Sensitivity Analysis for Missing Data: The "how to" for the "what if"

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Missing Data

- Exposure
  - (e.g. missed visits, blood draw issue)
- Confounders
  - (e.g. incomplete medical records)
- Outcome
  - (e.g. withdrawal, pregnancy loss before measurement obtained)

The Prevention and Treatment of Missing Data in Clinical Trials

Key findings (paraphrased):

"...missing data are a **serious problem** that undermines the scientific credibility of causal conclusions... "

"…in studies with missing data, analysis methods that are based on plausible scientific assumptions should be used… they all require **unverifiable assumptions**."

"Thus, **sensitivity analyses** should be conducted to assess the robustness of findings to plausible alternative assumptions about the missing data."

RJ Little et al. 2012. N Engl J Med. Oct 4;367(14):1355-60.

“…missing data are a serious problem…”

Power

- Missing data is lost efficiency, no matter what.

“…missing data are a serious problem…”

Power

- Missing data is lost efficiency, no matter what.

Potential Bias

- Missing data mechanisms (Influenced by)
  - MCAR – missing completely at random (random)
  - MAR – missing at random (observed data)
  - MNAR – missing not at random (unobserved data)

Mitigating the effects of Missing Data

1. Study Design!
   - An ounce of prevention is worth a pound of cure

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2. Analysis Techniques
   - Complete Case Analysis
   - Single Imputation
   - Estimating Equations
   - Multiple Imputation

Naïve, easy but sometimes useful

More work but more rigorous

Mitigating the effects of Missing Data

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} "…analysis methods that are based on plausible scientific assumptions…"

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"…all require unverifiable assumptions."

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"…analysis methods that are based on plausible scientific assumptions…"

"…all require unverifiable assumptions."

3. Sensitivity Analysis
   - "What if ?"

"…**sensitivity analyses** should be conducted to assess the robustness of findings to plausible alternative assumptions about the missing data."

Sensitivity Analysis for Missing Data

What if I had *observed* the *unobserved*?

1. Would my conclusions have changed?
2. What scenarios would have led to a change or not change?
3. What is the plausibility of these scenarios?

Sensitivity Analysis for Missing Outcome

EAGeR
The Effects of Aspirin in Gestation & Reproduction

- Is low dose aspirin an effective therapy for women with trying to conceive?
- Preconception Treatment: 81mg Aspirin versus Placebo
- Block randomized by Site and Eligibility Strata
  - ***Original*** and ***Expanded***
- Follow up: 6 cycles or through pregnancy
- Primary Endpoint: Live Birth

Sensitivity analysis: overall

	LDA	Placebo	Total
Randomized	**615**	**613**	**1228**

Sensitivity analysis: overall

Information available for 1088 of 1228

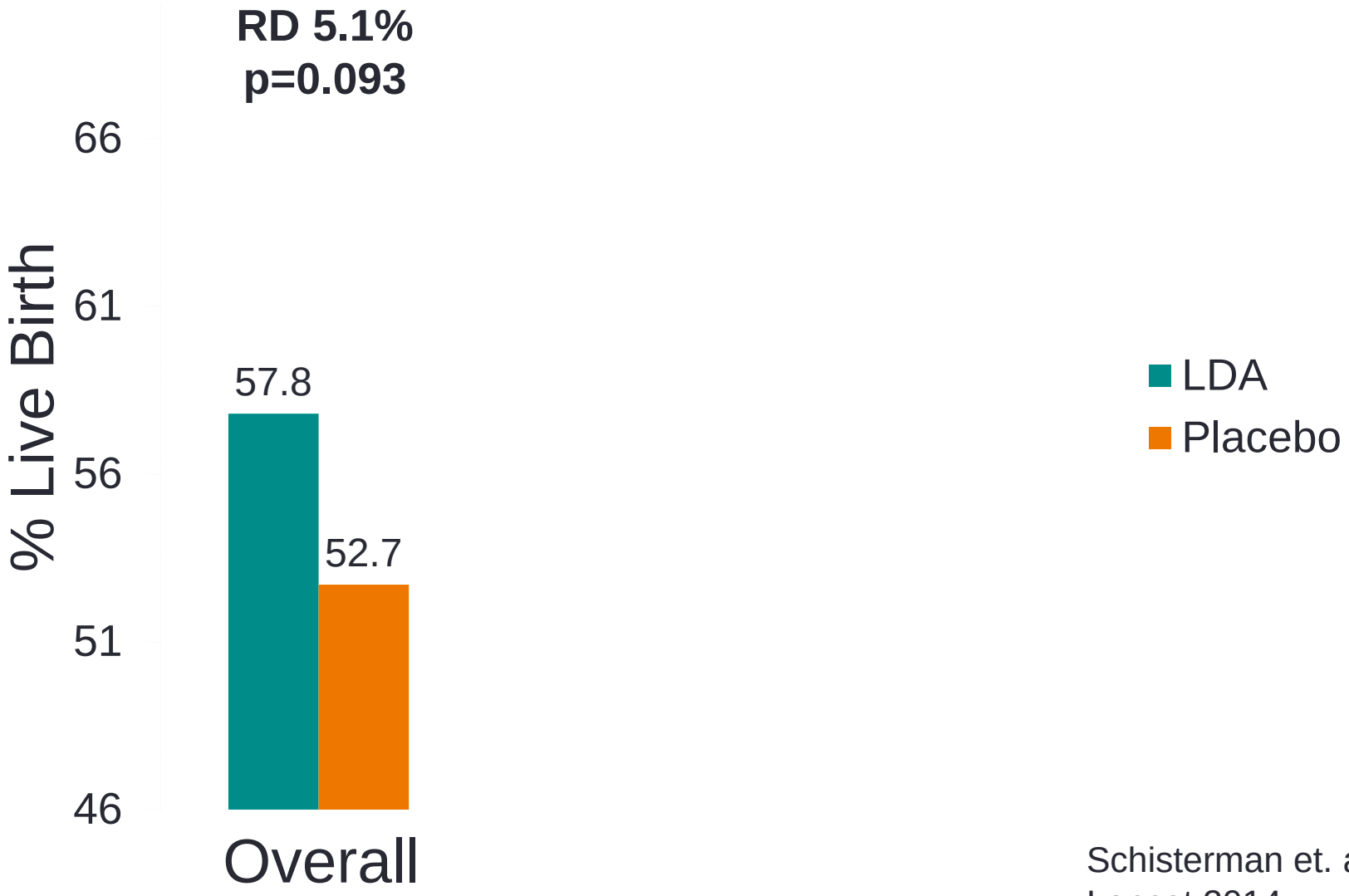
	LDA	Placebo	Total
Randomized	615	613	1228
Live Birth	**309**	**288**	**597**
No Live Birth	**228**	**263**	**491**

Sensitivity analysis: overall

Missing outcome on 140 of 1228 (12%)

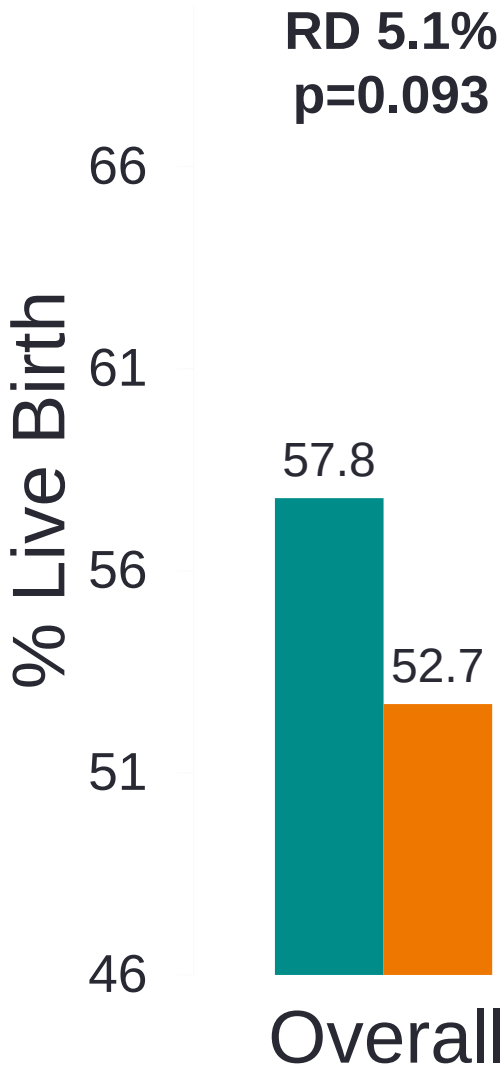
	LDA	Placebo	Total
Total	615	613	1228
Live Birth	309	288	597
No Live Birth	228	263	491
Unknown	**78**	**62**	**140**

Live Births: Overall



Schisterman et. al. The Lancet 2014

Live Births: Overall



Would the conclusions have changed if we had observed all of the data?

LDA
Placebo

Schisterman et. al. The Lancet 2014

Sensitivity analysis: methods

- Idea: impute missing outcome to:
  - success (live birth)
  - failure (no live birth)

- Consider all possible imputations between the two randomized treatment arms (uniformly)

- For each possible imputation, calculate the difference in probability of live birth and calculate the p-value for the chi-square test (n = 1228)

(Hollis et al Stat Med 2002)

Sensitivity analysis: overall

Success rates with various methods of allocating missing outcomes to success (live birth) or failure.

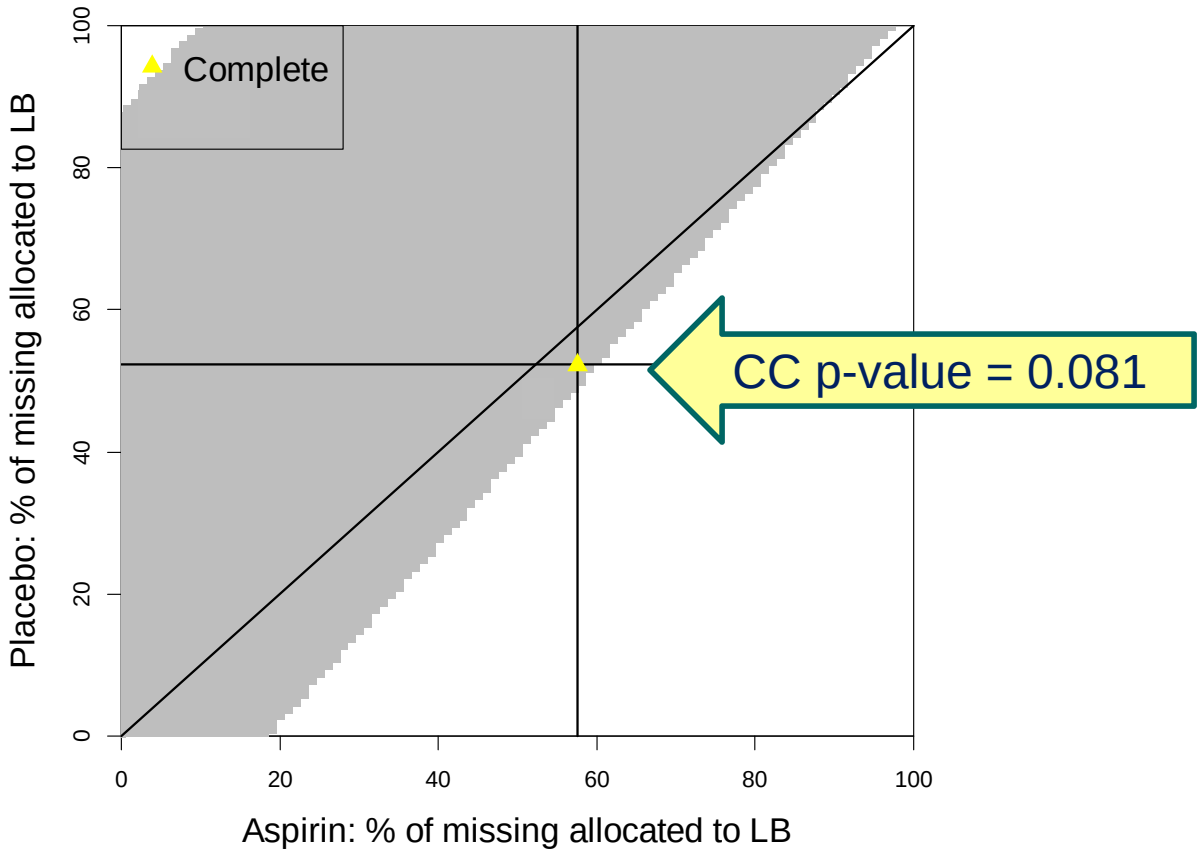
	LDA	Placebo	P-value
Complete cases	57.54	52.27	0.0805
Allocation to poor outcome	50.24	46.98	0.2528
Allocation to good outcome	62.93	57.10	0.0370
Best Case	62.93	46.98	<0.0001
Worst Case	50.24	57.10	0.0161
***Multiple Imputation**	**52.32**	**47.69**	**0.0945**

*Model: Rx, nulliparity, age, race, married, eligibility strata, BMI, time since loss, Log CRP

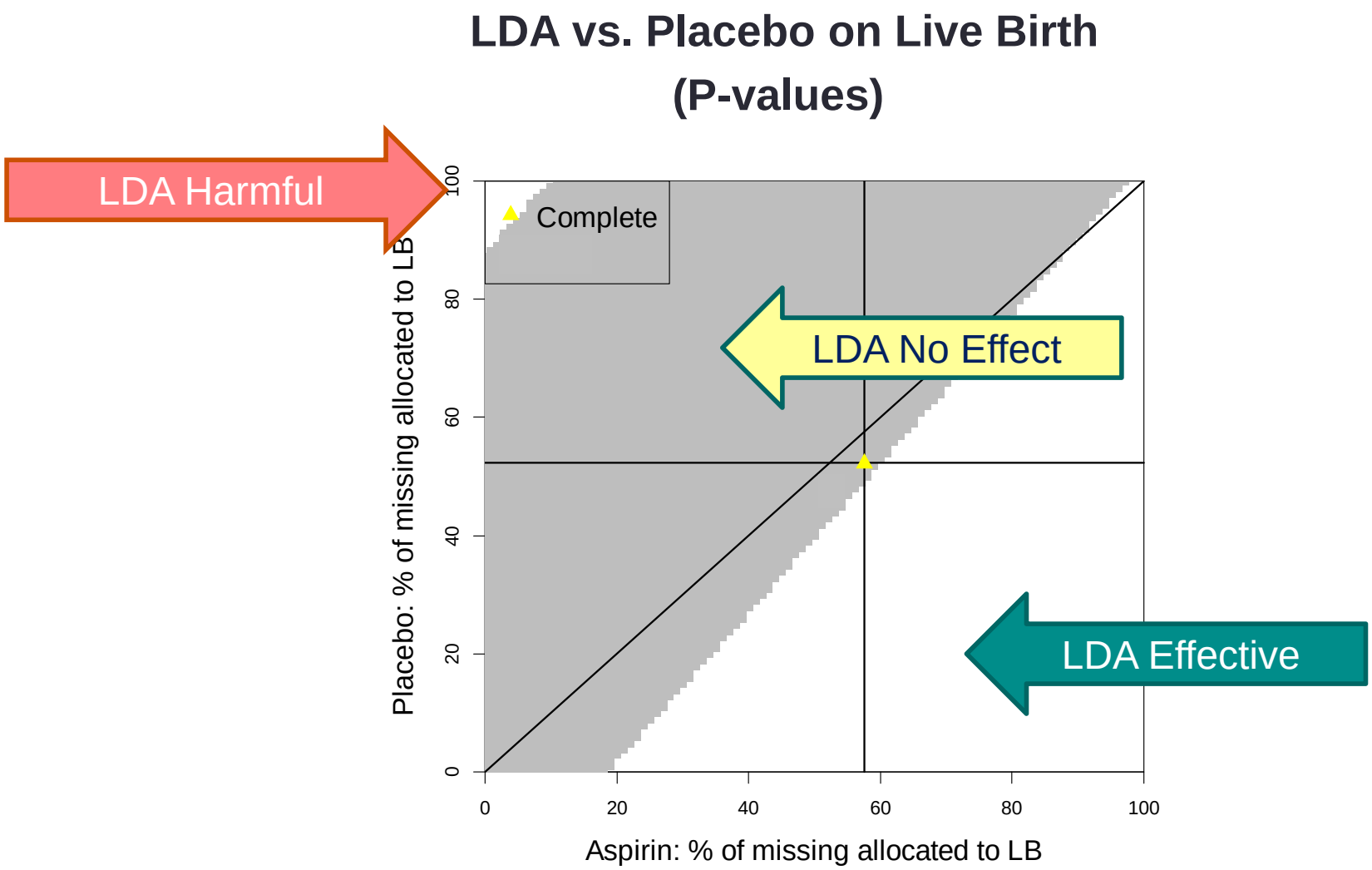
Sensitivity analysis: Plot

Placebo:
62 missing

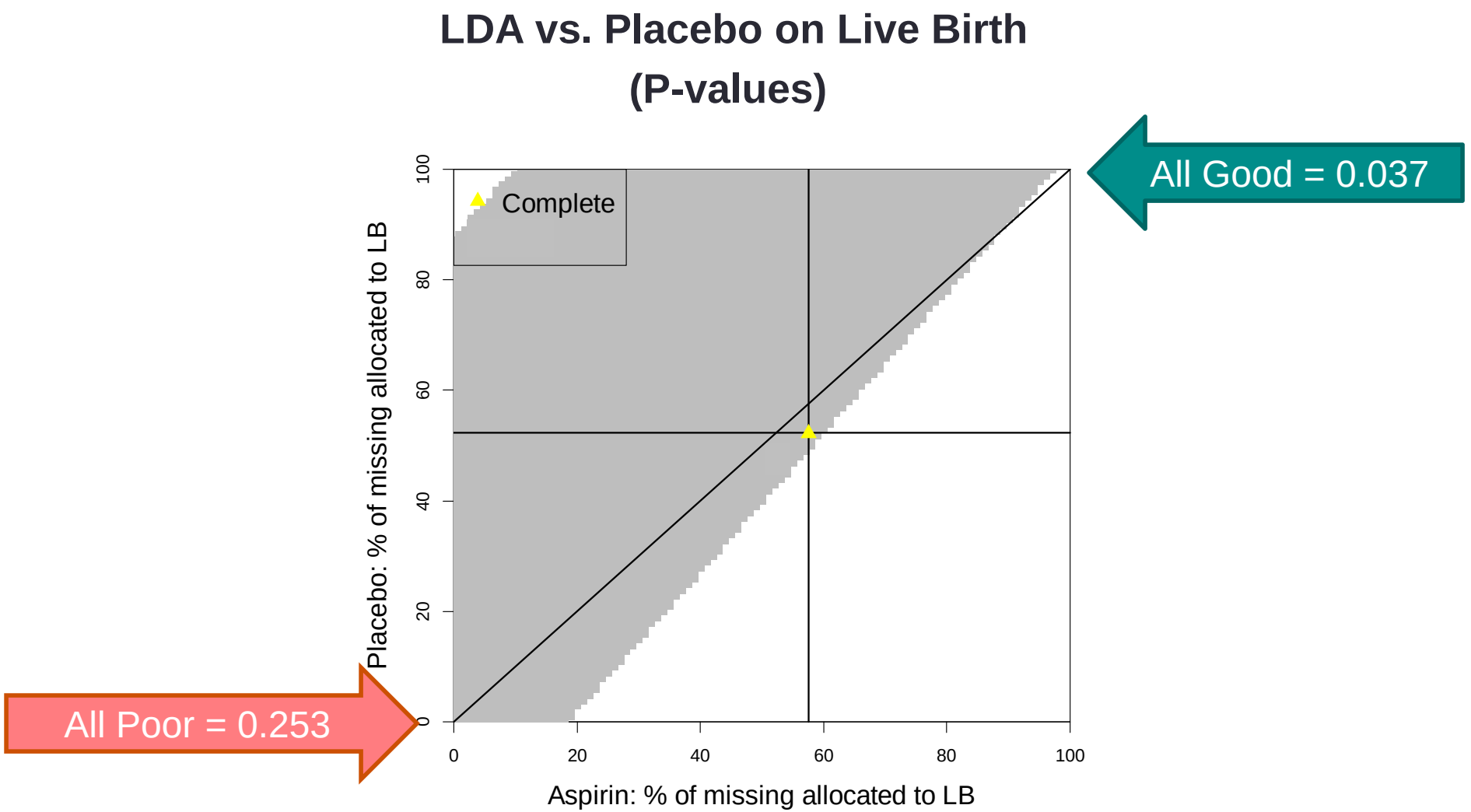
LDA:
78 missing



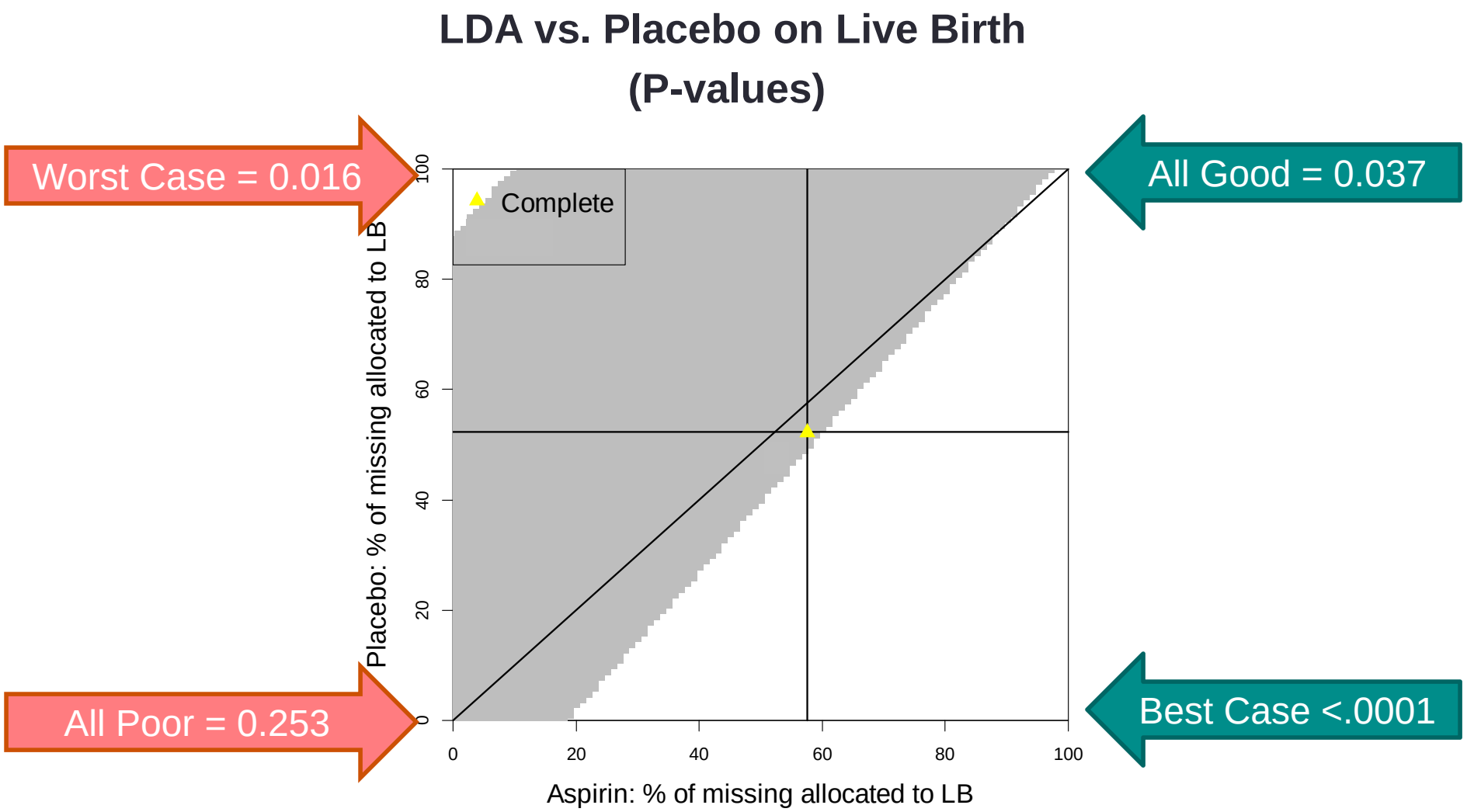
Sensitivity analysis: Plot Regions



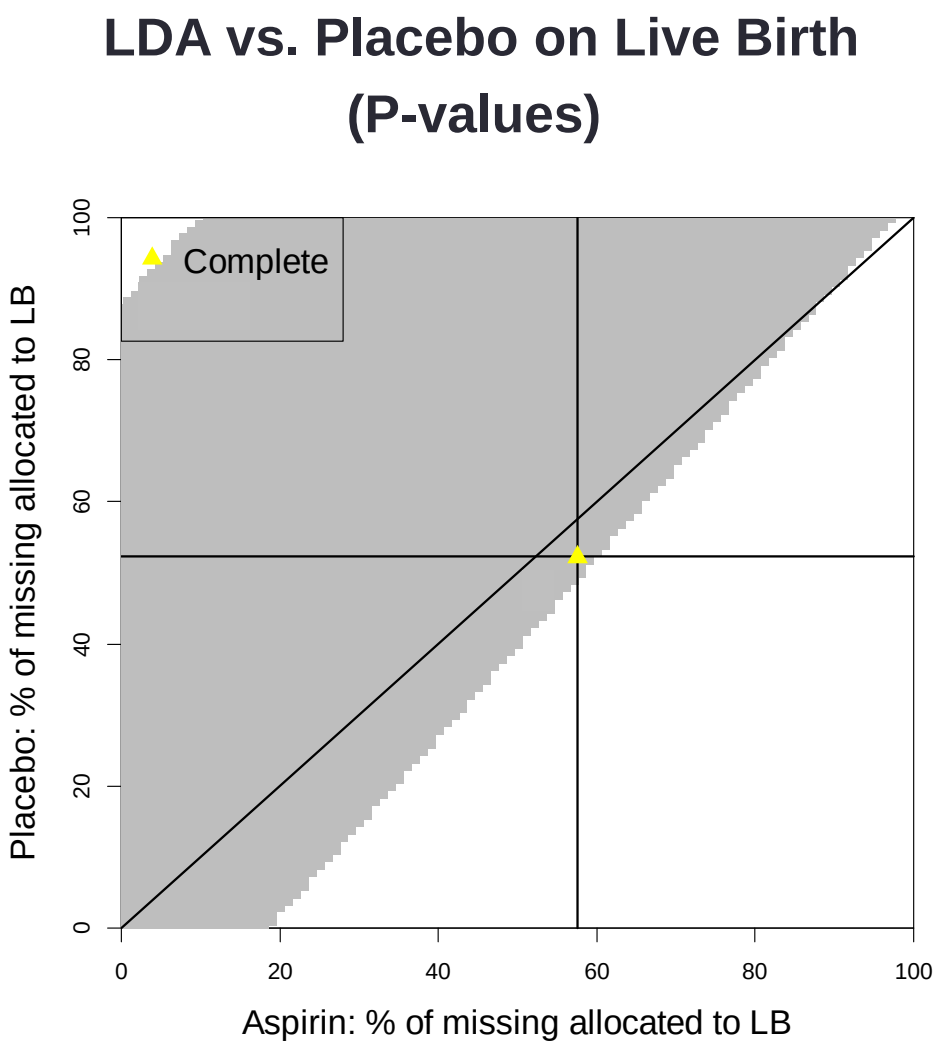
Sensitivity analysis: Plot Extremes



Sensitivity analysis: Plot Extremes



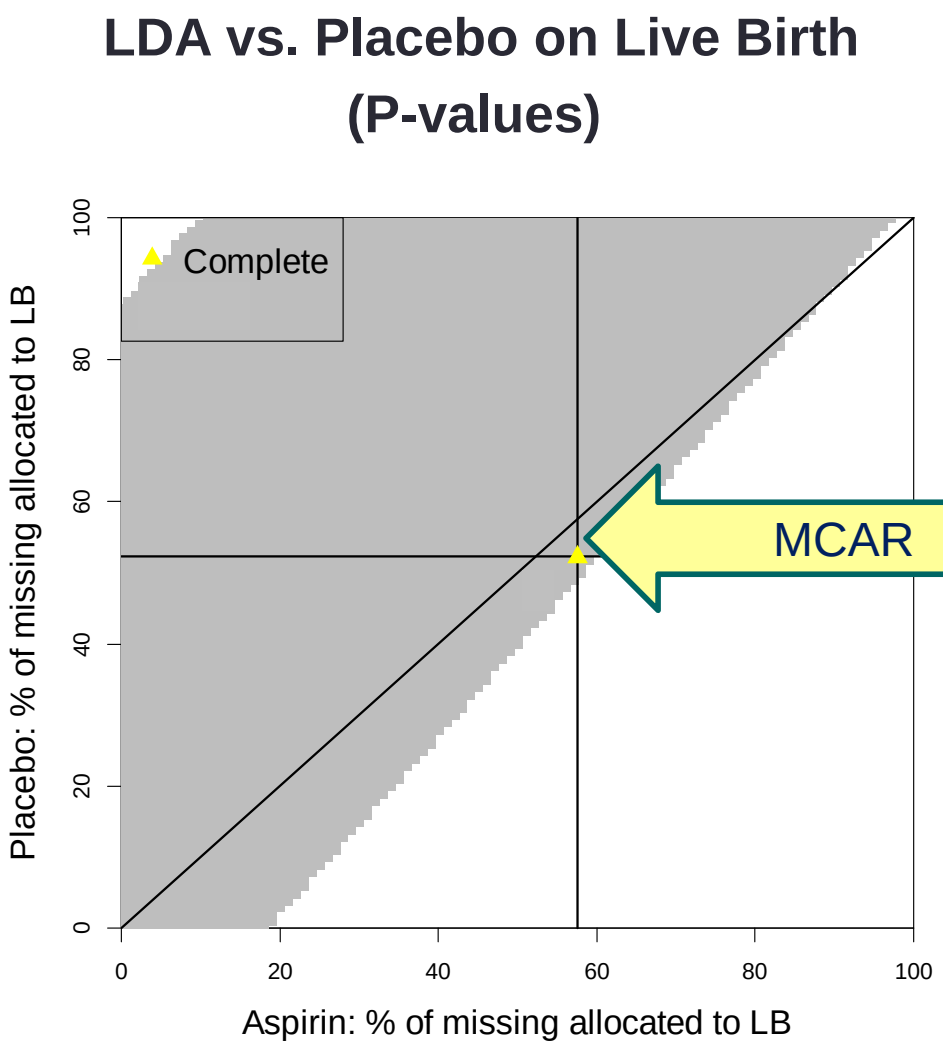
Sensitivity analysis: What's resonable?



MNAR

Bounds contain even the most extreme mechanism

Sensitivity analysis: What's resonable?



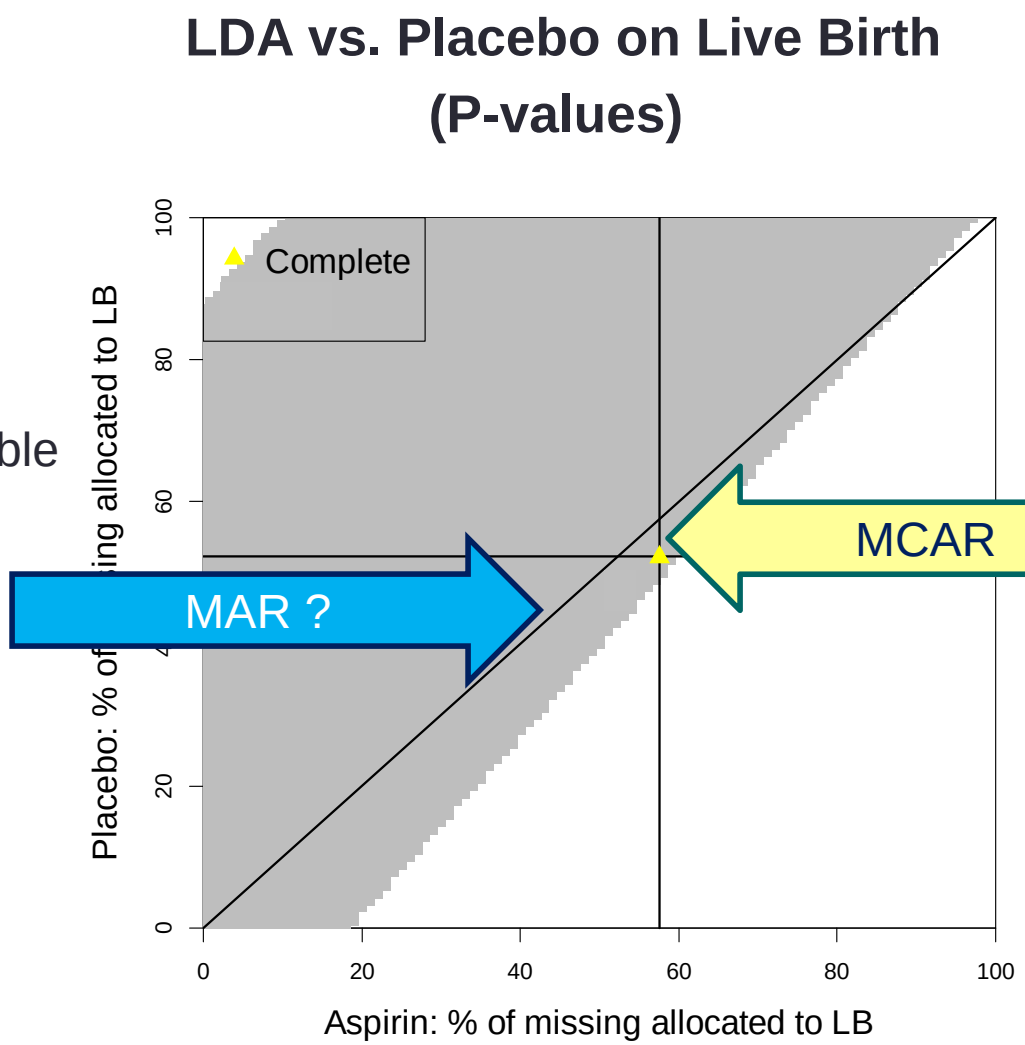
MNAR

Bounds contain even the most extreme mechanism

MCAR

Triangle region is what is intuitively reasonable under completely random missingness

Sensitivity analysis: What's resonable?

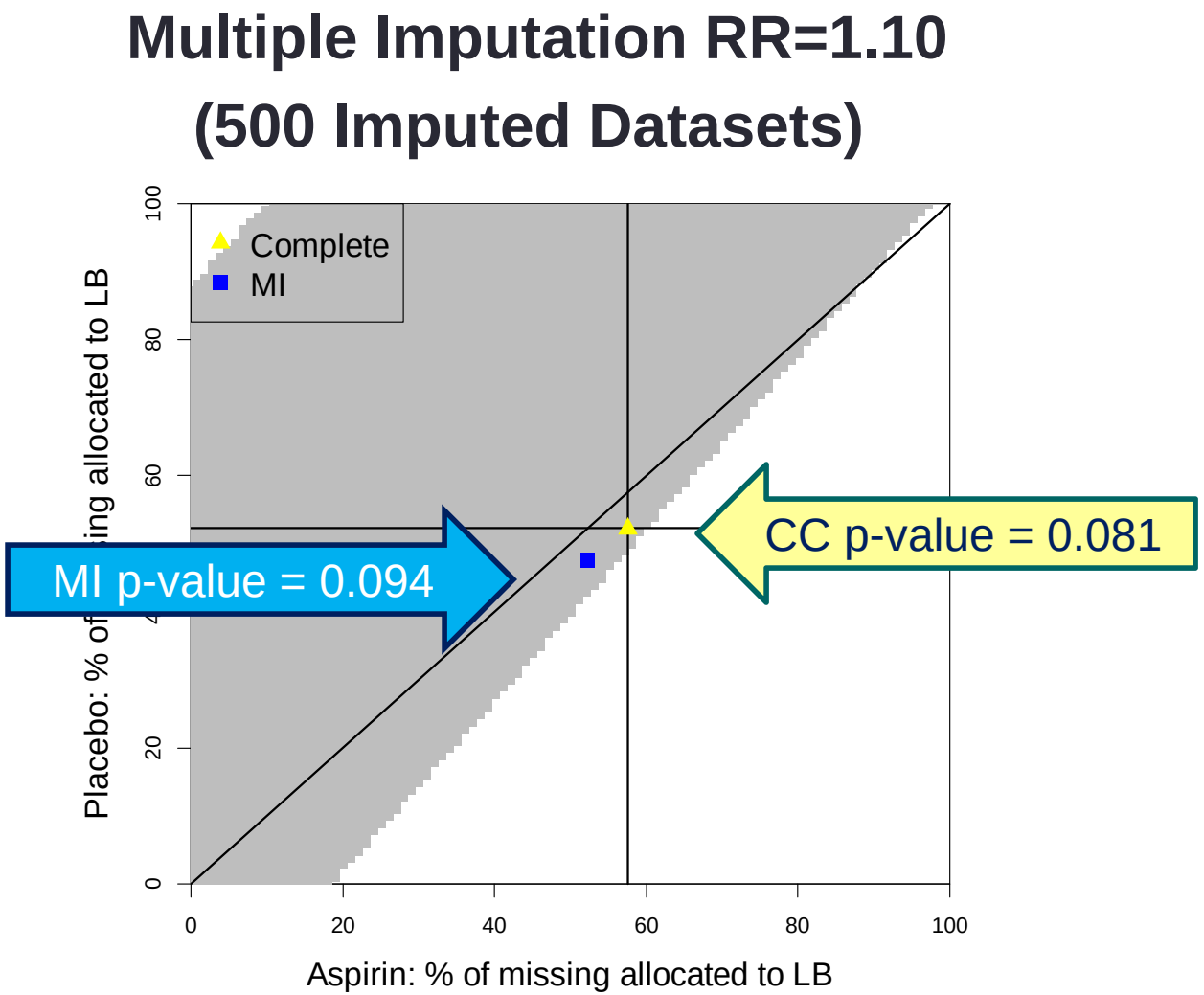


What is reasonable under missing at random?

Bounds contain even the most extreme mechanism

Triangle region is what is intuitively reasonable under missing completely at random

Sensitivity analysis: MI

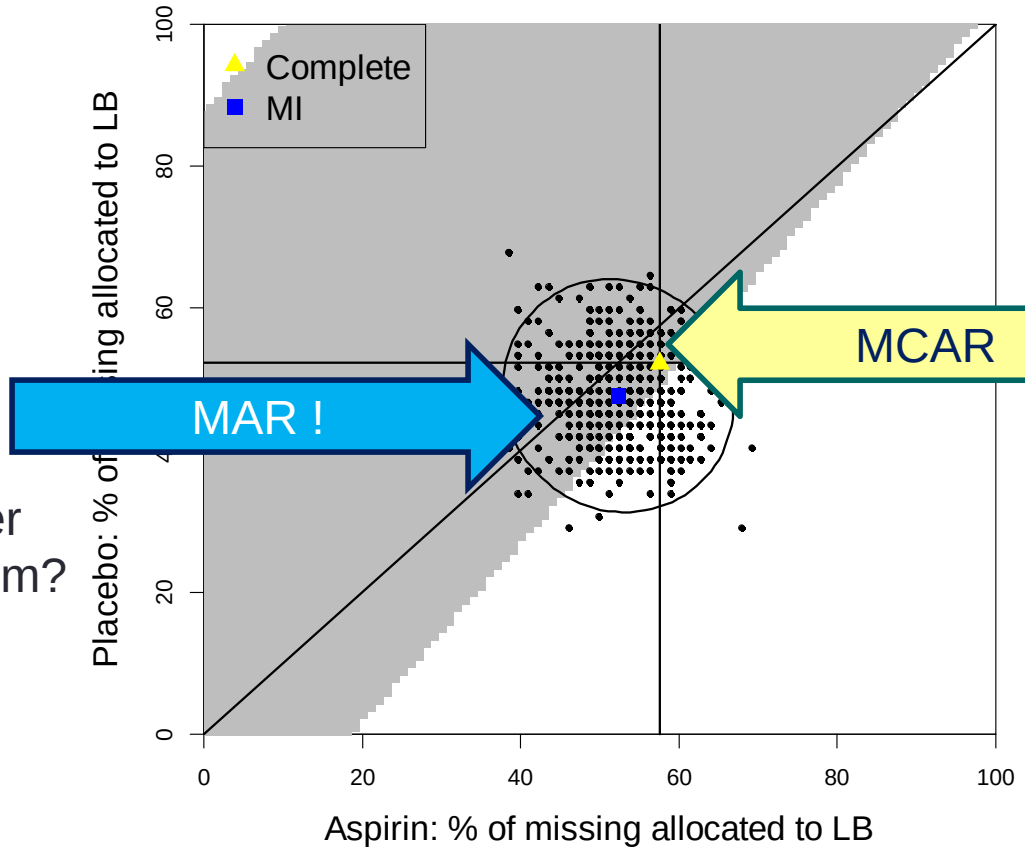


*Model: Rx, nulliparity, age, race, married, eligibility strata, BMI, time since loss, Log CRP

Sensitivity analysis: overall

Multiple Imputation RR=1.10

(500 Imputed Datasets)



MNAR

Bounds contain even the most extreme mechanism

MCAR

MAR !

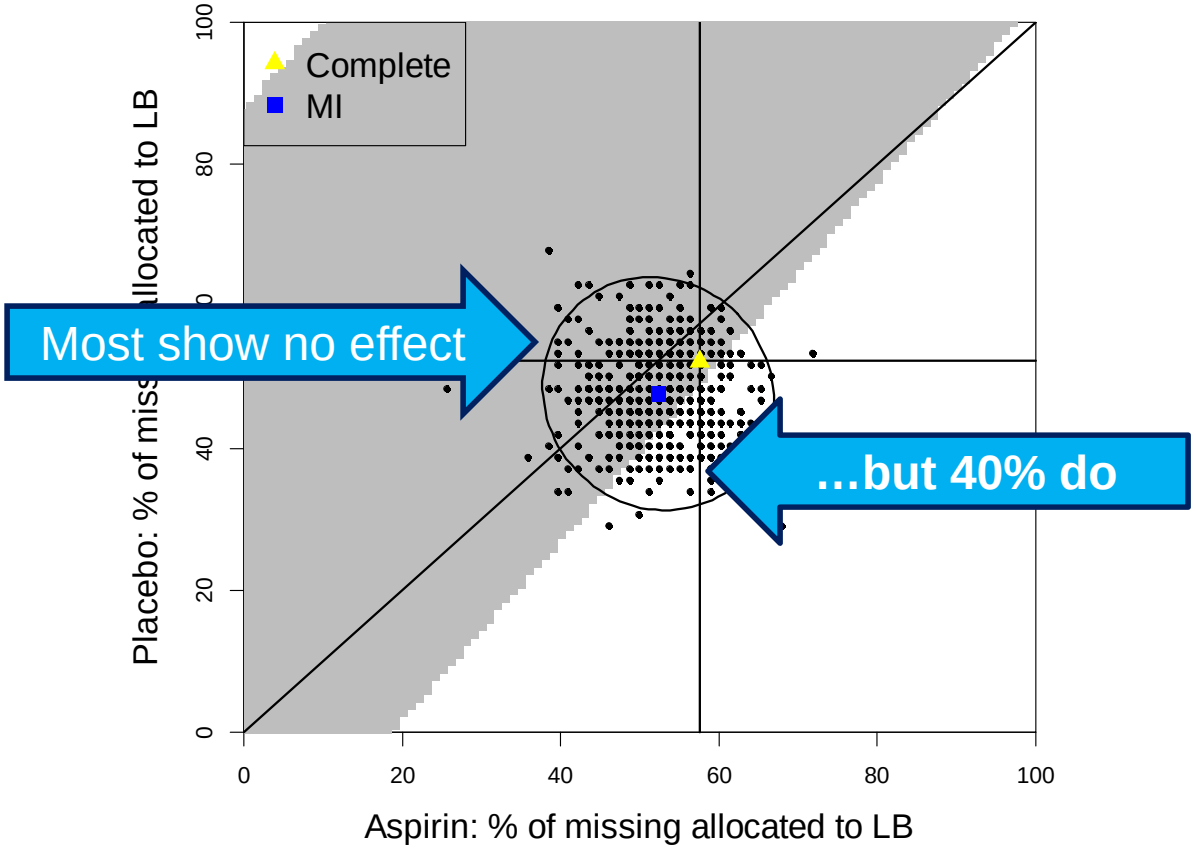
500 imputed datasets give a region that is reasonable under missing at random?

Triangle region is what is intuitively reasonable under missing completely at random

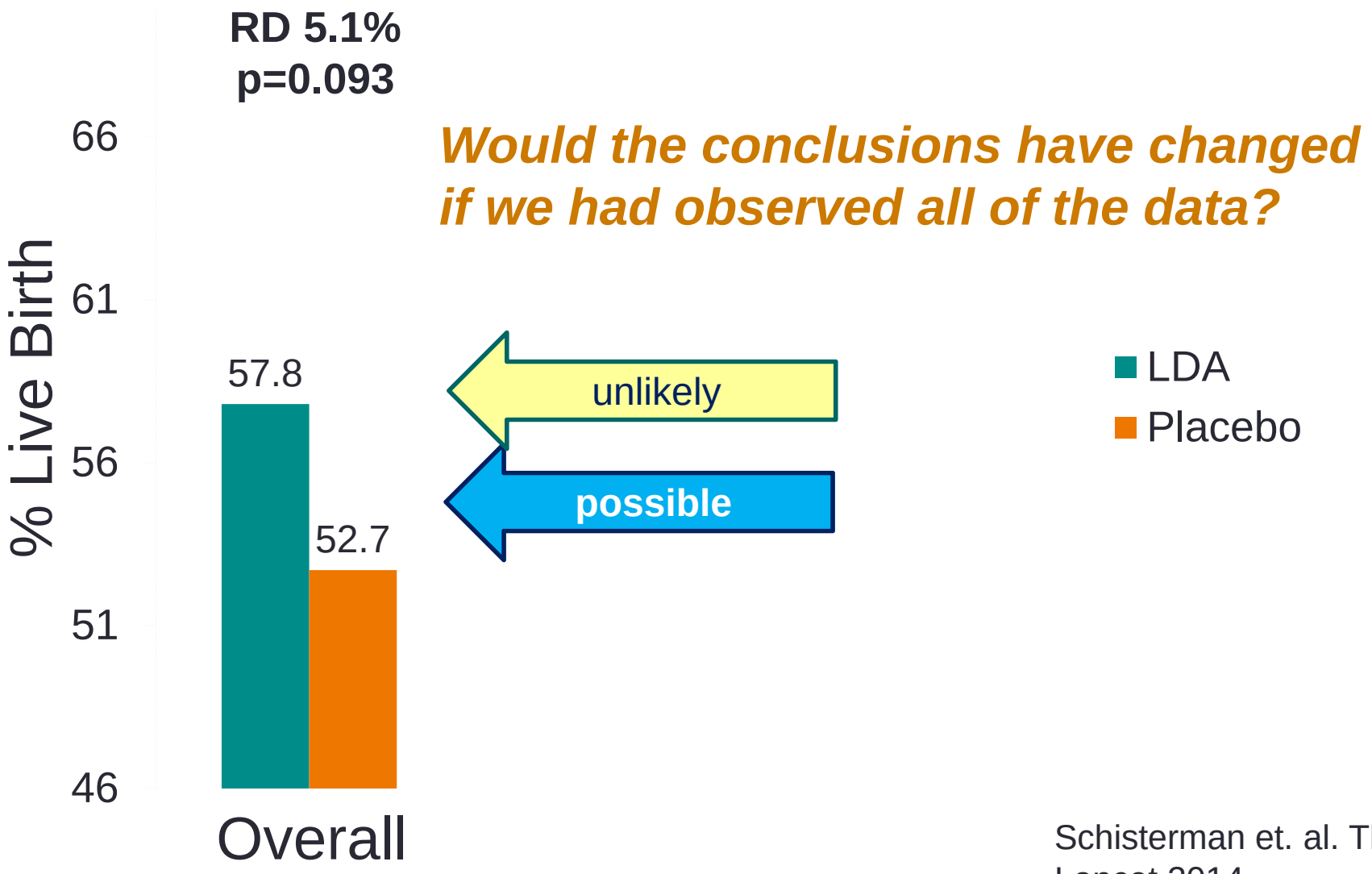
Sensitivity analysis: overall

Multiple Imputation RR=1.10

(500 Imputed Datasets)



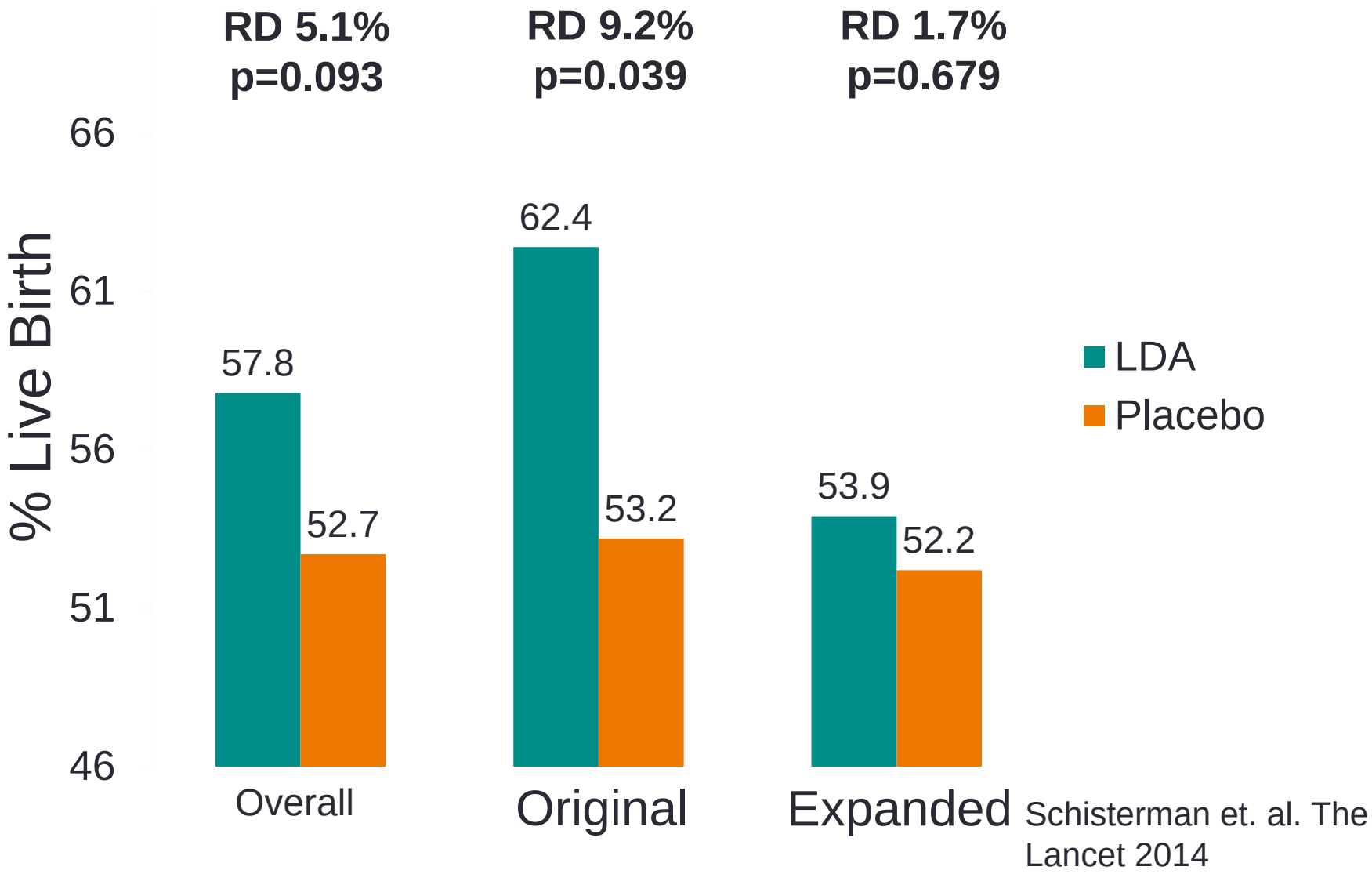
Live Births: Overall



Would the conclusions have changed if we had observed all of the data?

Schisterman et. al. The Lancet 2014

Live Births: By Stratum



Schisterman et. al. The Lancet 2014

Sensitivity analysis: **By Stratum**

Original

- **Information available for 495 of the 549 participants (90%)**
- **Missing Outcome:**
  - **22 Placebo**
  - **32 LDA**

Expanded

- **Information available for 593 of the 679 participants (87%)**
- **Missing Outcome:**
  - **40 Placebo**
  - **46 LDA**

Sensitivity analysis: **By Stratum**

	Original			Expanded		
	LDA	Placebo	P-value	LDA	Placebo	P-value
Complete cases	62.14	53.17	0.0443	53.74	51.51	0.5856
All poor	54.91	48.91	0.1592	46.47	45.43	0.7856
All good	66.55	56.93	0.0205	60.00	57.23	0.5033
Best Case	66.55	48.91	<0.0001	60.00	57.23	0.0002
Worst Case	54.91	56.93	0.6330	46.47	45.43	0.0050
***MI**	59.33	50.64	0.0458	46.41	44.59	0.6139

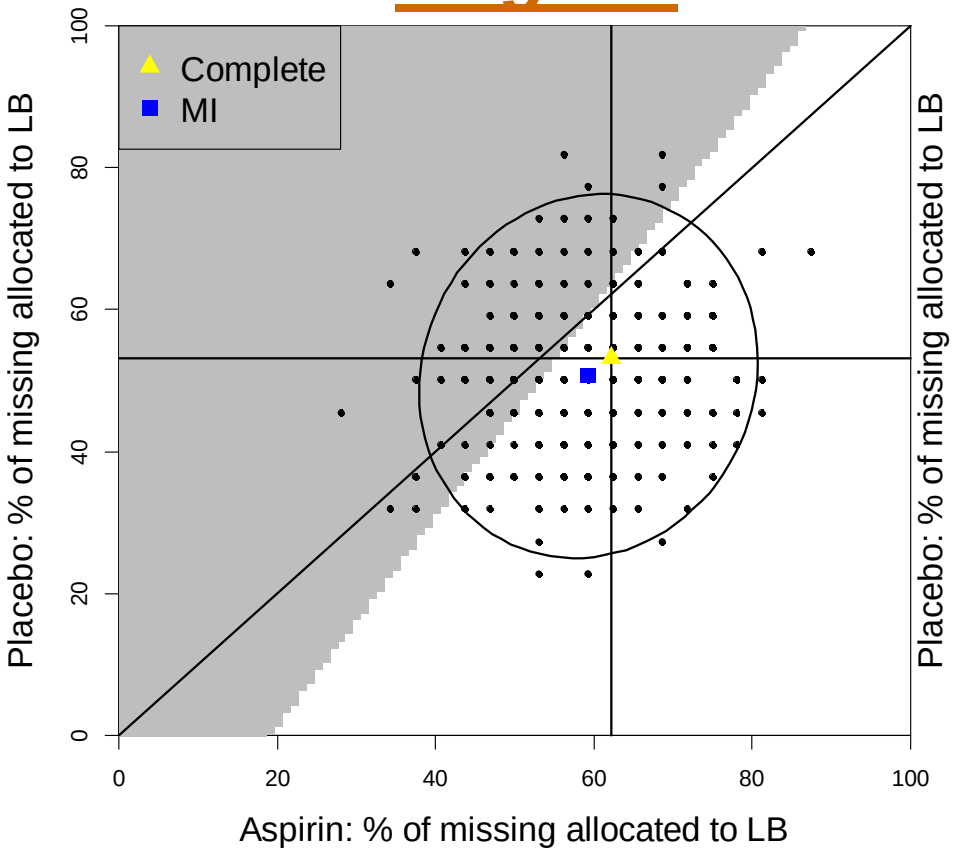
*Model: Rx, nulliparity, age, race, married, eligibility strata, BMI, time since loss

Sensitivity analysis: **By Stratum**

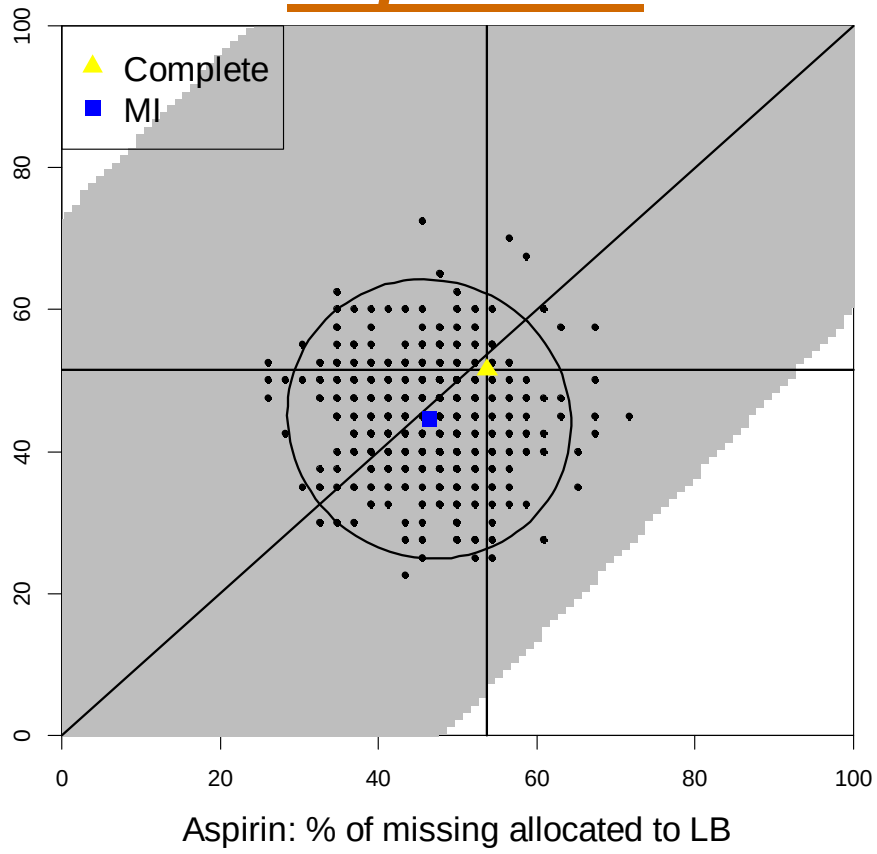
LDA vs. Placebo on Live Birth

(P-values)

Original



Expanded

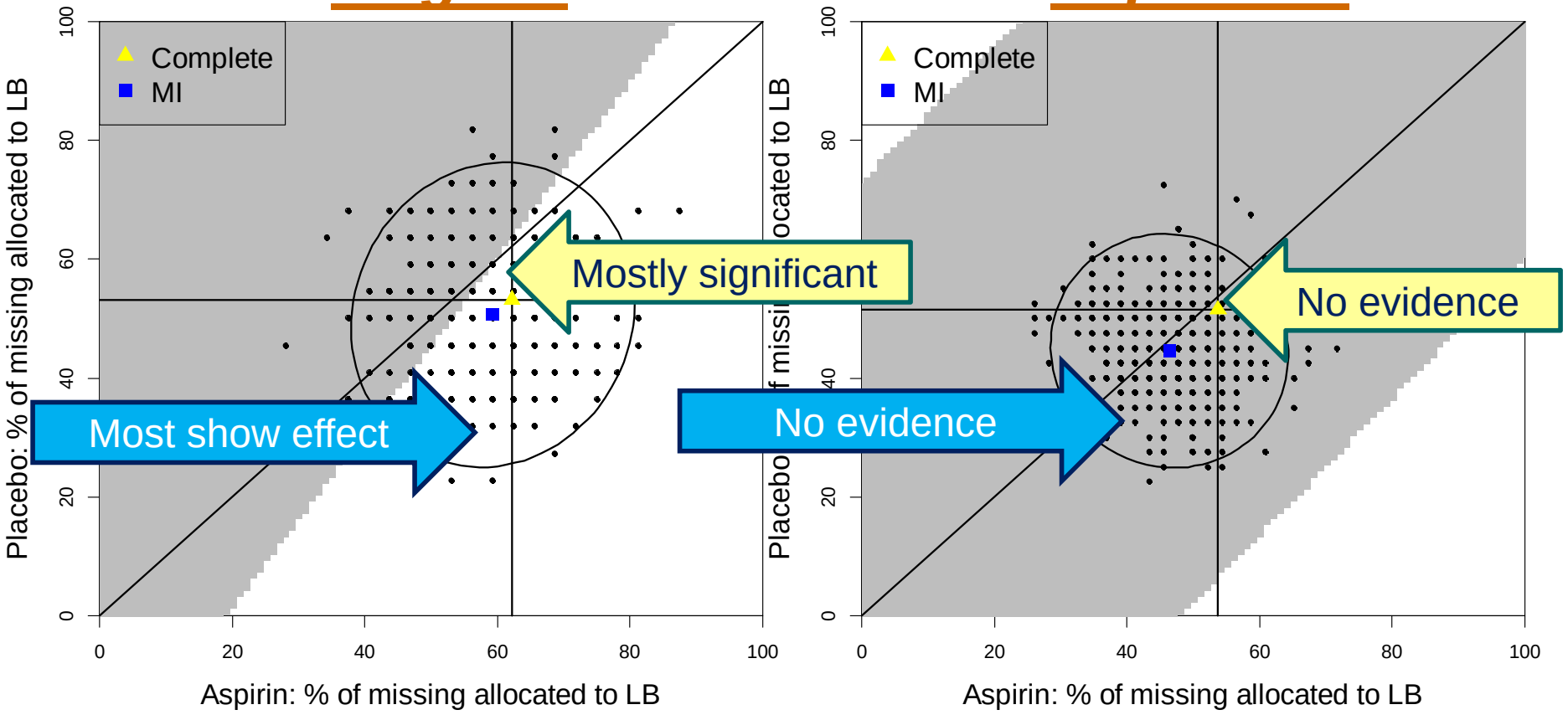


Sensitivity analysis: **By Stratum**

LDA vs. Placebo on Live Birth

(P-values)

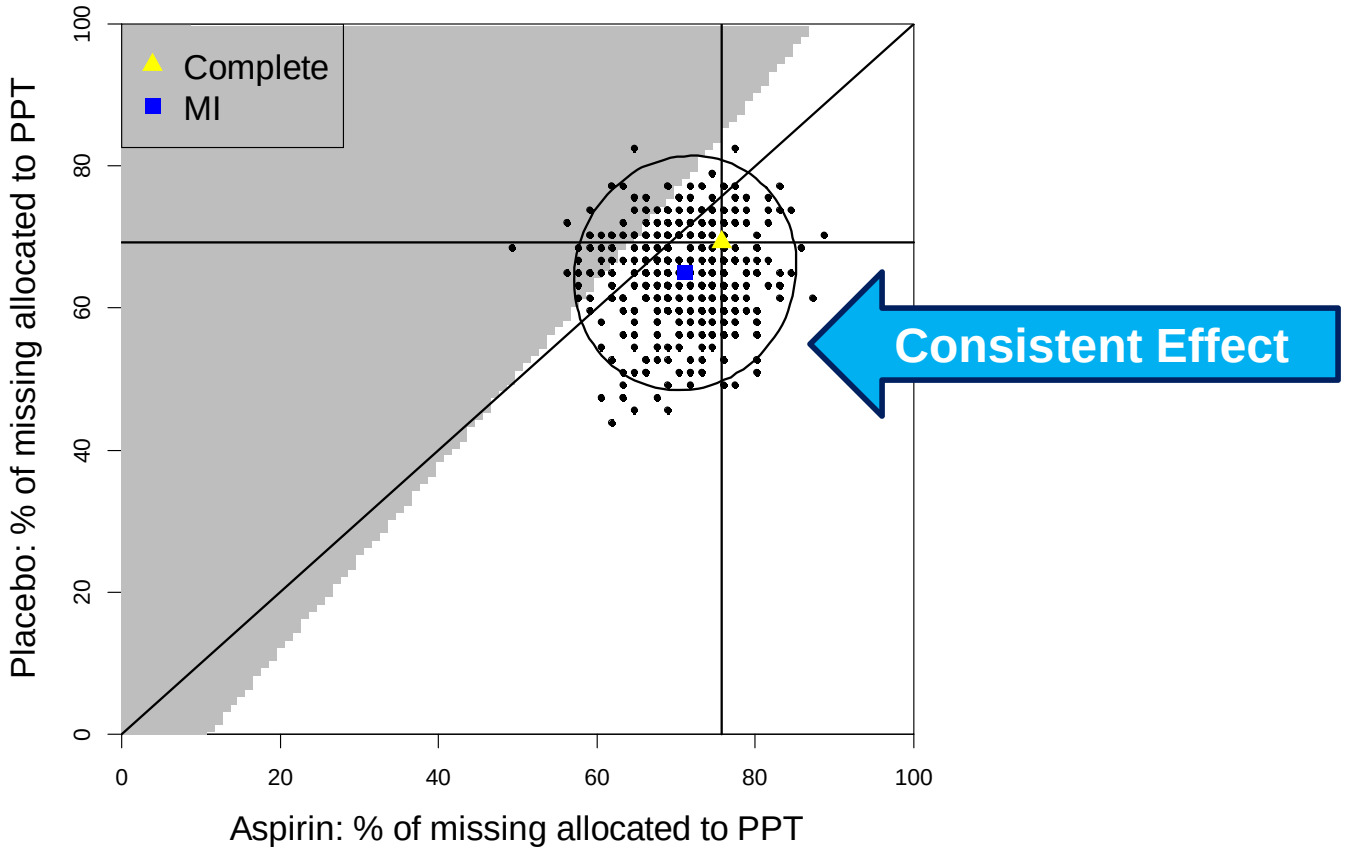
Original ***Expanded***



Sensitivity analysis: overall

LDA vs. Placebo on Positive Pregnancy Test

(P-values)

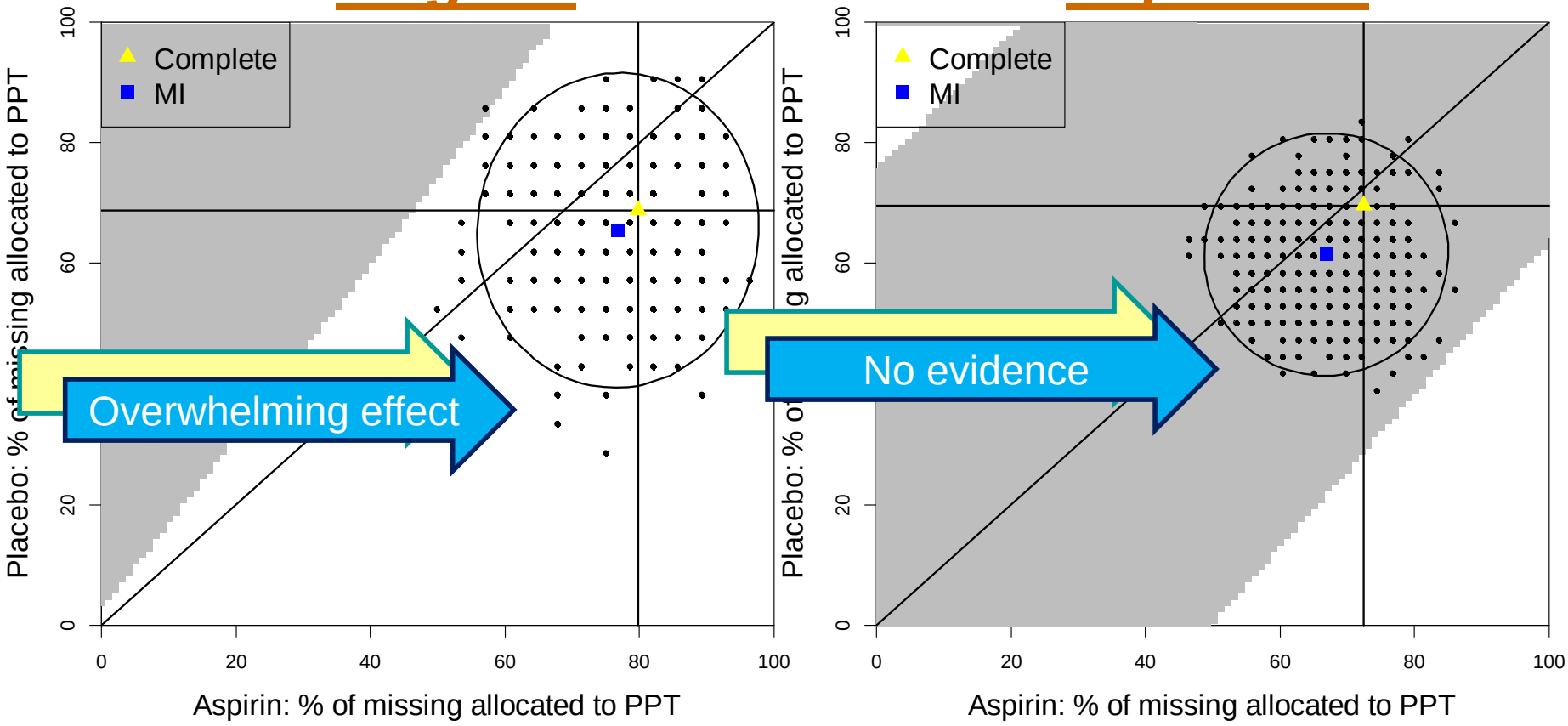


Sensitivity analysis: **By Stratum**

LDA vs. Placebo on Positive Pregnancy Test

(P-values)

Original ***Expanded***



The Prevention and Treatment of Missing Data in Clinical Trials

Key finding:

"Substantial instances of missing data are a serious problem that undermines the scientific credibility of causal conclusions from clinical trials. The assumption that analysis methods can compensate for such missing data are not justified, so aspects of trial design that limit the likelihood of missing data should be an important objective. In addition to specific aspects of trial design, many components of clinical-trial conduct can limit the extent of missing data. Finally, in studies with missing data, analysis methods that are based on plausible scientific assumptions should be used. For example, this consideration often rules out simple fixes, such as imputation by the last observation carried forward.[10] Although there are better analysis alternatives to that method, they all require unverifiable assumptions. Thus, **sensitivity analyses** should be conducted to assess the robustness of findings to plausible alternative assumptions about the missing data."

RJ Little et al. 2012. N Engl J Med. Oct 4;367(14):1355-60.

Missing outcome data: “How to”
What is the impact on the risk ratio?

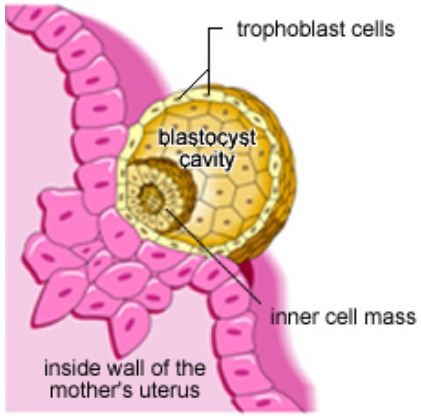
LDA and pregnancy with male offspring

What this section will cover

- Motivating example
- Plot: sensitivity of RR to missing outcome data
- SAS program
  - Addresses confounding, selection with weights (optional)
  - Generates data
  - Analyzes data
  - (R program)

Inflammation and implantation

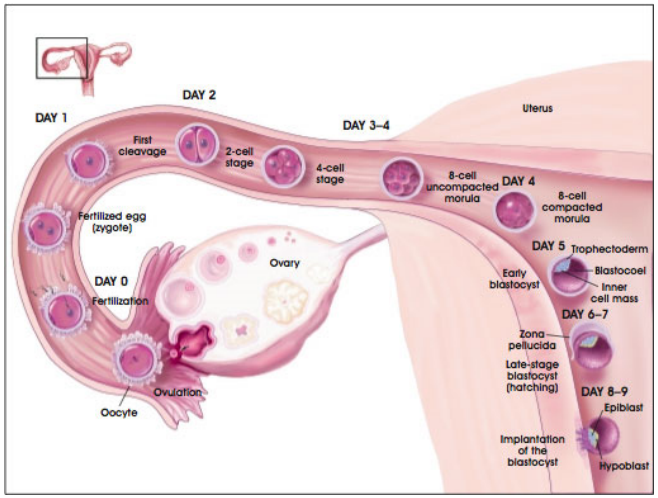
- Endometrium as biosensor
  - Responds to embryonic signals
  - Appropriate regulation of inflammatory response
  - LDA may modulate overactive inflammation



Macklon and Brosens *Biol Reprod* 2014
Quenby *Human Reprod* 1999

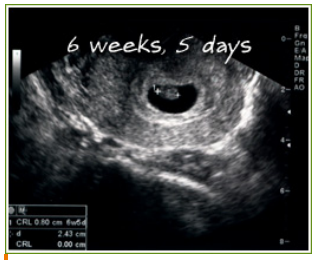
Are male embryos more vulnerable?

- Male and female pre-implantation embryos differ on:
  - Response to maternal inflammation
  - Gene expression
  - Metabolism



References:
Perez-Crespo *Mol Rep Dev* 2005,
Dobbs *Biol Rep* 2014,
Kay *Cell* 1994,
Bermejo-Alvarez *PNAS* 2010,
Ray *J Reprod Fertil* 1995

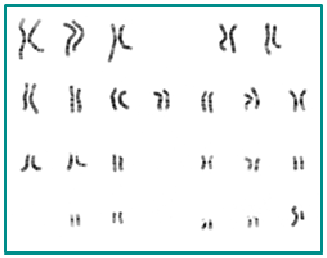
Pregnancy Follow-up



Study pill plus folic acid

Genetic testing of clinical pregnancy losses

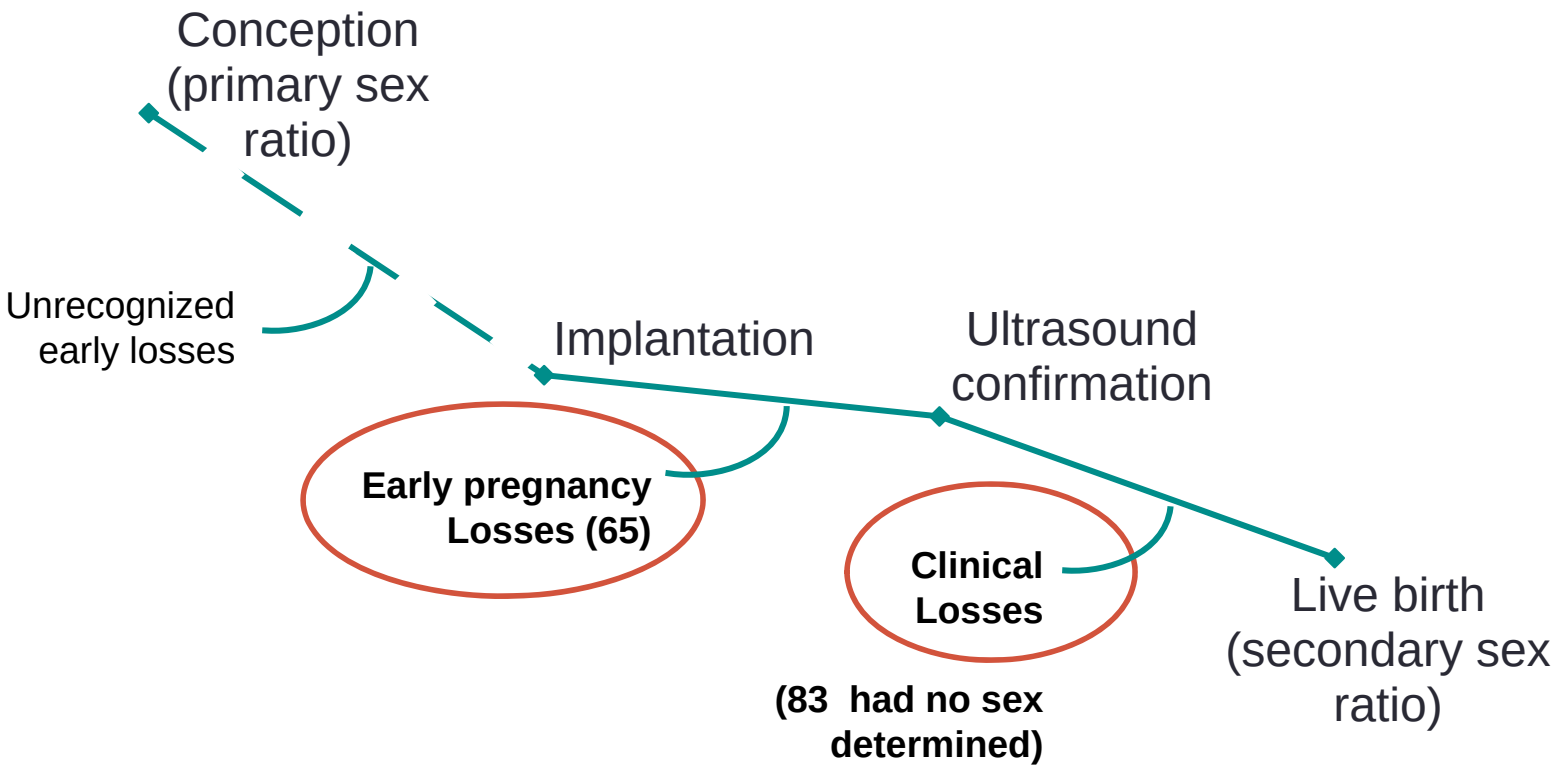
4 weeks' GA –
end-cycle study visit



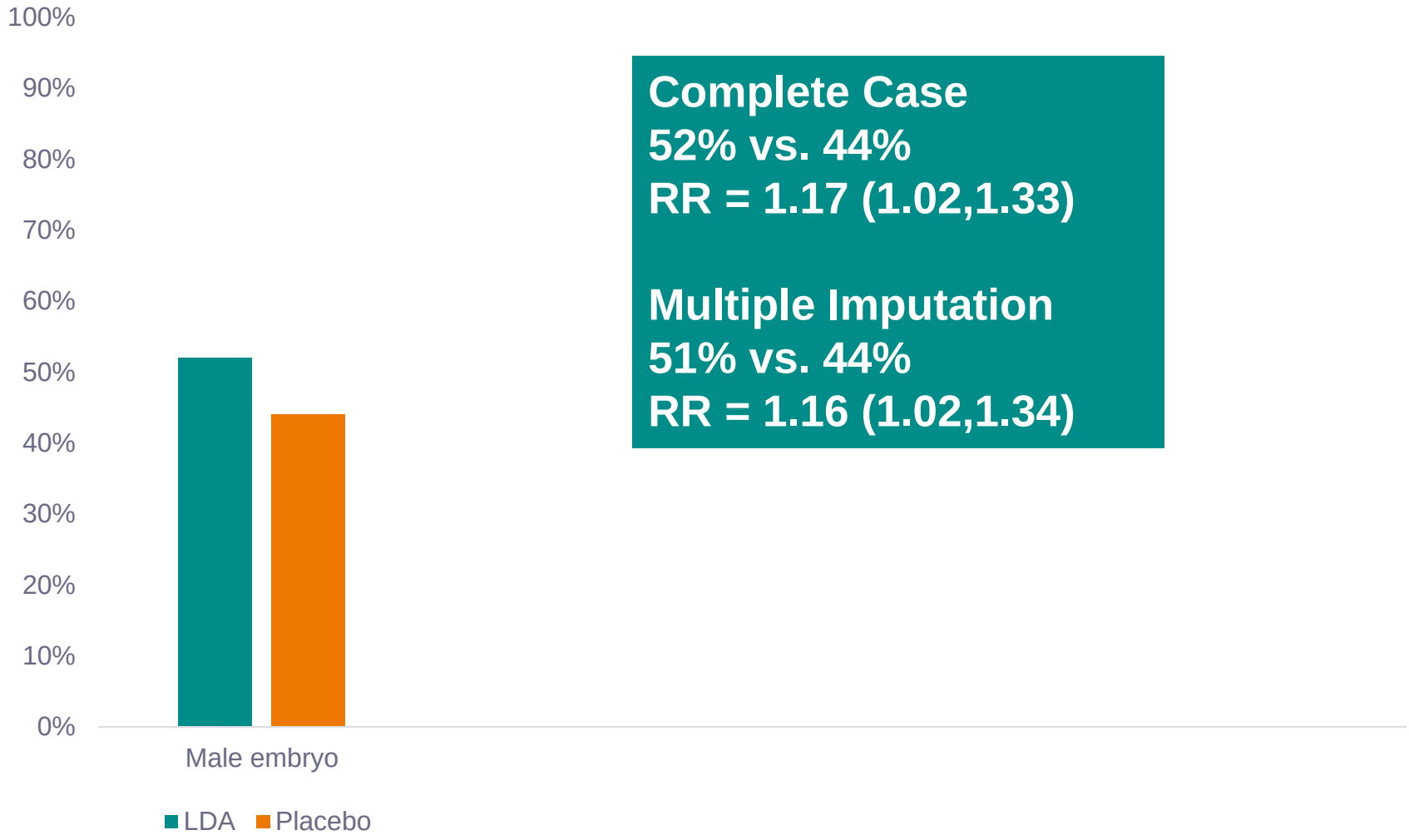
Intent-to-treat analysis

	LDA	Placebo
No pregnancy detected	203 (33%)	228 (37%)
Pregnancy:	412	385
Pregnancy loss – no sex determined	73 (12%)	75 (12%)
female offspring	164 (27%)	173 (28%)
male offspring	**175 (28%)**	**137 (22%)**
Total	*615 (100%)*	*613 (100%)*

What about sex ratio at implantation?



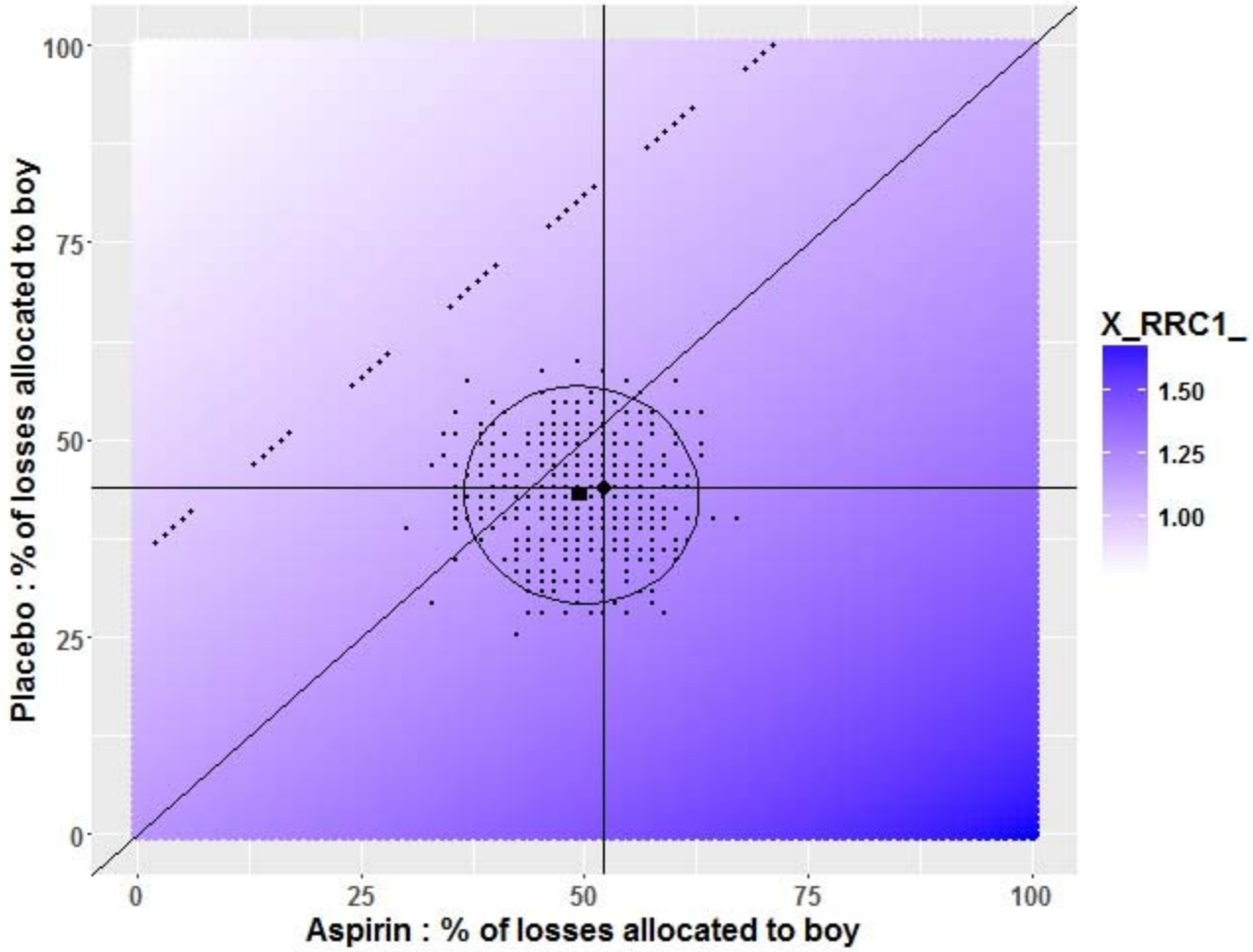
Male offspring among pregnancies: LDA vs. placebo



Complete Case
52% vs. 44%
RR = 1.17 (1.02,1.33)

Multiple Imputation
51% vs. 44%
RR = 1.16 (1.02,1.34)

Male offspring among pregnancies: LDA vs. placebo



- SAS program –
  - Addresses confounding, selection with weights (optional)
  - Generates data for every scenario
  - Analyzes data

Cross tab

	LDA	Placebo
Boy	175	137
Girl	164	173
Missing	73	75
TOTAL	**412**	**385**

```
/* distribution of girls, boys, and missings by exposure among women with PPT */
/* N = number observed, M = number missing in that exposure arm */
data mylib.crosstab;
input exposure$ outcome$ N M;
cards;
Aspirin boy     175 73
Aspirin girl    164 73
Placebo boy     137 75
Placebo girl    173 75
;run;
```

Apply weights (optional)

- Address confounding or selection in your data

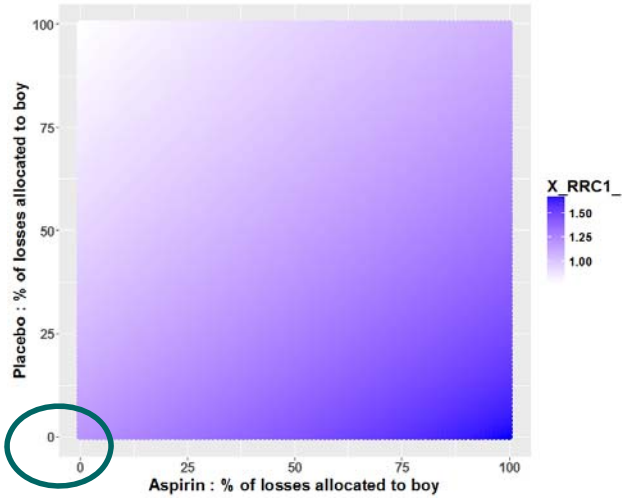
	LDA	Placebo
Boy	175	137
Girl	164	173
Missing	73	75
TOTAL	**412**	**385**

	LDA	Placebo
Boy	261.23	218.13
Girl	244.81	275.45
Missing	108.96	119.42
TOTAL	**615**	**613**

```
data mylibwts.crosstabwt; set mylibwts.crosstab;

w_LDA_preg = 1 / (412/615);
w_Placebo_preg = 1 /(385/613);

if exposure = 'Aspirin' then do;
 N = N * w_lda_preg;  M = M * w_lda_preg; end;
else if exposure = 'Placebo' then do;
 N = N * w_placebo_preg;  M = M * w_placebo_preg; end;
```

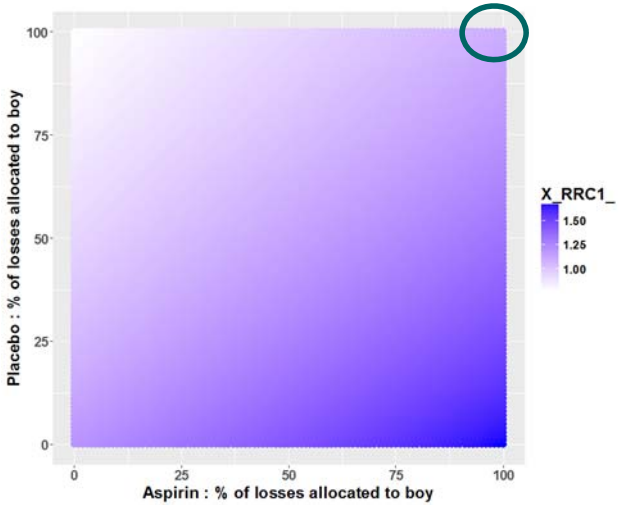
- SAS program –
  - Addresses confounding, selection with weights (optional)
  - Generates data for every scenario
  - Analyzes data
  - R program

Create the outcome distribution under every scenario (0 – 100%)



exposure	outcome	x1	x2	.....	x10200	x10201
Aspirin	boy	261.23	261.23		370.19	370.19
Aspirin	girl	353.77	353.77		244.81	244.81
Placebo	boy	218.13	219.33		336.35	337.55
Placebo	girl	394.87	393.67		276.65	275.45
Aspirin	pct	0.00	0.00		100.00	100.00
Placebo	pct	0.00	1.00		99.00	100.00

Create the outcome distribution under every scenario (0 – 100%)



exposure	outcome	x1	x2	.....	x10200	x10201
Aspirin	boy	261.23	261.23		370.19	370.19
Aspirin	girl	353.77	353.77		244.81	244.81
Placebo	boy	218.13	219.33		336.35	337.55
Placebo	girl	394.87	393.67		276.65	275.45
Aspirin	pct	0.00	0.00		100.00	100.00
Placebo	pct	0.00	1.00		99.00	100.00

```
data mylibwts.wide_data;set mylibwts.crosstabwt;
array new x1-x10201;
j=1;
do a=0 to 100 by 1;  * do loop in aspirin *;
 do p=0 to 100 by 1; * do loop in placebo *;
  if exposure in ('Aspirin') and outcome in ('boy') then new[j]=N+((a/100)*M);
  if exposure in ('Aspirin') and outcome in ('girl') then new[j]=N+(((100-a)/100)*M);

  if exposure in ('Placebo') and outcome in ('boy') then new[j]=N+((p/100)*M);
  if exposure in ('Placebo') and outcome in ('girl') then new[j]=N+(((100-p)/100)*M);

  if exposure in ('Aspirin') and outcome in ('pct') then new[j]=a;
  if exposure in ('Placebo') and outcome in ('pct') then new[j]=p;
  j+1;
 end;
end;
```

exposure	outcome	x1	x2	.....	x10200	x10201
Aspirin	boy	261.23	261.23		370.19	370.19
Aspirin	girl	353.77	353.77		244.81	244.81
Placebo	boy	218.13	219.33		336.35	337.55
Placebo	girl	394.87	393.67		276.65	275.45
Aspirin	pct	0.00	0.00		100.00	100.00
Placebo	pct	0.00	1.00		99.00	100.00

Alternative approach to creating the outcome distribution (whole numbers)

Alternative approach you could use when analyzing unweighted data

```
data mylibnum.wide_data;set mylibnum.crosstab;
 array new x1-x5624;
 j=1;
 do i=0 to 73 by 1;   * do loop in aspirin *;
  do k=0 to 75 by 1; * do loop in placebo *;
   if exposure in ('Aspirin') and outcome in ('boy') then new[j]=N+i;
   if exposure in ('Aspirin') and outcome in ('girl') then new[j]=N+(73-i);
   if exposure in ('Placebo') and outcome in ('boy') then new[j]=N+k;
   if exposure in ('Placebo') and outcome in ('girl') then new[j]=N+(75-k);

   if exposure in ('Aspirin') and outcome in ('pct') then new[j]=i;
   if exposure in ('Placebo') and outcome in ('pct') then new[j]=k;
   j+1;
  end;
 end;
```

- SAS program –
  - Addresses confounding, selection with weights (optional)
  - Generates data for every scenario
  - Analyzes data
  - R program

Wide data set for analysis

exposure	outcome	x1	x2	……..	x10200	x10201
Aspirin	boy	261.226	261.226	……..	370.194	370.194
Aspirin	girl	353.774	353.774	……..	244.806	244.806
Placebo	boy	218.132	219.327	……..	336.354	337.548
Placebo	girl	394.868	393.673	……..	276.646	275.452

Analyze tabular data

exposure	outcome	N	M	x1	x2	…….	x10200	x10201
Aspirin	boy	175	73	261.226	261.226	…….	370.194	370.194
Aspirin	girl	164	73	353.774	353.774	…….	244.806	244.806
Placebo	boy	137	75	218.132	219.327	…….	336.354	337.548
Placebo	girl	173	75	394.868	393.673	…….	276.646	275.452

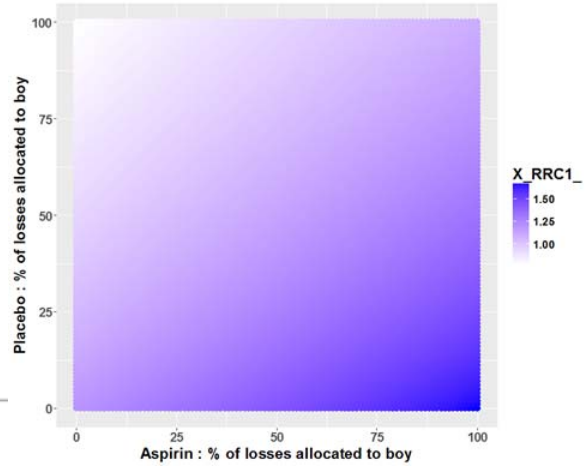
	boy	girl
Aspirin	261.226	353.774
Placebo	218.132	394.868

P_PCHI	_RDIF1_	_RRC1_
0.013318	0.068913	1.19366

```
proc freq data=mylibwts.wide_data noprint;
 tables exposure*outcome
 /chisq relrisk riskdiff nopercent;
 weight x1;
 output out=out1(keep=p_pchi _RDIF1_ _RRC1_) chisq relrisk riskdiff;
run;
```

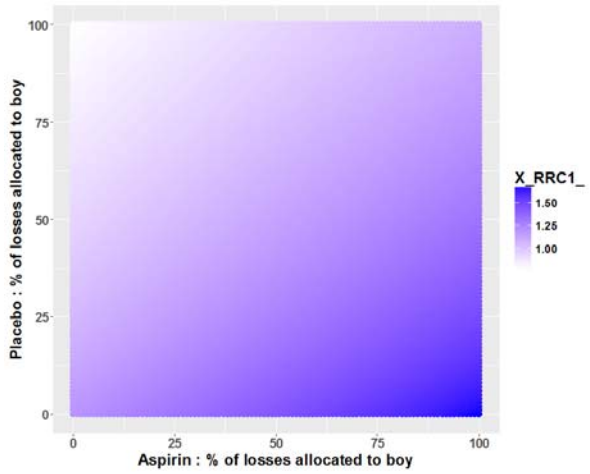
Analyze tabular data…10,201 times

```
data mylibwts.chisq_results_w;
input a;
cards;
1
2
3
;

%macro DOCHISQ_W;
%do i=1 %to 10201;

proc freq data=mylibwts.wide_data(where=(outcome in ("boy","girl"))) noprint;
 tables exposure*outcome
 /chisq relrisk riskdiff nopercent;
 weight x&i;
 output out=out&i(keep=p_pchi _RDIF1_ _RRC1_) chisq relrisk riskdiff;
run;

data mylibwts.chisq_results_w;
 set mylibwts.chisq_results_w out&i;
run;

proc datasets;
 delete out&i;
run;
%end;
%mend DOCHISQ_W;

%DOCHISQ_W;
quit;
```



Results from 10,201 allocation scenarios

NAME	Aspirin	Placebo	P_PCHI	_RDIF1_	_RRC1_
x1	0	0	0.013	0.069	1.194
x2	0	1	0.016	0.067	1.187
x3	0	2	0.020	0.065	1.181
⋮					
x10199	100	98	0.050	0.055	1.101
x10200	100	99	0.059	0.053	1.097
x10201	100	100	0.069	0.051	1.093



Make wide data tall: transpose

exposure	outcome	x1	x2	…….	x10200	x10201
Aspirin	boy	261.226	261.226	…….	370.194	370.194
Aspirin	girl	353.774	353.774	…….	244.806	244.806
Placebo	boy	218.132	219.327	…….	336.354	337.548
Placebo	girl	394.868	393.673	…….	276.646	275.452
Aspirin	pct	0	0		100	100
Placebo	pct	0	1		99	100

NAME	Aspirin_ boy	Aspirin_ girl	Placebo_ boy	Placebo_ girl	Aspirin	Placebo
x1	261.226	353.774	218.132	394.868	0	0
x2	261.226	353.774	219.327	393.673	0	1
⋮						
x10200	370.194	244.806	336.354	276.646	100	99
x10201	370.194	244.806	337.548	275.452	100	100

Make wide data tall: transpose

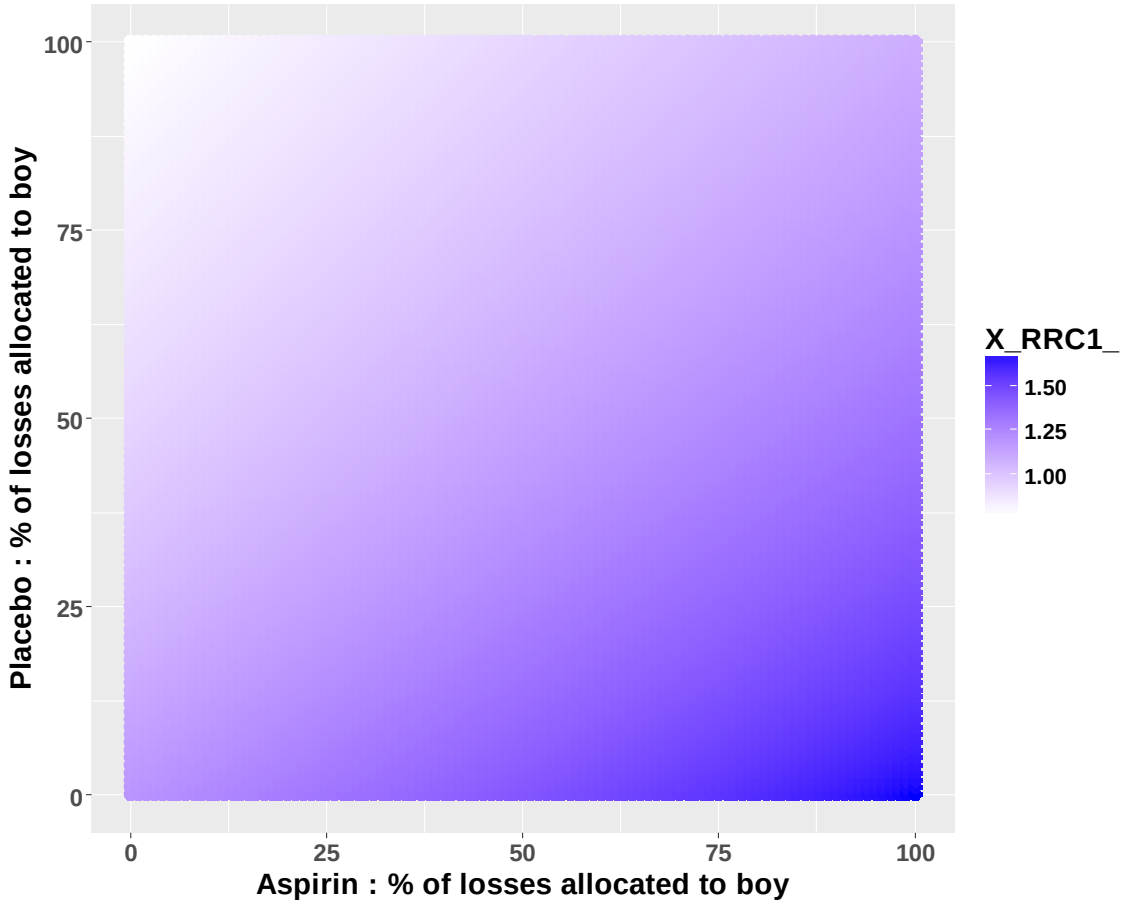
```
proc transpose data=mylibwts.wide_data out=mylibwts.tall_data;run;

data mylibwts.tall_data2; set mylibwts.tall_data;
 * delete any row that is not an allocation scenario;
 if _NAME_ in ('N' 'M' 'j' 'i' 'k' 'a' 'p' 'w_LDA_preg' 'w_Placebo_preg') then delete;
 rename COL1=Aspirin_boy COL2=Aspirin_girl
        COL3=Placebo_boy COL4=Placebo_girl
        COL5=Aspirin COL6=Placebo;
 id+1;
```

Export results to .csv file

```
data mylibwts.data_To_Plot_wt;
 merge   mylibwts.tall_data2(keep=_NAME_ Aspirin Placebo id)
         mylibwts.chisq_results_w ;
 by id;
 drop id;
 run;
```

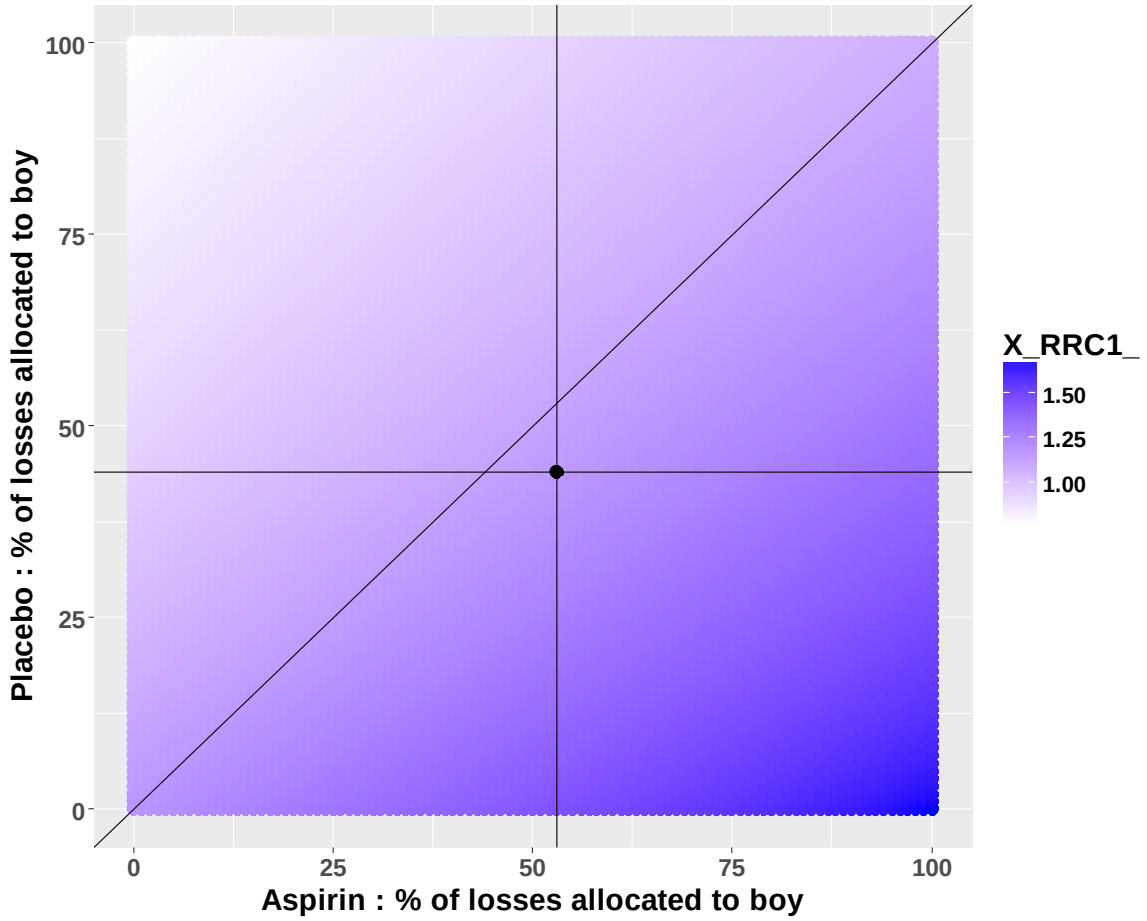
```
PROC EXPORT DATA= mylibwts.data_To_Plot_wt
            OUTFILE= "C:\Users\radinrg\Documents\Advanced Methods Workshop\data\sensitivity_results_wt.csv"
            DBMS=CSV REPLACE;
     PUTNAMES=YES;
RUN;
```

Heat Map: all possible scenarios



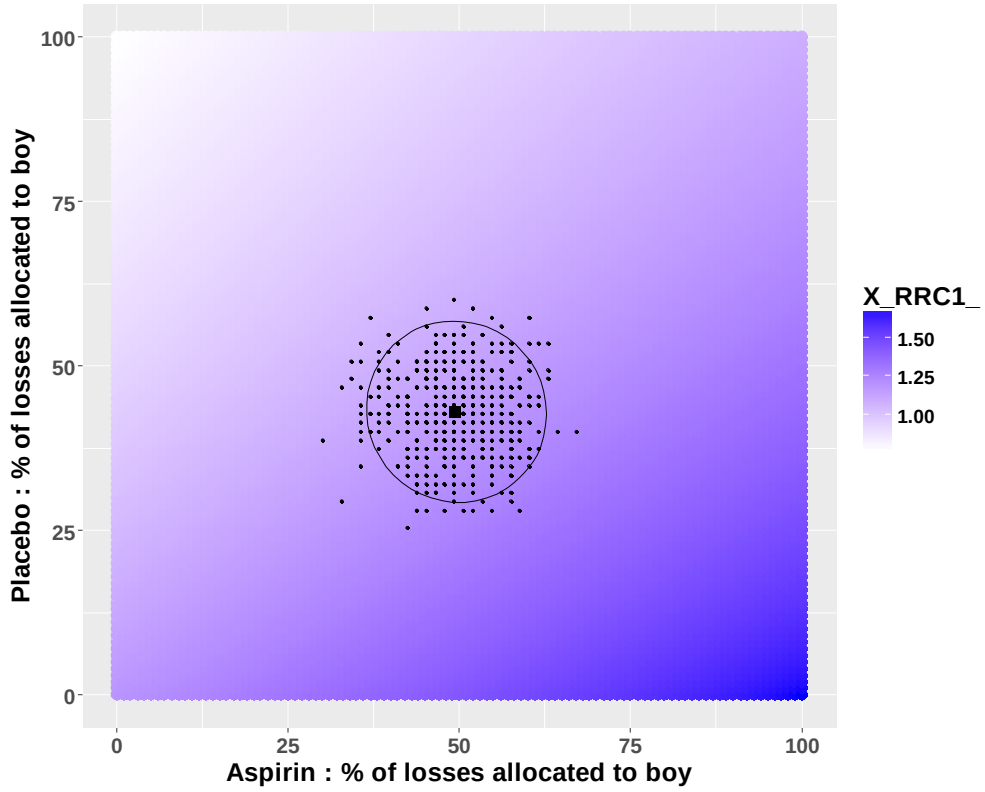
Overlay lines, dot: plausible scenarios

R Function plots the complete case and three lines to define plausible scenarios



Make the oval and dots: PROC MI

- Define plausible scenarios
- Each imputed data set represents one plausible scenario



SAS Code: PROC MI

```
proc mi data=complete seed=12345 out=MIdata nimpute=500;
    class boy1 time_last_loss1;
    fcs logistic(boy1/details) discrim(time_last_loss1/details);
    var  boy1
    is_treatment PriorLB0 bmi logcrp
    age white married time_last_loss1 ;
run;
```

Associated with outcome

Associated with missingness

SAS Log: PROC MI

- Fully conditional specification uses continuous predictors only.

```
514  proc mi data=preg seed=12345 out=boyMIdata nimpute=500;
515     class boy1 time_last_loss1;
516     fcs logistic(boy1/details) discrim(time_last_loss1/details);
517     var  boy1 is_treatment PriorLBO age white married bmi time_last_loss1 logcrp;
518
519  run;

WARNING: The covariates are not specified in an FCS discriminant method for variable time_last_loss1, only remaining
         continuous variables will be used as covariates with the default CLASSEFFECTS=EXCLUDE option.
NOTE: The data set WORK.BOYMIDATA has 398500 observations and 354 variables.
NOTE: PROCEDURE MI used (Total process time):
      real time           2:19.12
      cpu time            2:18.18
```

Each imputation: % allocated to male

		Number of males		Number of pregnancies	Percent of missing allocated to male
Imputation	is_treatment	Imputed data set	Complete case	Missing outcome	
1	0	286.60	218.13	119.42	57.33
2	0	277.04	218.13	119.42	49.33
3	0	272.27	218.13	119.42	45.33
4	0	265.90	218.13	119.42	40.00

Imputed = observed + (Missing * percent * 0.01)

Calculate the % allocated to male

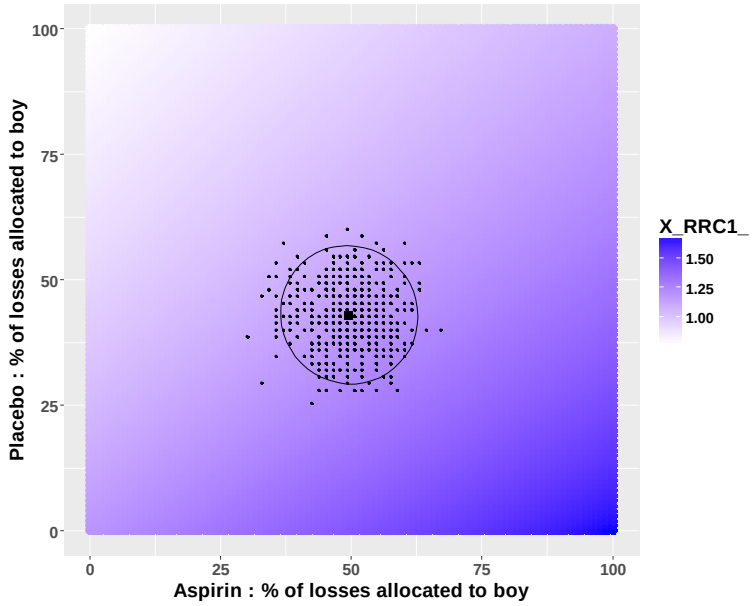
```
proc freq data=complete;
tables is_treatment*boy1/missing nocol norow nopercent chisq relrisk;
weight mypregwt;
ods output  CrossTabFreqs=cross0;
run;
```

```
* complete case: get number of boys in LDA and placebo groups *;
data male;
set cross0;
if boy1=1 and is_treatment~=. and _type_=11;
rename Frequency=n0;
label Frequency=n0;
keep is_treatment Frequency;
run;
```

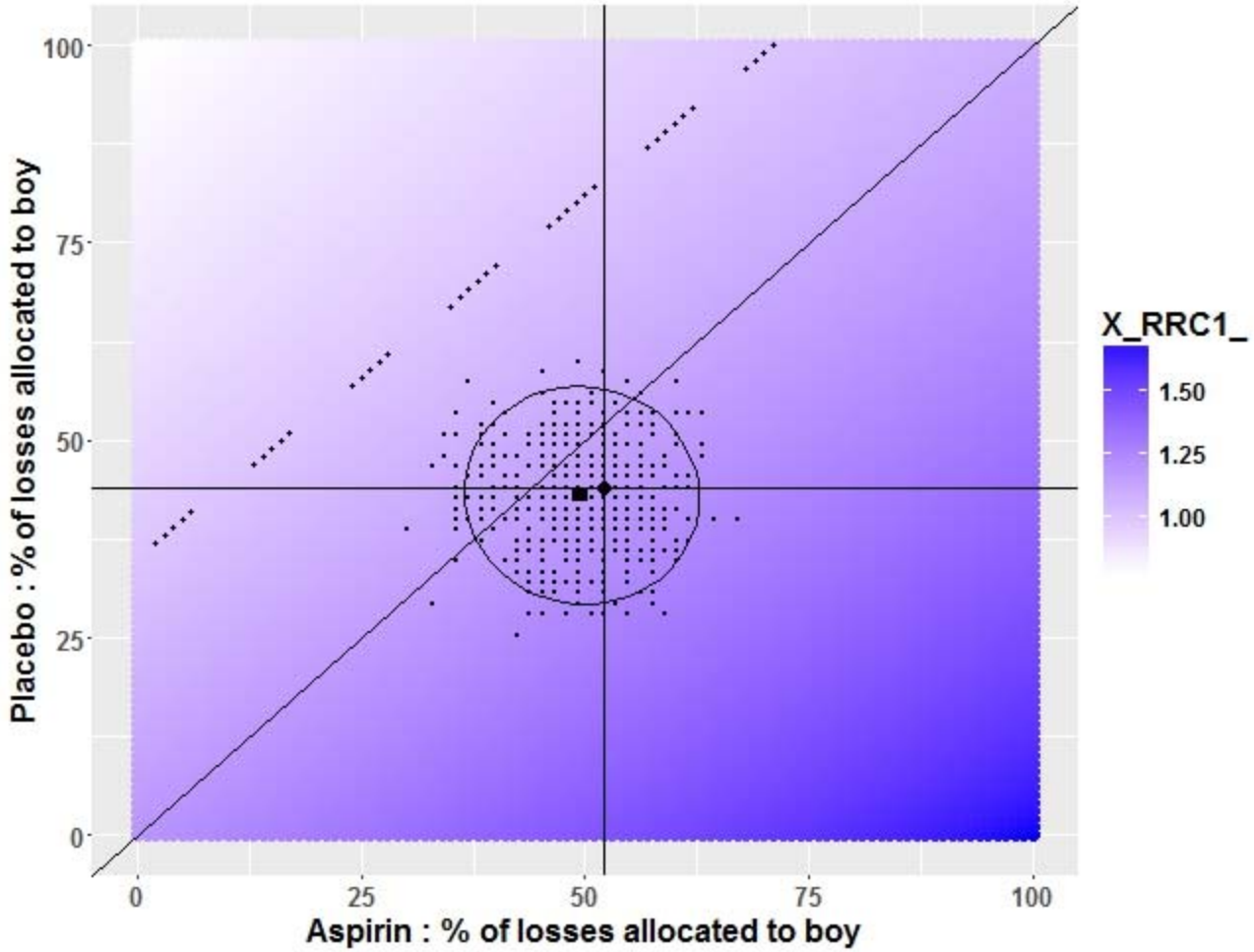
```
* complete case: get number of missing observations in LDA and placebo
data missing;
set cross0;
if boy1=. and is_treatment~=. and _type_=11;
rename Frequency=missing;
label Frequency=missing;
keep is_treatment Frequency;
run;
```

Calculate the % allocated to male

```
proc freq data=MIdata;
 tables is_treatment*boy1/norow nocol nopercent;
 by _imputation_;
 weight mypregwt;
 ods output  CrossTabFreqs=cross;
 run;
 * MI data: get number of boys in LDA and placebo groups *;
data cross2;
 set cross;
 if boy1=1 and is_treatment~=.;
 keep _imputation_ is_treatment Frequency;
 rename Frequency=n;
 label Frequency=n;
 run;

proc sort data=cross2;
 by is_treatment;
 run;

 * Step 4: calculate % of missing allocated to male in LDA,
data cross3;
 merge cross2 male missing;
 by is_treatment;

 percent=(n-n0)/missing*100;
 label percent='percent of missing allocated to male';
 run;
```



Sensitivity Plot R function



senPlot function in R

```
senPlot=function(dat, imp=NA, obs.per=c(.5,.5), null.para=NA, null.tol=0.001,
                 pvplot=TRUE, XY.names=list("X","Y"), missing="missing",
                 outcome.name="Yes", obs.col="black", imp.col="black",
                 pv.col=c("white","gray"), gradient.col=c("white","gray")){
```

- Data
- Plot type
- Axis labels
- Point estimate colors
- Background colors

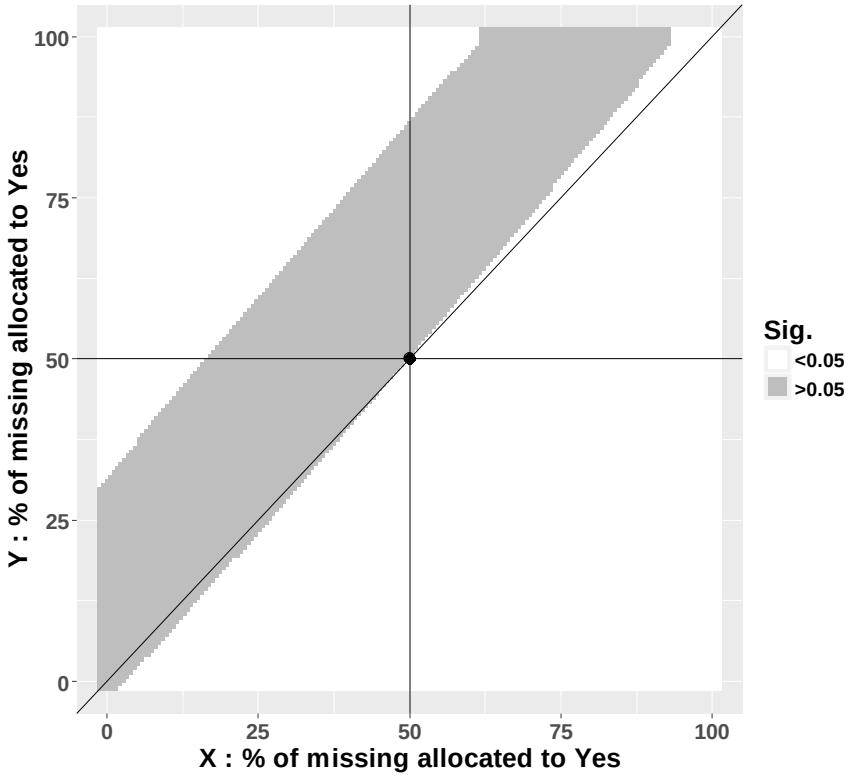
senPlot function in R

```
> senPlot(dat=dat[,c(1,2,5)])
```

- Data: dat=c(X, Y, background)

```
> head(dat[,c(1,2,5)])
```

1	0	fisher.exact
0.0000000	0	0.12317317
0.5882353	0	0.10591367
1.1764706	0	0.09065954
1.7647059	0	0.07724975
2.3529412	0	0.06552393
2.9411765	0	0.05532477

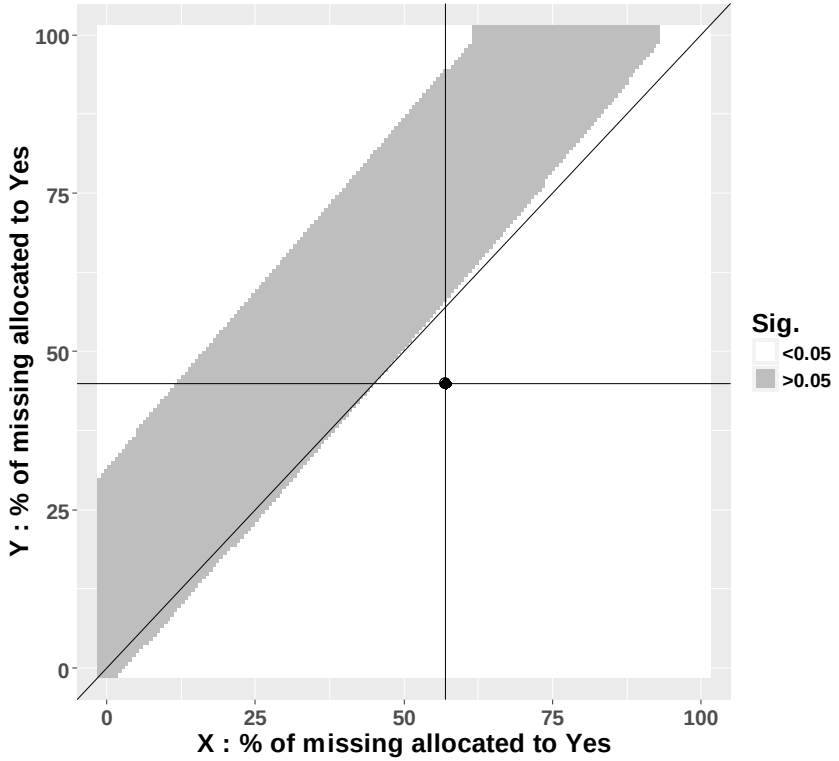


senPlot function in R

- senPlot(dat=dat[,c(1,2,5)], obs.per=per.obs[2:1])

- Data

```
> head(dat[,c(1,2,5)])
        1         0          fisher.exact
 0.0000000         0           0.12317317
 0.5882353         0           0.10591367
 1.1764706         0           0.09065954
 1.7647059         0           0.07724975
 2.3529412         0           0.06552393
 2.9411765         0           0.05532477
> per.obs[2:1]
       1        0
56.95652 44.89796
```

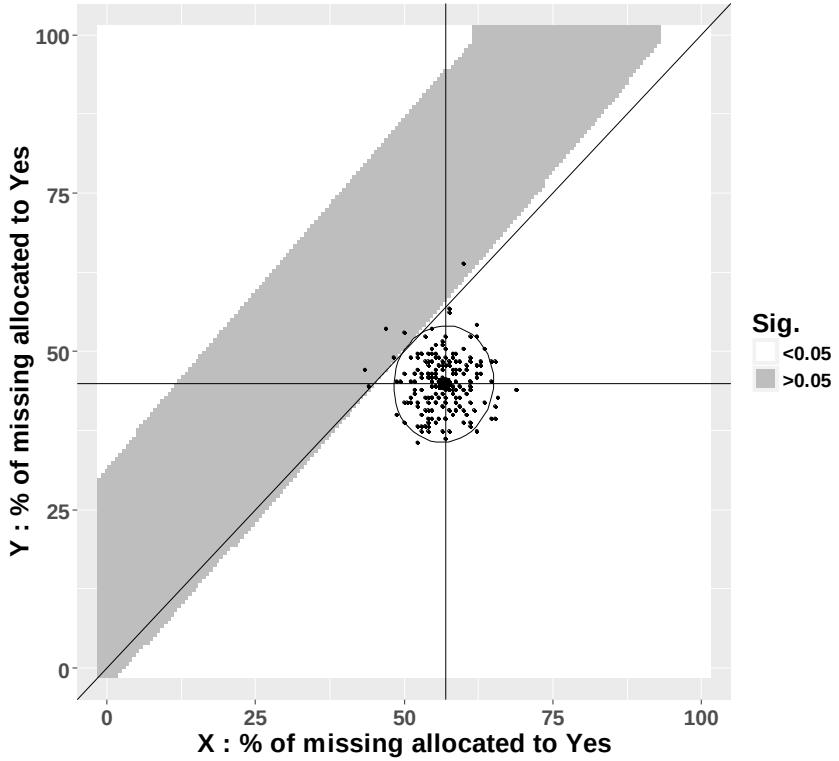


senPlot function in R

```
> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1])
```

- Data: imp=c(X, Y)

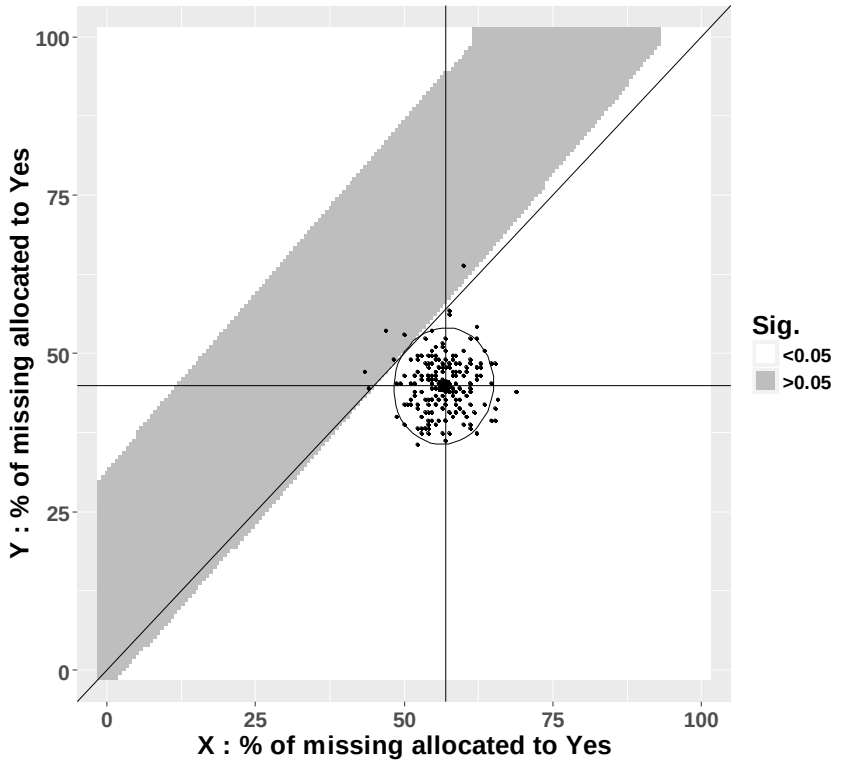
```
> head(imp.sen)
       1        0
52.35294 49.03226
50.00000 46.45161
55.29412 46.45161
54.70588 42.58065
54.11765 45.80645
57.05882 47.74194
```



senPlot function in R

> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1], pvplot=TRUE)

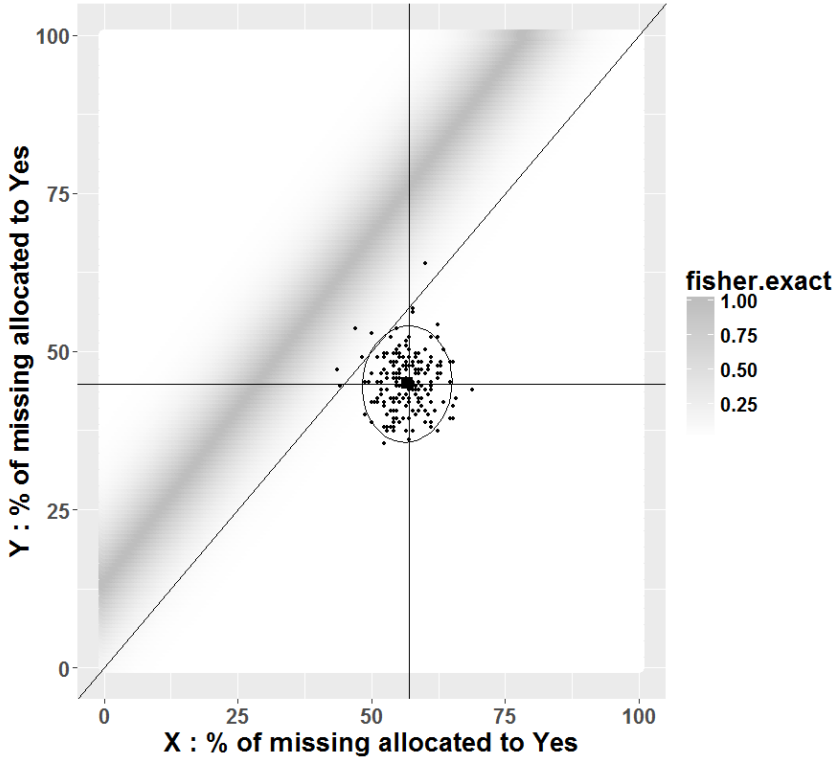
- Plot type

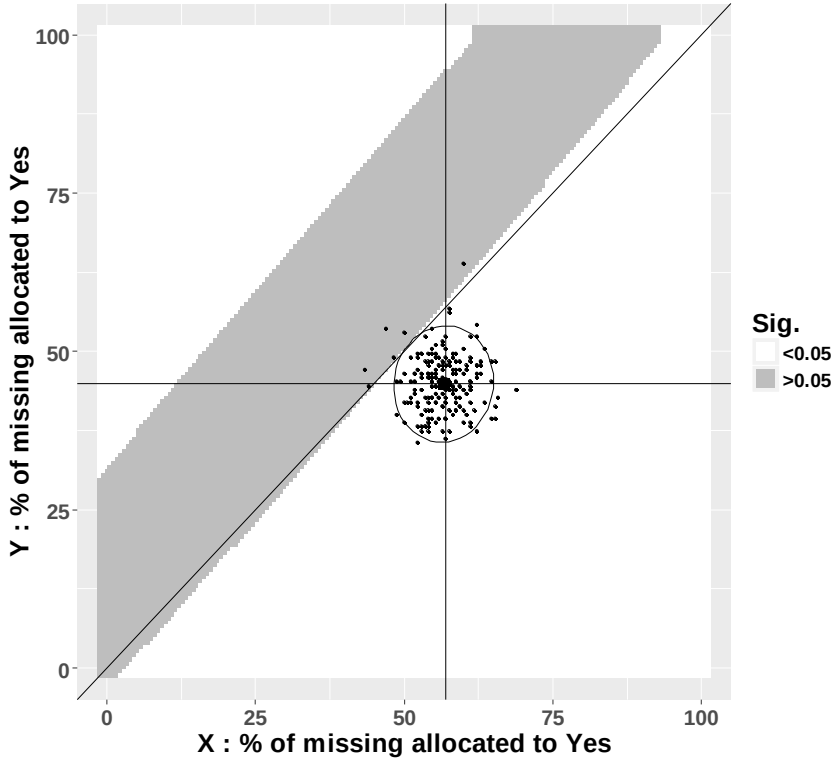


senPlot function in R

> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1], pvplot=FALSE)

- Plot type

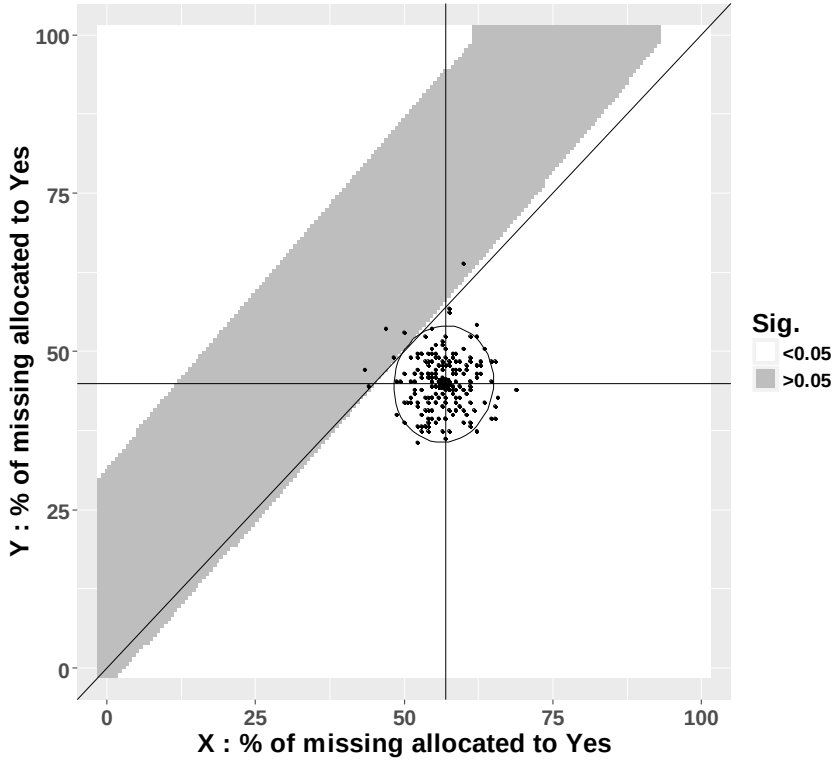




senPlot function in R

> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1],pvplot=TRUE,
XY.names=list("X","Y"), missing="missing",
outcome.name="Yes")

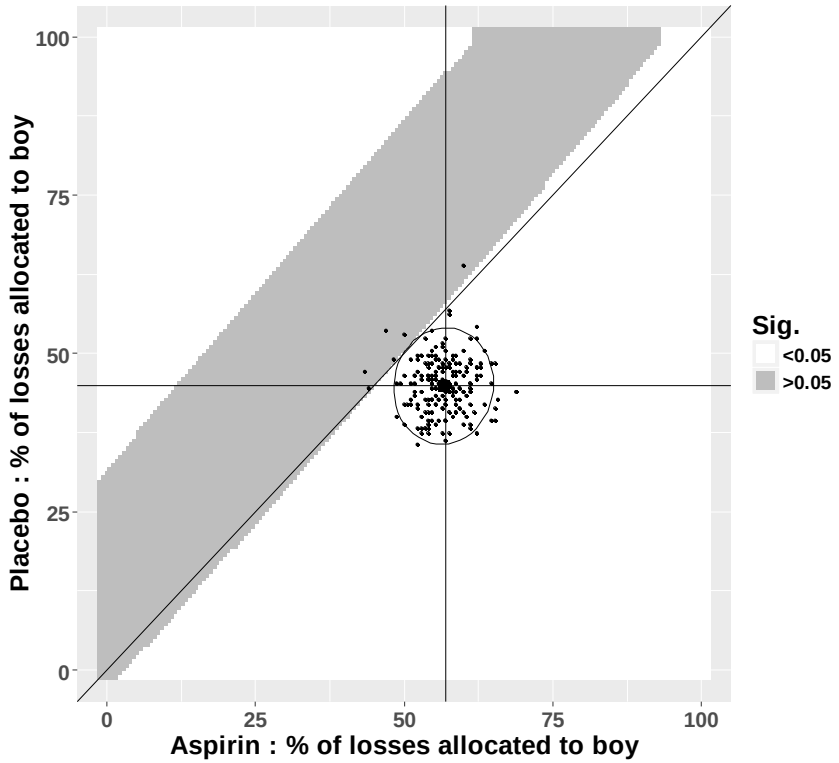
- Axis Labels



senPlot function in R

> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1],pvplot=TRUE,
XY.names=list("Aspirin","Placebo"), missing="losses",
outcome.name="boy")

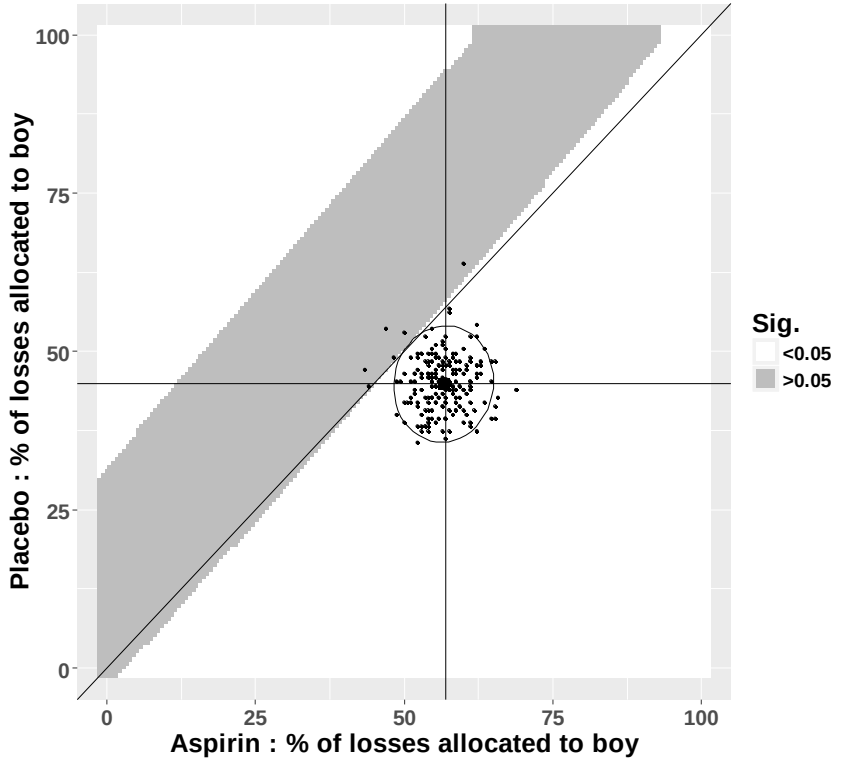
- Axis Labels



senPlot function in R

> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1],pvplot=TRUE,
XY.names=list("Aspirin","Placebo"), missing="losses",
outcome.name="boy“, obs.col=“black”, imp.col=“black”)

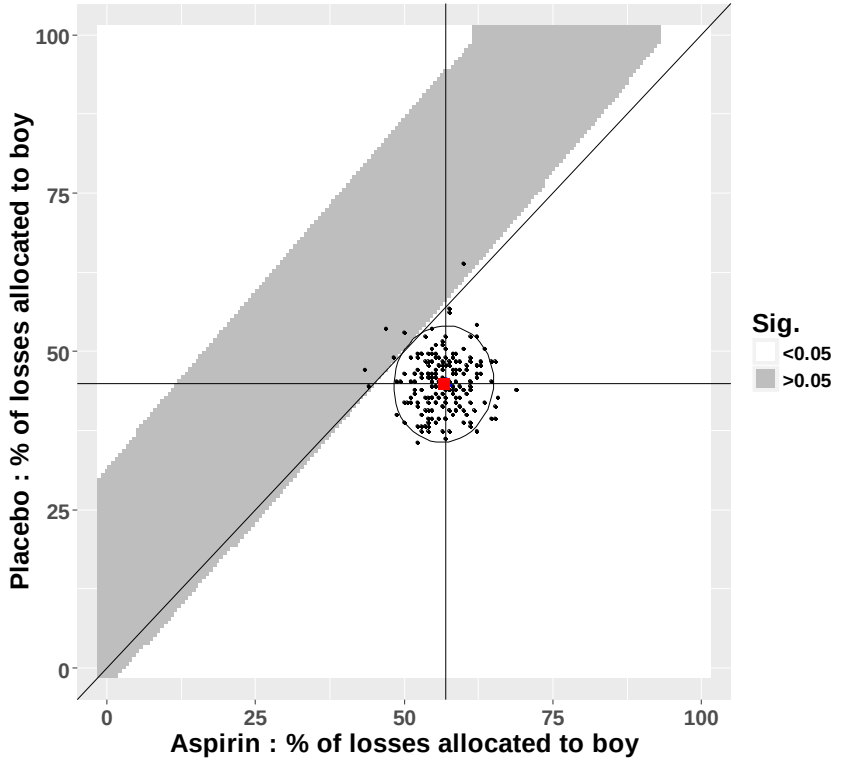
- Point estimate colors



senPlot function in R

> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1],pvplot=TRUE,
XY.names=list("Aspirin","Placebo"), missing="losses",
outcome.name="boy“, obs.col=“blue”, imp.col=“red”)

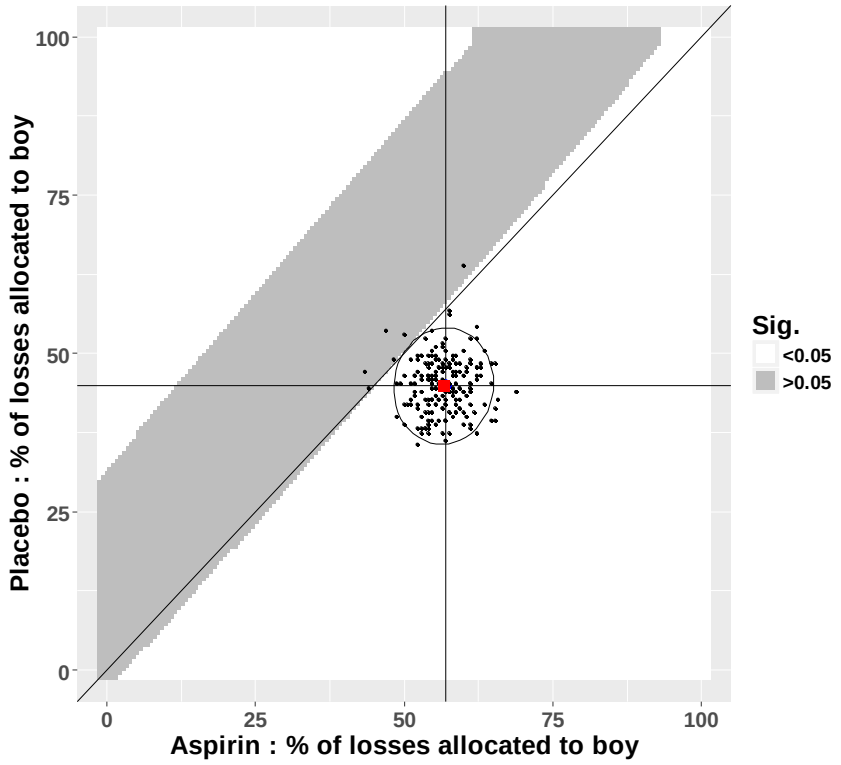
- Point estimate colors



senPlot function in R

> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1],pvplot=TRUE,
XY.names=list("Aspirin","Placebo"), missing="losses",
outcome.name="boy“, obs.col=“blue”, imp.col=“red”,
pv.col=c(“white”,”black”))

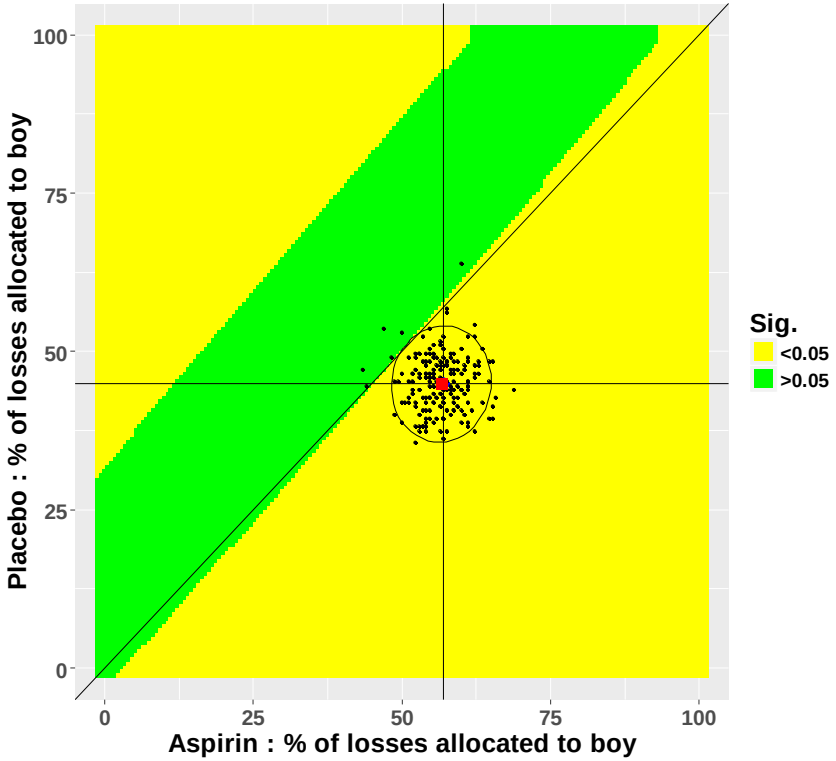
- Background colors



senPlot function in R

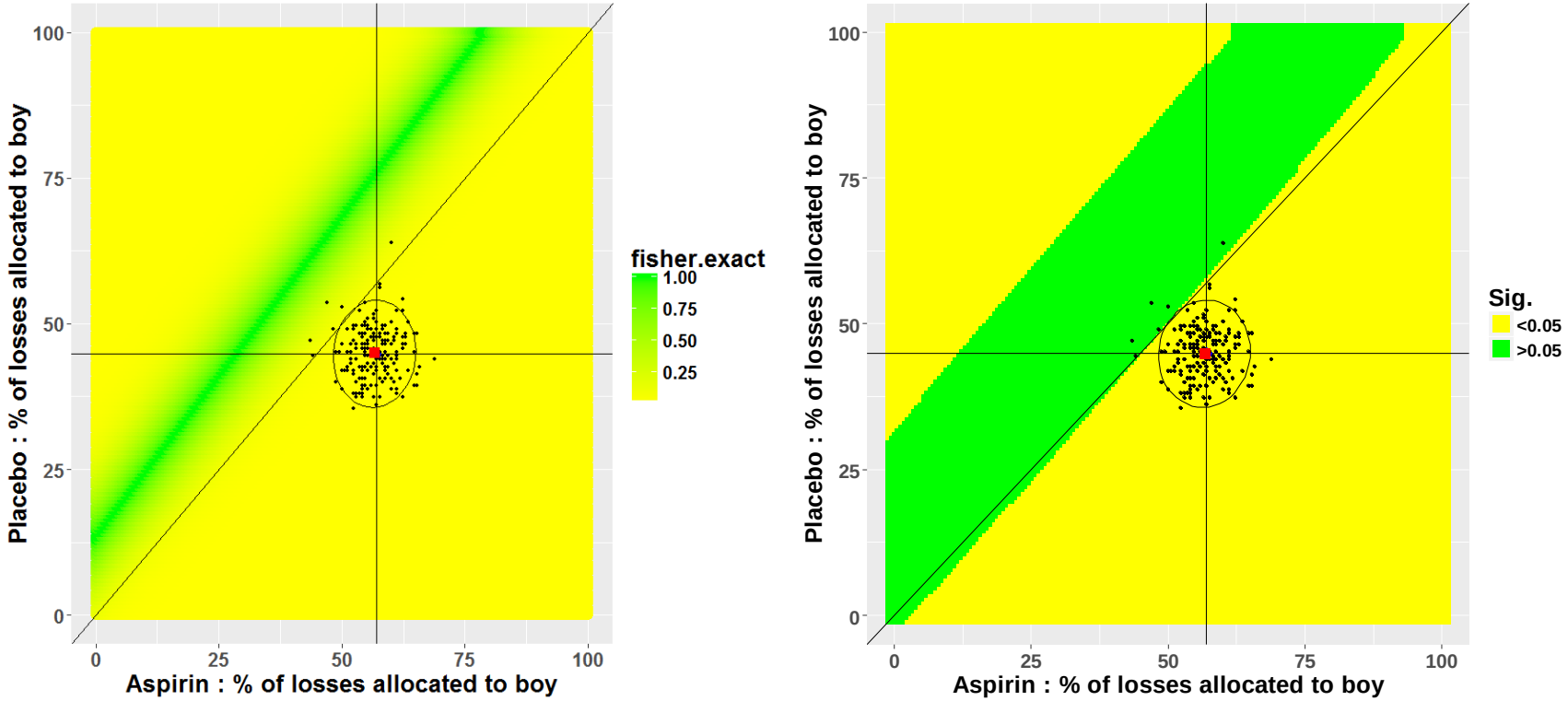
> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1],pvplot=TRUE,
XY.names=list("Aspirin","Placebo"), missing="losses",
outcome.name="boy“, obs.col=“blue”, imp.col=“red”,
pv.col=c(“yellow”,”green”))

- Background colors



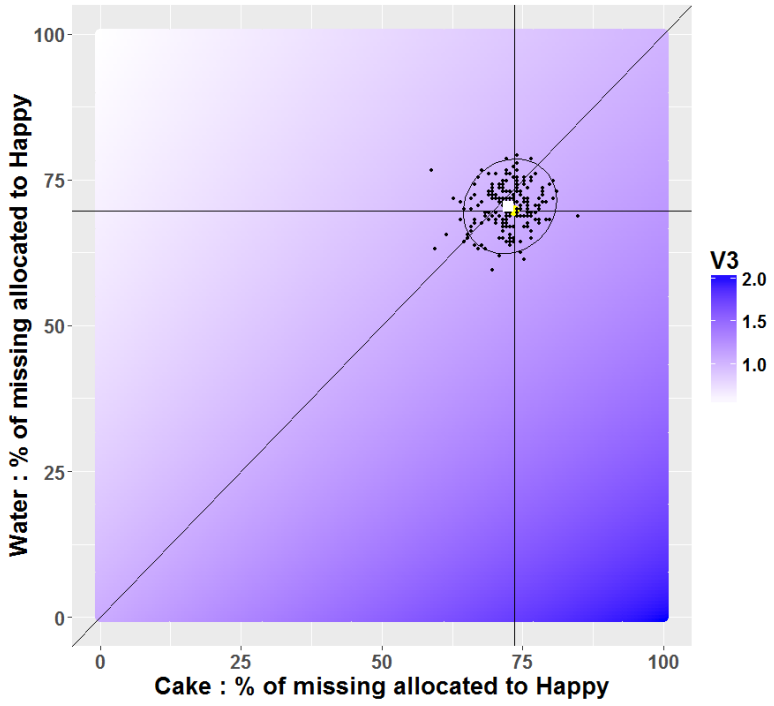
senPlot function in R

```
> senPlot(dat=dat[,c(1,2,5)],imp=imp.sen,obs.per=per.obs[2:1],pvplot=FALSE,
        XY.names=list("Aspirin","Placebo"), missing="losses",
        outcome.name="boy“, obs.col=“blue”, imp.col=“red”,
        Gradient.col=c(“yellow”,”green”))
```



senPlot function in R

- Gradient examples



Sensitivity Analysis: Take home

- Sensitivity analysis are essential to evaluate the potential effect of missing data on study findings under various assumptions.
- Visualizing sensitivity analysis is a concise way to convey those potential effects under numerous situations.

- Thanks to:
- Enrique F. Schisterman, PhD
- The EAGeR Trial Team
- SPER
- And…

NIH

Eunice Kennedy Shriver National Institute of Child Health and Human Development