```
                                              __ __  __  __  ___(R)
                                             /_  / __/ / / __/
                                            __/ / /__/ / / /__/
                                              Statistics/Data analysis
```

```
 1 .
 2 .
 3 .
 4 . **ANALYSIS B: **
 5 .
 6 . use finaldata_imputedFINAL, clear

 7 .
 8 . mi extract 0

 9 .
10 . save finaldata_unimputedFINAL, replace
   file finaldata_unimputedFINAL.dta saved

11 .
12 . **foreach y1 of varlist FA_mean MD_mean {
13 . **reg `y1' infectionburden AGE SEX  i.RACE_ETHN AD_PGS householdsize TIME_V0V2  invmillsMRIINF if sample_final=
14 . **}
15 .
16 .
17 . global tflist ""

18 . global modseq=0

19 . foreach X of var infectionburdentert {
    2. foreach Y of var ISOVF_mean ICVF_mean OD_mean  {
    3. global modseq=$modseq+1
    4. tempfile tfcur
    5. parmby "regr `Y' `X'  AGE SEX  NonWhite AD_PGS householdsize TIME_V0V2  invmillsMRIINF if sample_final==1, b
  >  replace) flist(tflist)
    6.  }
    7.  }
   Command: regr ISOVF_mean infectionburdentert  AGE SEX  NonWhite AD_PGS householdsize TIME_V0V2  invmillsMRIINF if
```

Source	SS	df	MS	Number of obs	=	38,705
				F(8, 38696)	=	1213.46
Model	1.34003908	8	.167504885	Prob > F	=	0.0000
Residual	5.34156468	38,696	.000138039	R-squared	=	0.2006
				Adj R-squared	=	0.2004
Total	6.68160376	38,704	.000172633	Root MSE	=	.01175

ISOVF_mean	Coefficient	Std. err.	t	P>|t|	Beta
infectionburdentert	.0003132	.0000683	4.59	0.000	.0208875
AGE	.0007328	8.59e-06	85.35	0.000	.4189682
SEX	-.001516	.0001205	-12.58	0.000	-.0575875
NonWhite	.0003406	.0007667	0.44	0.657	.0020223
AD_PGS	.0000893	.0000606	1.47	0.140	.0067064
householdsize	-.0002261	.0000526	-4.30	0.000	-.0210053
TIME_V0V2	2.35e-06	9.43e-08	24.88	0.000	.1132148
invmillsMRIINF	-4.73e-07	5.24e-07	-0.90	0.367	-.004104
_cons	.0484476	.0010035	48.28	0.000	.

```
   (file C:\Users\baydounm\AppData\Local\Temp\ST_62c8_000001.tmp not found)
   file C:\Users\baydounm\AppData\Local\Temp\ST_62c8_000001.tmp saved as .dta format
   Command: regr ICVF_mean infectionburdentert  AGE SEX  NonWhite AD_PGS householdsize TIME_V0V2  invmillsMRIINF if
```

Source	SS	df	MS			
				Number of obs	=	38,705
				F(8, 38696)	=	482.88
Model	2.7077124	8	.33846405	Prob > F	=	0.0000
Residual	27.123009	38,696	.000700925	R-squared	=	0.0908
				Adj R-squared	=	0.0906
Total	29.8307214	38,704	.00077074	Root MSE	=	.02647

ICVF_mean	Coefficient	Std. err.	t	P>|t|	Beta
infectionburdentert	-.0000618	.0001539	-0.40	0.688	-.00195
AGE	-.0010984	.0000193	-56.77	0.000	-.2972033
SEX	-.0002798	.0002715	-1.03	0.303	-.0050304
NonWhite	-.0017346	.0017277	-1.00	0.315	-.0048744
AD_PGS	-.0003053	.0001365	-2.24	0.025	-.0108483
householdsize	.0002569	.0001185	2.17	0.030	.0112951
TIME_V0V2	-8.05e-08	2.13e-07	-0.38	0.705	-.001839
invmillsMRIINF	3.73e-07	1.18e-06	0.32	0.752	.0015324
_cons	.6746145	.0022612	298.34	0.000	.

(file **C:\Users\baydounm\AppData\Local\Temp\ST_62c8_000002.tmp** not found)
file **C:\Users\baydounm\AppData\Local\Temp\ST_62c8_000002.tmp** saved as .dta format
Command: **regr OD_mean infectionburdentert AGE SEX NonWhite AD_PGS householdsize TIME_V0V2 invmillsMRIINF if sa**

Source	SS	df	MS			
				Number of obs	=	38,705
				F(8, 38696)	=	393.04
Model	.207283759	8	.02591047	Prob > F	=	0.0000
Residual	2.5509386	38,696	.000065923	R-squared	=	0.0752
				Adj R-squared	=	0.0750
Total	2.75822236	38,704	.000071265	Root MSE	=	.00812

OD_mean	Coefficient	Std. err.	t	P>|t|	Beta
infectionburdentert	.0001996	.0000472	4.23	0.000	.0207149
AGE	.0002396	5.93e-06	40.38	0.000	.2132099
SEX	.0003675	.0000833	4.41	0.000	.0217264
NonWhite	-.0026175	.0005298	-4.94	0.000	-.0241885
AD_PGS	.0000419	.0000419	1.00	0.317	.0048992
householdsize	-.0002076	.0000363	-5.71	0.000	-.0300164
TIME_V0V2	2.14e-06	6.52e-08	32.82	0.000	.1606379
invmillsMRIINF	-3.26e-07	3.62e-07	-0.90	0.368	-.004399
_cons	.1094786	.0006935	157.87	0.000	.

(file **C:\Users\baydounm\AppData\Local\Temp\ST_62c8_000003.tmp** not found)
file **C:\Users\baydounm\AppData\Local\Temp\ST_62c8_000003.tmp** saved as .dta format

20 .
21 . drop _all

22 . append using $tflist

23 . sort idnum command `Y' parmseq

24 . describe

Contains data
 Observations: **27**
   Variables: **12**

Variable name	Storage type	Display format	Value label	Variable label
parmseq	byte	%12.0g		**Parameter sequence number**
command	str126	%126s		**Estimation command**
idnum	byte	%10.0g		**Numeric ID**
parm	str19	%19s		**Parameter name**
label	str31	%31s		**Parameter label**
estimate	double	%8.2f		**Parameter estimate**
stderr	double	%10.0g		**SE of parameter estimate**
dof	long	%10.0g		**Degrees of freedom**
t	double	%10.0g		**t-test statistic**
p	double	%8.1e		**P-value**
min95	double	%8.2f		**Lower 95% confidence limit**
max95	double	%8.2f		**Upper 95% confidence limit**

Sorted by: **idnum   command   parmseq**
      Note: Dataset has changed since last saved.

25 . by idnum command:list `Y' parm label estimate min95 max95 p, noobs

-> idnum = 1, command = regr ISOVF_mean infectionburdentert A..

parm	label	estimate	min95	max95	p
infectionburdentert	3 quantiles of infectionburden	0.00	0.00	0.00	4.5e-06
AGE		0.00	0.00	0.00	0.0e+00
SEX		-0.00	-0.00	-0.00	3.1e-36
NonWhite		0.00	-0.00	0.00	6.6e-01
AD_PGS		0.00	-0.00	0.00	1.4e-01
householdsize	Number of household members	-0.00	-0.00	-0.00	1.7e-05
TIME_V0V2		0.00	0.00	0.00	2.e-135
invmillsMRIINF		-0.00	-0.00	0.00	3.7e-01
_cons	Constant	0.05	0.05	0.05	0.0e+00

-> idnum = 2, command = regr ICVF_mean infectionburdentert AG..

parm	label	estimate	min95	max95	p
infectionburdentert	3 quantiles of infectionburden	-0.00	-0.00	0.00	6.9e-01
AGE		-0.00	-0.00	-0.00	0.0e+00
SEX		-0.00	-0.00	0.00	3.0e-01
NonWhite		-0.00	-0.01	0.00	3.2e-01
AD_PGS		-0.00	-0.00	-0.00	2.5e-02
householdsize	Number of household members	0.00	0.00	0.00	3.0e-02
TIME_V0V2		-0.00	-0.00	0.00	7.0e-01
invmillsMRIINF		0.00	-0.00	0.00	7.5e-01
_cons	Constant	0.67	0.67	0.68	0.0e+00

-> idnum = 3, command = regr OD_mean infectionburdentert AGE ..

parm	label	estimate	min95	max95	p
infectionburdentert	3 quantiles of infectionburden	0.00	0.00	0.00	2.3e-05
AGE		0.00	0.00	0.00	0.0e+00
SEX		0.00	0.00	0.00	1.0e-05
NonWhite		-0.00	-0.00	-0.00	7.8e-07
AD_PGS		0.00	-0.00	0.00	3.2e-01
householdsize	Number of household members	-0.00	-0.00	-0.00	1.1e-08
TIME_V0V2		0.00	0.00	0.00	6.e-233
invmillsMRIINF		-0.00	-0.00	0.00	3.7e-01
_cons	Constant	0.11	0.11	0.11	0.0e+00

```
26 .
27 . save Outputdata_overall_B, replace
   file Outputdata_overall_B.dta saved

28 .
29 .
30 .
31 . **Smile plot**
32 . use Outputdata_overall_B, clear

33 .
34 . keep if parmseq==1
   (24 observations deleted)

35 .
36 .
37 . sort parm

38 . multproc, pval(p) meth(bonferroni) gpunc(uncp) gpcor(corp) rej(signif)

   Method: bonferroni
   Uncorrected overall critical P-value: .05
   Number of P-values: 3
   Corrected overall critical P-value: .01666667
   Number of rejected P-values: 2

39 . smileplot7, est(estimate) pval(p) punc(uncp) pcor(corp) ptl(command)  t1(" ")

   Method: userspecified
   Uncorrected overall critical P-value: .05
   Number of P-values: 3
   Corrected overall critical P-value: .01666667
   Number of rejected P-values: 2
```

```
40 . list if signif, nodisp
```

```
    >  ┌──────────────────────────────────────────────────────────────────────┐
       │  parmseq    command                                                   
    >  │ estimate      stderr      dof         t        p   min95   max95   uncp       corp   signif │
       ├──────────────────────────────────────────────────────────────────────┤
    >  ──────────────────────────────────────────────────────────────────────
   1. │         1   regr ISOVF_mean infectionburdentert  AGE SEX  NonWhite AD_PGS householdsize TIME_V0V2  invmillsM
    >  │     0.00   .00006829    38696   4.5870679   4.5e-06    0.00    0.00     .05   .01666667        1 │
   3. │         1   regr OD_mean infectionburdentert  AGE SEX  NonWhite AD_PGS householdsize TIME_V0V2  invmillsMRII
    >  │     0.00   .00004719    38696   4.2295224   2.3e-05    0.00    0.00     .05   .01666667        1 │
    >  ──────────────────────────────────────────────────────────────────────
```

```
41 .
42 .
43 .
44 . //q-value: FDR//
45 .
46 . capture drop myqvallargervolumes
```

```
47 .
48 . qqvalue p, method(simes) qvalue(myqvallargervolumes)
```

```
49 . sort myqvallargervolumes
```

```
50 .
51 . list parm myqvallargervolumes command p  estimate stderr if p<0.05
```

1.	parm **infectionburdentert**		myqvall~s **.00001353**
	command **regr ISOVF_mean infectionburdentert AGE SEX NonWhite AD_PGS householdsize TIME_V0V2 invmillsMRIINF if s**		
	p **4.5e-06**	estimate **0.00**	st **.00006**

2.	parm **infectionburdentert**		myqvall~s **.00003521**
	command **regr OD_mean infectionburdentert AGE SEX NonWhite AD_PGS householdsize TIME_V0V2 invmillsMRIINF if samp**		
	p **2.3e-05**	estimate **0.00**	st **.00004**

```
52 .
53 .
54 . save, replace
   file Outputdata_overall_B.dta saved
```

```
55 .
56 . capture log close
```