

Log files of the data analyses

For the analyses of the dichotomous scan result (variable `outcome` in print screen below), based on individual scan interpretations, the following syntax in STATA © 14 was used:

```
melogit outcome i.method || PIN: || observer:, or
```

For the analyses of the number of lesions (variable `Nlesions` in print screen below), the following syntax in Stata 14 was used:

```
mepoisson Nlesions i.method || PIN: || observer:, irr
```

Data Editor (Browse) - [Reconstudy_Revisions_2 - extra lang_2.0.dta]

File Edit View Data Tools

PIN[1] 1

	PIN	Reading	observer	method	outcome	Nlesions
1	1	1	1	4mm	yes	1
2	1	25	2	4mm	yes	1
3	1	49	3	4mm	yes	1
4	1	73	4	4mm	no	0
5	1	1	1	4mm+PSF	yes	1
6	1	25	2	4mm+PSF	yes	1
7	1	49	3	4mm+PSF	yes	1
8	1	73	4	4mm+PSF	no	0
9	1	1	1	2mm	yes	2
10	1	25	2	2mm	yes	1
11	1	49	3	2mm	yes	1
12	1	73	4	2mm	yes	1
13	1	1	1	2mm+PSF	yes	2
14	1	25	2	2mm+PSF	yes	1
15	1	49	3	2mm+PSF	yes	1
16	1	73	4	2mm+PSF	yes	1
17	2	2	1	4mm	yes	11
18	2	26	2	4mm	yes	20
19	2	50	3	4mm	yes	6
20	2	74	4	4mm	yes	1

PIN=patient identification number

For the analyses of the agreement (variable `agree` in print screen below), the following syntax in Stata 14 was used:

```
melogit agree i.method || PIN: || pair:, or
```

Data Editor (Browse) - [Reconstudy_Revisions_2 - agreement_2.0.dta]

File Edit View Data Tools

PIN[1] 1

	PIN	method	pair	agree
1	1	4mm	12	yes
2	1	4mm	13	yes
3	1	4mm	14	no
4	1	4mm	23	yes
5	1	4mm	24	no
6	1	4mm	24	no
7	1	4mm+PSF	12	yes
8	1	4mm+PSF	13	yes
9	1	4mm+PSF	14	no
10	1	4mm+PSF	23	yes
11	1	4mm+PSF	24	no
12	1	4mm+PSF	24	no
13	1	2mm	12	yes
14	1	2mm	13	yes
15	1	2mm	14	yes
16	1	2mm	23	yes
17	1	2mm	24	yes
18	1	2mm	24	yes
19	1	2mm+PSF	12	yes
20	1	2mm+PSF	13	yes
21	1	2mm+PSF	14	yes
22	1	2mm+PSF	23	yes
23	1	2mm+PSF	24	yes
24	1	2mm+PSF	24	yes
25	2	4mm	12	yes
26	2	4mm	13	yes
27	2	4mm	14	yes
28	2	4mm	23	yes
29	2	4mm	24	yes
30	2	4mm	24	yes

PIN=patient identification number