Its levels correspond to the names of the variables specified in ttest.

```
. collect clear
. collect r(mu_1) r(mu_2) r(p), tags(varname[age]): ttest age, by(highbp)
Two-sample t test with equal variances
------------------------------------------------------------------------------
   Group |     Obs        Mean    Std. err.   Std. dev.   [95% conf. interval]
---------+--------------------------------------------------------------------
       0 |   5,975    42.16502    .2169725    16.77157    41.73968    42.59037
       1 |   4,376    54.97281    .2253767    14.90897    54.53095    55.41466
---------+--------------------------------------------------------------------
Combined |  10,351    47.57965    .1692044    17.21483    47.24798    47.91133
---------+--------------------------------------------------------------------
    diff |           -12.80779    .3185604               -13.43223   -12.18335
------------------------------------------------------------------------------
    diff = mean(0) - mean(1)                                      t = -40.2052
H0: diff = 0                                     Degrees of freedom =    10349
    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

```
. collect r(mu_1) r(mu_2) r(p), tags(varname[weight]): ttest weight, by(highbp)
Two-sample t test with equal variances
───────────────────────────────────────────────────────────────────────────────
   Group │     Obs        Mean    Std. err.   Std. dev.   [95% conf. interval]
─────────┼─────────────────────────────────────────────────────────────────────
       0 │   5,975    68.26626    .1755737    13.57152    67.92207    68.61045
       1 │   4,376    76.85565    .2455179    16.24134    76.37431    77.33699
─────────┼─────────────────────────────────────────────────────────────────────
Combined │  10,351    71.89752    .1509381    15.35642    71.60165    72.19339
─────────┼─────────────────────────────────────────────────────────────────────
    diff │           -8.589386    .2936615               -9.165019   -8.013753
───────────────────────────────────────────────────────────────────────────────
    diff = mean(0) - mean(1)                                      t = -29.2493
H0: diff = 0                                     Degrees of freedom =    10349

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

```
. collect r(mu_1) r(mu_2) r(p), tags(varname[bmi]): ttest bmi, by(highbp)
Two-sample t test with equal variances
------------------------------------------------------------------------------
   Group |     Obs        Mean    Std. err.   Std. dev.   [95% conf. interval]
---------+--------------------------------------------------------------------
       0 |   5,975    24.20231     .053045    4.100279    24.09832    24.30629
       1 |   4,376    27.36081    .0806049    5.332119    27.20279    27.51884
---------+--------------------------------------------------------------------
Combined |  10,351     25.5376    .0483092    4.914969     25.4429    25.63229
---------+--------------------------------------------------------------------
    diff |           -3.158506    .0927376               -3.34029   -2.976723
------------------------------------------------------------------------------
    diff = mean(0) - mean(1)                                      t = -34.0585
H0: diff = 0                                     Degrees of freedom =    10349
    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

We see that the new varname dimension has been added to the collection.

```
. collect dims

Collection dimensions
Collection: default
-----------------------------------------
                   Dimension   No. levels
-----------------------------------------
Layout, style, header, label
                      cmdset   3
               program_class   1
                      result   14
                 result_type   1
                     varname   3

Style only
                border_block   4
                   cell_type   4
-----------------------------------------
```

The levels of this dimension are age, bmi, and weight, as we requested.

```
. collect label list varname, all

  Collection: default
   Dimension: varname
       Label:
Level labels:
         age
         bmi
      weight
```

We can now specify that the `varname` dimension be used to construct the rows of our table.

```
. collect layout (varname) (result)
Collection: default
      Rows: varname
   Columns: result
   Table 1: 3 x 3
----------------------------------------------------------------------------
       |  x1 mean for population 1 x2 mean for population 2 Two-sided p-value
-------+--------------------------------------------------------------------
age    |                  42.16502                  54.97281                 0
weight |                  68.26626                  76.85565         9.1e-181
bmi    |                  24.20231                  27.36081         4.5e-241
----------------------------------------------------------------------------
```

We now have more meaningful labels on the rows, but the column headers have default labels that we might want to modify.

We can use the `collect label` command to specify our preferred labels for the levels of the `result` dimension.

```
. collect label levels result
>   mu_1 "Normotensive" mu_2 "Hypertensive" p "p-value", modify

. collect preview

-------------------------------------------------
       |  Normotensive Hypertensive   p-value
-------+-----------------------------------------
age    |      42.16502     54.97281         0
weight |      68.26626     76.85565 9.1e-181
bmi    |      24.20231     27.36081 4.5e-241
-------------------------------------------------
```

`collect style cell` allows us to make a wide variety of formatting modifications to our table. First, we modify the numeric format of the *p*-values, and we request that numbers less than 0.001 be reported as `<0.001` in the table.

```
. collect style cell result[p], nformat(%5.3f) min(0.001)

. collect preview

-----------------------------------------------------
        |  Normotensive Hypertensive p-value
--------+--------------------------------------------
age     |      42.16502     54.97281  <0.001
weight  |      68.26626     76.85565  <0.001
bmi     |      24.20231     27.36081  <0.001
-----------------------------------------------------
```

We also request that only two decimal places be reported for the means.

```
. collect style cell result[mu_1 mu_2], nformat(%5.2f)

. collect preview

-------------------------------------------------
        |  Normotensive Hypertensive  p-value
--------+----------------------------------------
age     |         42.17        54.97   <0.001
weight  |         68.27        76.86   <0.001
bmi     |         24.20        27.36   <0.001
-------------------------------------------------
```

We specify that the values (`cell_type[item]`) be centered horizontally within in the columns.

```
. collect style cell cell_type[item], halign(center)

. collect preview

───────────┬─────────────────────────────────────
           │  Normotensive Hypertensive p-value
───────────┼─────────────────────────────────────
age        │     42.17        54.97      <0.001
weight     │     68.27        76.86      <0.001
bmi        │     24.20        27.36      <0.001
───────────┴─────────────────────────────────────
```

Finally, we request that the border be removed from the right side of the row headers.

```
. collect style cell border_block, border(right, pattern(nil))

. collect preview
────────────────────────────────────────
       Normotensive Hypertensive p-value
────────────────────────────────────────
age           42.17        54.97  <0.001
weight        68.27        76.86  <0.001
bmi           24.20        27.36  <0.001
────────────────────────────────────────
```

Once the table is formatted to our liking, we can export to a number of different formats by specifying the appropriate suffix. Below, we export the table to HTML.

```
. collect export ttest_tab.html, replace
(collection default exported to file ttest_tab.html)
```

If we create tables of a similar style repeatedly, there is no need to remember the collect commands each time we create a new table. Instead, we can save the style we like and apply it to tables we create in the future.

```
. collect style save ttest_style, replace
(style from default saved to file ttest_style.stjson)
```

Now, we can apply this style to tables using different variables and even different datasets.

```
. clear all
. sysuse auto, clear
. collect r(mu_1) r(mu_2) r(p), tags(varname[price]): ttest price, by(foreign)
. collect r(mu_1) r(mu_2) r(p), tags(varname[weight]): ttest weight, by(foreign)
. collect r(mu_1) r(mu_2) r(p), tags(varname[length]): ttest length, by(foreign)
. collect style use ttest_style, replace
. collect preview
----------------------------------------------------------------------------
       x1 mean for population 1 x2 mean for population 2 Two-sided p-value
----------------------------------------------------------------------------
price           6072.42                  6384.68                 0.680
weight          3317.12                  2315.91                 <0.001
length          196.13                   168.55                  <0.001
----------------------------------------------------------------------------
```

Now, we need only to make modifications specific to this dataset, such as the labels in the column headers.

```
. collect label levels result
>   mu_1 "Domestic cars" mu_2 "Foreign cars" p "p-value", modify

. collect preview
─────────────────────────────────────────
       Domestic cars Foreign cars p-value
─────────────────────────────────────────
price      6072.42        6384.68    0.680
weight     3317.12        2315.91   <0.001
length      196.13         168.55   <0.001
─────────────────────────────────────────
```

As we have seen previously, `dtable`, `etable`, and `table` make it easy to create tables. They have many options for formatting, but when we don't get exactly what we want from one of these commands, we can often use just a few `collect` commands to finish the customization.

We can put the finishing touches on our table of logistic regression results.

```
. quietly logistic highbp bmi age
. quietly etable
. quietly logistic highbp bmi age i.sex
. quietly etable, append
. quietly logistic highbp bmi c.age##i.sex
. etable, append column(index)
          mstat(aic) mstat(bic)
          title("Table 2: Logistic regression results")
          notes("Odds ratio (Std. Err.)")
Table 2: Logistic regression results
------------------------------------------------
                          1        2        3
------------------------------------------------
Body mass index (BMI)    1.145    1.147    1.148
                       (0.006)  (0.006)  (0.006)
Age (years)              1.046    1.047    1.034
                       (0.001)  (0.001)  (0.002)
Sex
  Female                          0.617    0.152
                                (0.028)  (0.023)
Sex # Age (years)
  Female                                   1.028
                                         (0.003)
Intercept                0.002    0.003    0.005
                       (0.000)  (0.000)  (0.001)
AIC                   11812.48 11698.99 11605.77
BIC                   11834.21 11727.97 11642.00
------------------------------------------------
Odds ratio (Std. Err.)
```

Because sex is a binary variable, we do not need the variable label and the level labels. We hide the title for this dimension. We also specify a split row style with an x for the interaction delimiter instead of #. We again add some vertical space to the table.

```
. collect style header sex, title(hide)
. collect style row split, dups(first) delimiter(" x ") spacer
. collect preview
Table 2: Logistic regression results
────────────────────────────────────────────────
                             1        2        3
────────────────────────────────────────────────
Body mass index (BMI)    1.145    1.147    1.148
                       (0.006)  (0.006)  (0.006)
Age (years)              1.046    1.047    1.034
                       (0.001)  (0.001)  (0.002)
Female                            0.617    0.152
                                (0.028)  (0.023)
Female x Age (years)                       1.028
                                         (0.003)
Intercept                0.002    0.003    0.005
                       (0.000)  (0.000)  (0.001)

AIC                   11812.48 11698.99 11605.77

BIC                   11834.21 11727.97 11642.00
────────────────────────────────────────────────
Odds ratio (Std. Err.)
```

We now have a clean table that can be used alone or included in complete reports.

Complete reports

Stata offers the following suites of commands for creating full reports that include customized text, formatted tables, Stata results, and images:

- `putdocx` creates Word documents
- `putpdf` creates PDFs
- `putexcel` creates Excel files
- `dyndoc` and Markdown together create HTML files and Word documents

A basic outline for commands used to create a Word document is shown below.

```
putdocx begin

  putdocx paragraph
  putdocx text = ("mytext")

  putdocx textblock begin
    my paragraph text
  putdocx textblock end

  putdocx paragraph
  putdocx image myimage.png

  putdocx table tablename = etable

  putdocx collect

putdocx save myfile.docx
```

We demonstrate how to incorporate tables in a Word document by using `putdocx` to generate a complete Word document with text, the tables we created previously, and a graph.

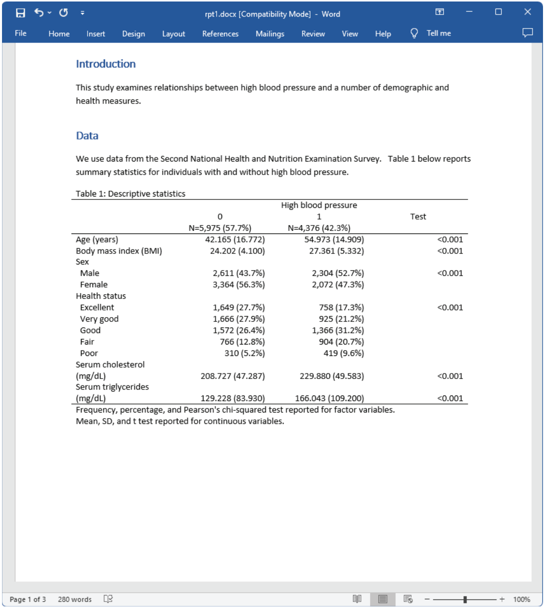
```
version 18.5
clear all
putdocx begin

putdocx paragraph, style(Heading1)
putdocx text ("Introduction")

putdocx textblock begin, hardbreak
This study examines relationships between high blood pressure and
a number of demographic and health measures.
putdocx textblock end

putdocx paragraph, style(Heading1)
putdocx text ("Data")

putdocx textblock begin, hardbreak
We use data from the Second National Health and Nutrition
Examination Survey.  Table 1 below reports summary statistics
for individuals with and without high blood pressure.
putdocx textblock end
```

```
webuse nhanes2l

dtable age bmi i.sex i.hlthstat tcresult tgresult,
    by(highbp, nototals tests notestnotes)
    sample(, place(seplabels)) sformat("N=%s" frequency)
    title("Table 1: Descriptive statistics")
    note("Frequency, percentage, and Pearson's chi-squared
          test reported for factor variables.")
    note("Mean, SD, and t test reported for continuous variables.")

putdocx collect

putdocx paragraph, style(Heading1)
putdocx text ("Results")

putdocx textblock begin, hardbreak
We fit three logistic regression models of high blood pressure on BMI,
age, sex, and the interaction of age and sex.  Results of the three
models are presented in Table 2.
putdocx textblock end
```

```
logistic highbp bmi age
etable
logistic highbp bmi age i.sex
etable, append
logistic highbp bmi c.age##i.sex
etable, append column(index)
    mstat(aic) mstat(bic)
    title("Table 2: Logistic regression results")
    notes("Odds ratio (Std. Err.)")

collect style header sex, title(hide)
collect style row split, dups(first) delimiter(" x ") spacer
putdocx collect

putdocx textblock begin, hardbreak
The model with the interaction provided best fit. The graph below
plots explores the interaction effect. Probability of high blood
pressure increases with age. For younger individuals, males
have a higher probability of having high blood pressure, but this
changes with age.
putdocx textblock end
```

```
margins sex, at(age=(20(5)75))

marginsplot, ytitle("Probability of high blood pressure")
  title("Interaction of age and sex")
  graphregion(fcolor(white))
  legend(cols(1) bplacement(5) ring(0))
  ylabel(, angle(horizontal)) xlabel(, grid)

graph export marginsplot.png, replace

putdocx paragraph, halign(center)
putdocx image marginsplot.png, height(3.5in)

putdocx save rpt1.docx, replace
```

When we run the do-file, we create the following Word document.



Introduction

This study examines relationships between high blood pressure and a number of demographic and health measures.

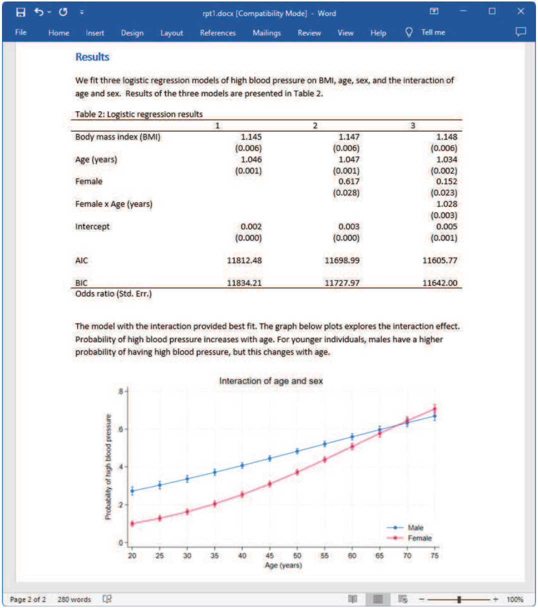
Data

We use data from the Second National Health and Nutrition Examination Survey. Table 1 below reports summary statistics for individuals with and without high blood pressure.

Table 1: Descriptive statistics

	High blood pressure		
	0	1	Test
	N=5,975 (57.7%)	N=4,376 (42.3%)	
Age (years)	42.165 (16.772)	54.973 (14.909)	<0.001
Body mass index (BMI)	24.202 (4.100)	27.361 (5.332)	<0.001
Sex			
Male	2,611 (43.7%)	2,304 (52.7%)	<0.001
Female	3,364 (56.3%)	2,072 (47.3%)	
Health status			
Excellent	1,649 (27.7%)	758 (17.3%)	<0.001
Very good	1,666 (27.9%)	925 (21.2%)	
Good	1,572 (26.4%)	1,366 (31.2%)	
Fair	766 (12.8%)	904 (20.7%)	
Poor	310 (5.2%)	419 (9.6%)	
Serum cholesterol (mg/dL)	208.727 (47.287)	229.880 (49.583)	<0.001
Serum triglycerides (mg/dL)	129.228 (83.930)	166.043 (109.200)	<0.001

Frequency, percentage, and Pearson's chi-squared test reported for factor variables.
Mean, SD, and t test reported for continuous variables.



Results

We fit three logistic regression models of high blood pressure on BMI, age, sex, and the interaction of age and sex. Results of the three models are presented in Table 2.

Table 2: Logistic regression results

	1	2	3
Body mass index (BMI)	1.145	1.147	1.148
	(0.006)	(0.006)	(0.006)
Age (years)	1.046	1.047	1.034
	(0.001)	(0.001)	(0.002)
Female		0.617	0.152
		(0.028)	(0.023)
Female x Age (years)			1.028
			(0.003)
Intercept	0.002	0.003	0.005
	(0.000)	(0.000)	(0.001)
AIC	11812.48	11698.99	11605.77
BIC	11834.21	11727.97	11642.00

Odds ratio (Std. Err.)

The model with the interaction provided best fit. The graph below plots explores the interaction effect. Probability of high blood pressure increases with age. For younger individuals, males have a higher probability of having high blood pressure, but this changes with age.

We used putdocx as an example of incorporating tables in complete reports. We can similarly create

- PDFs by using putpdf or docx2pdf after putdocx
- Excel files by using putexcel
- HTML files by using dyndoc

Thank you!