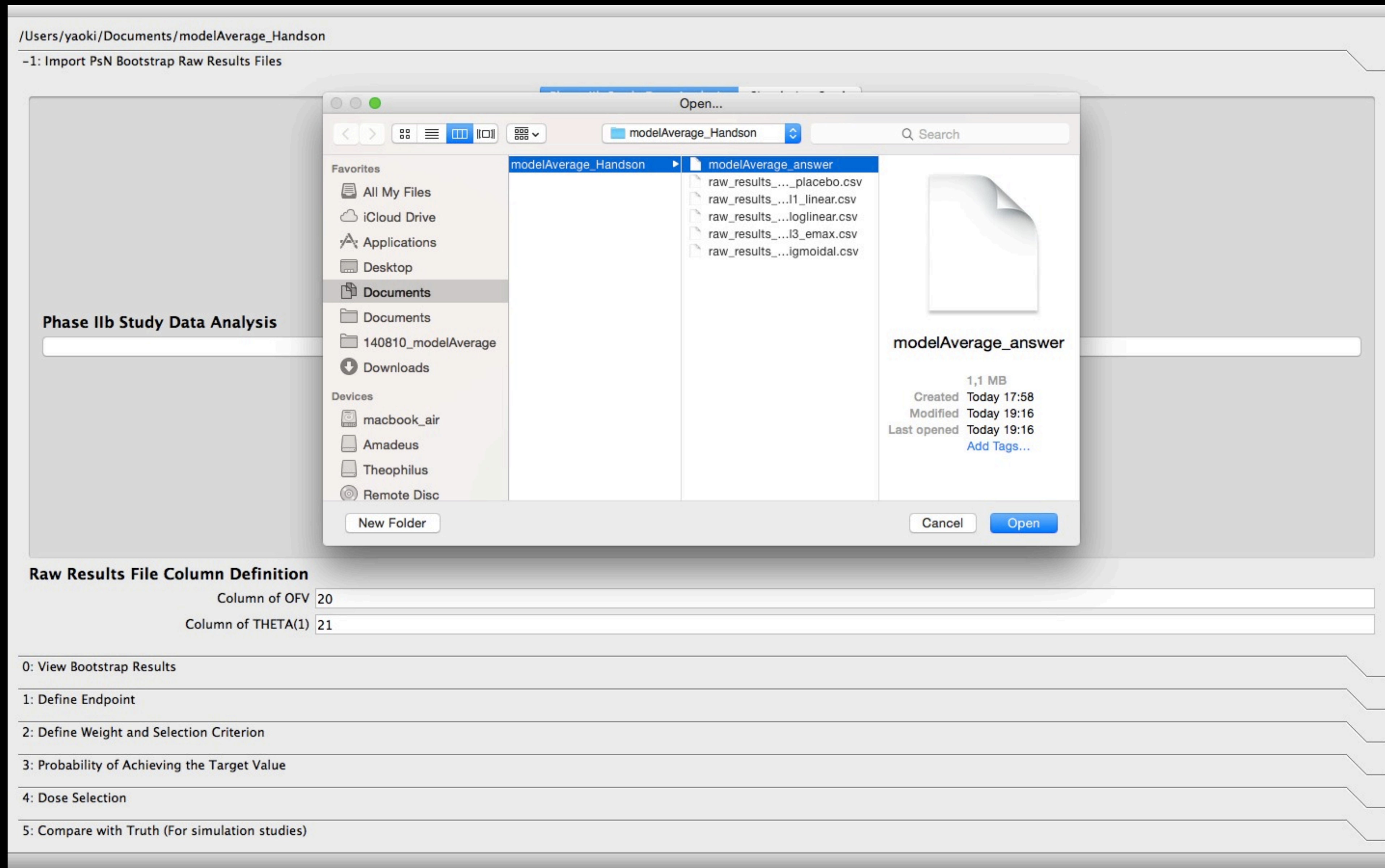


modelAVERAGE

hands-on answer



You can load all the correct input to the software by opening
"modelAverage_answer".

exercise 0

Write a shell script (unix command) to run the bootstrap analyses of candidate models

exercise 0

Write a shell script (unix command) to run the bootstrap analyses of candidate models

```
rm -rf bootstrap_dir*
bootstrap -seed=0 model0_placebo.mod
cp bootstrap_dir1/raw_results_model0_placebo.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model1_linear.mod
cp bootstrap_dir1/raw_results_model1_linear.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model2_loglinear.mod
cp bootstrap_dir1/raw_results_model2_loglinear.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model3_emax.mod
cp bootstrap_dir1/raw_results_model3_emax.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model4_sigmoidal.mod
cp bootstrap_dir1/raw_results_model4_sigmoidal.csv .
```

exercise 0

Write a shell script (unix command) to run the bootstrap analyses of candidate models

```
rm -rf bootstrap_dir*
bootstrap -seed=0 model0_placebo.mod
cp bootstrap_dir1/raw_results_model0_placebo.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model1_linear.mod
cp bootstrap_dir1/raw_results_model1_linear.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model2_loglinear.mod
cp bootstrap_dir1/raw_results_model2_loglinear.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model3_emax.mod
cp bootstrap_dir1/raw_results_model3_emax.csv .
rm -rf bootstrap_dir1
bootstrap -seed=0 model4_sigmoidal.mod
cp bootstrap_dir1/raw_results_model4_sigmoidal.csv .
```

Ph11b Data

Bootstrap Data I

Model1 P.E.

Model2 P.E.

Model3 P.E.

Model4 P.E.

Model1 P.E.

Model2 P.E.

Model3 P.E.

Model4 P.E.

Model1 P.E.

Model2 P.E.

Model3 P.E.

Model4 P.E.

AIC/BIC/Likelihood X

AIC/BIC/Likelihood X

AIC/BIC/Likelihood X

AIC/BIC/Likelihood X

model
AVERAGE

Distribution of Endpoint
Averaged

Probability of Success

dose

NONMEM + PsN bootstrap

exercise 1

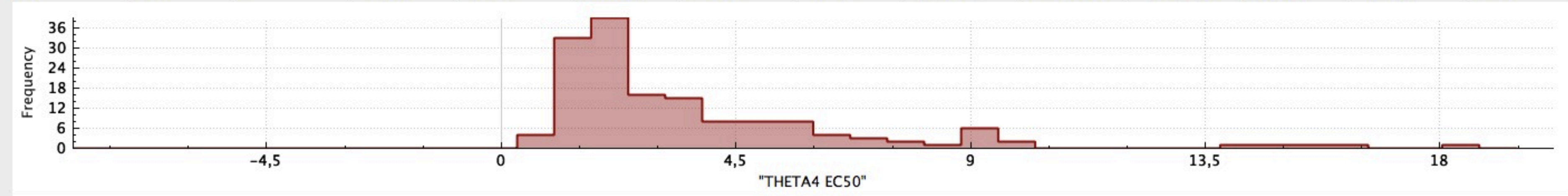
Can we use variance covariance matrix?

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

Model 4

'model_run_time'	subprob_est_time	subprob_cov_time	"ofv"	"THETA1 BASE"	"THETA2 KOUT"	"THETA3 EMAX"	"THETA4 EC50"	"THETA5 N"	"A6 PROP ERROR 0"	"HETA7 PBO EFFEC"	"HETA8 IIV_BASELI"	"THETA9 IIV_PBO"	THETA10 IIV_EPS
nan	64.19	0	-9758.71	9.22101	0.0255804	0.9581	3.73312	1.16434	0.0906149	-0.0239603	0.171924	0.113784	0.267216
nan	406.69	0	-10110.7	9.21404	0.0244908	65.3682	749.941	0.892205	0.0879335	-0.0164387	0.161953	0.106602	0.284585
nan	184.38	0	-9969.32	9.3259	0.0258434	5.74655	42.7899	0.922993	0.087145	-0.0196403	0.166384	0.119992	0.281643
nan	65.82	0	-9901.38	9.11626	0.0254865	1.18616	5.36935	1.13476	0.0899751	-0.0281212	0.17518	0.112283	0.292749
nan	162.07	0	-9925.23	9.20503	0.0277046	3.63817	28.0012	0.903498	0.0904599	-0.022037	0.174127	0.102701	0.287926
nan	261.63	0	-9825.13	9.20775	0.0251975	21.4408	201.283	0.926098	0.08624	-0.0333671	0.174786	0.114761	0.270423
nan	433.53	0	-9713.12	9.31372	0.0263222	39.3405	465.134	0.90517	0.0912276	-0.0383623	0.160475	0.108287	0.275613
nan	63.71	0	-9633.01	9.17187	0.0249377	0.902756	2.86938	1.57521	0.0906543	-0.0319385	0.177426	0.117964	0.289755
nan	91.55	0	-9663.44	9.25581	0.0279135	0.54757	1.82046	1.44075	0.0906579	-0.0345333	0.184103	0.110659	0.24319
nan	369.84	0	-9646.12	9.21821	0.0263436	35.147	390.13	0.887047	0.0866813	-0.0180337	0.176099	0.121083	0.277039
nan	72.78	0	-9831.15	9.23663	0.0274284	0.997444	5.61822	0.940903	0.0917081	-0.0244304	0.15654	0.102414	0.262015



1: Define Endpoint

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

4: Dose Selection

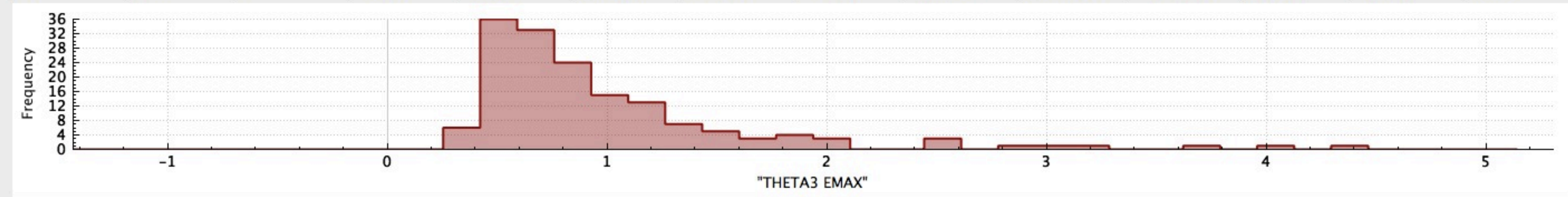
5: Compare with Truth (For simulation studies)

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

Model 4

"model_run_time"	subprob_est_time	subprob_cov_time	"ofv"	"THETA1 BASE"	"THETA2 KOUT"	"THETA3 EMAX"	"THETA4 EC50"	"THETA5 N"	"6 PROP ERROR 0"	"HETA7 PBO EFFEC"	"HETA8 IIV_BASELI"	"THETA9 IIV_PBO"	THETA10 IIV_EPS
nan	64.19	0	-9758.71	9.22101	0.0255804	0.9581	3.73312	1.16434	0.0906149	-0.0239603	0.171924	0.113784	0.267216
nan	406.69	0	-10110.7	9.21404	0.0244908	65.3682	749.941	0.892205	0.0879335	-0.0164387	0.161953	0.106602	0.284585
nan	184.38	0	-9969.32	9.3259	0.0258434	5.74655	42.7899	0.922993	0.087145	-0.0196403	0.166384	0.119992	0.281643
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nan	162.07	0	-9925.23	9.20503	0.0277046	3.63817	28.0012	0.903498	0.0904599	-0.022037	0.174127	0.102701	0.287926
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nan	91.55	0	-9663.44	9.25581	0.0279135	0.54757	1.82046	1.44075	0.0906579	-0.0345333	0.184103	0.110659	0.24319
nan	369.84	0	-9646.12	9.21821	0.0263436	35.147	390.13	0.887047	0.0866813	-0.0180337	0.176099	0.121083	0.277039
nan	72.78	0	-9831.15	9.23663	0.0274284	0.997444	5.61822	0.940903	0.0917081	-0.0244304	0.15654	0.102414	0.262015



1: Define Endpoint

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

4: Dose Selection

5: Compare with Truth (For simulation studies)

exercise 2

Derive Steady States and endpoint.

Model 0: Placebo

$$\text{End Point} = \theta_1 e^{\theta_8 \eta_1} \left(\frac{1 + \theta_7 + \theta_9 \eta_2}{1 + 0} - 1 \right)$$

Model 1: Linear

$$\text{End Point} = \theta_1 e^{\theta_8 \eta_1} \left(\frac{1 + \theta_7 + \theta_9 \eta_2}{1 + \theta_3 \text{dose}} - 1 \right)$$

Model 2: Loglinear

$$\text{End Point} = \theta_1 e^{\theta_8 \eta_1} \left(\frac{1 + \theta_7 + \theta_9 \eta_2}{1 + \theta_3 \log(\text{dose} + 1)} - 1 \right)$$

Model 3: Emax

$$\text{End Point} = \theta_1 e^{\theta_8 \eta_1} \left(\frac{1 + \theta_7 + \theta_9 \eta_2}{1 + \theta_3 \frac{\text{dose}}{\theta_4 + \text{dose}}} - 1 \right)$$

Model 4: Sigmoidal

$$\text{End Point} = \theta_1 e^{\theta_8 \eta_1} \left(\frac{1 + \theta_7 + \theta_9 \eta_2}{1 + \theta_3 \frac{\text{dose}^{\theta_5}}{\theta_4^{\theta_5} + \text{dose}^{\theta_5}}} - 1 \right)$$

exercise 3

How many simulations are enough?

-1: Import PsN Bootstrap Raw Results Files

1: Define Endpoint

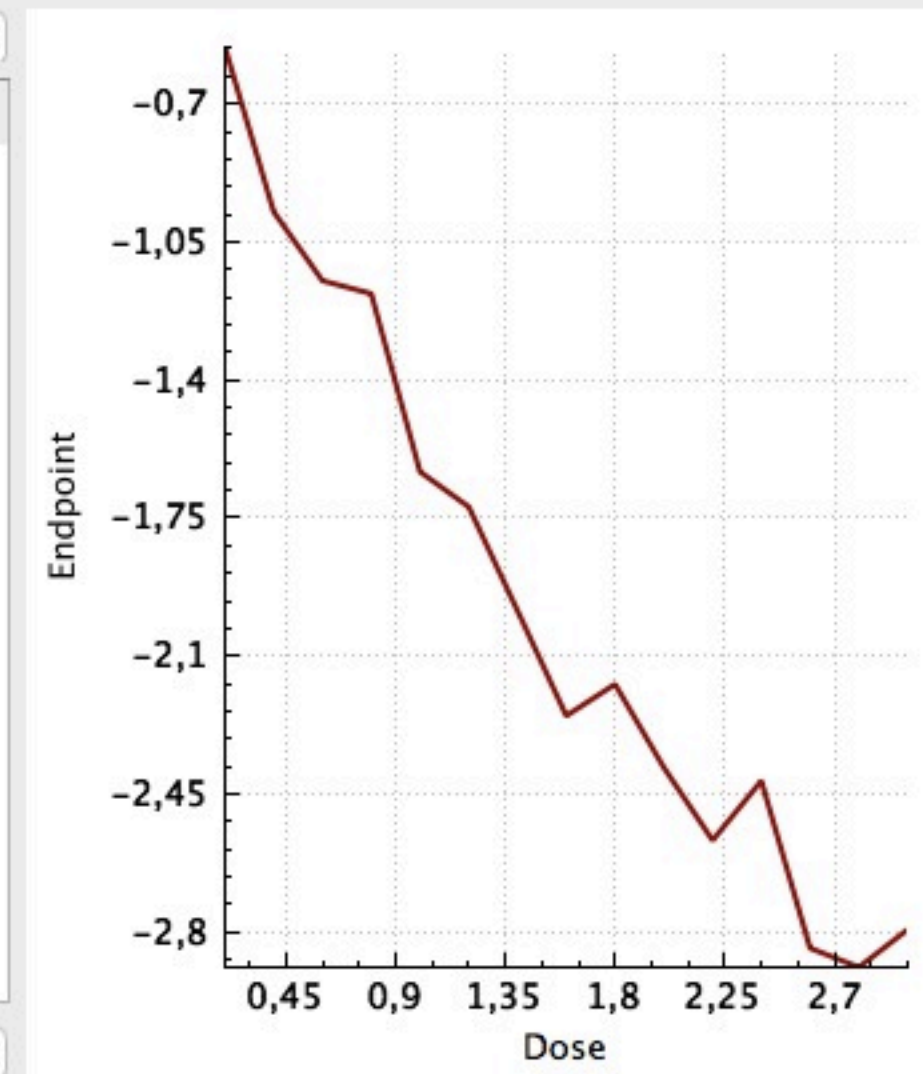
0.2:0.2:3

EndPoint Definition	
model0_placebo	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + 0) - 1)$
model1_linear	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose}) - 1)$
model2_loglinear	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \log(\text{Dose} + 1))) \dots$
model3_emax	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose} / (\text{Dose} \dots$
model4_sigmoidal	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose}^{\text{THETA4}}))$

2

	1	2
1	1	0
2	0	1

Mean of the Population



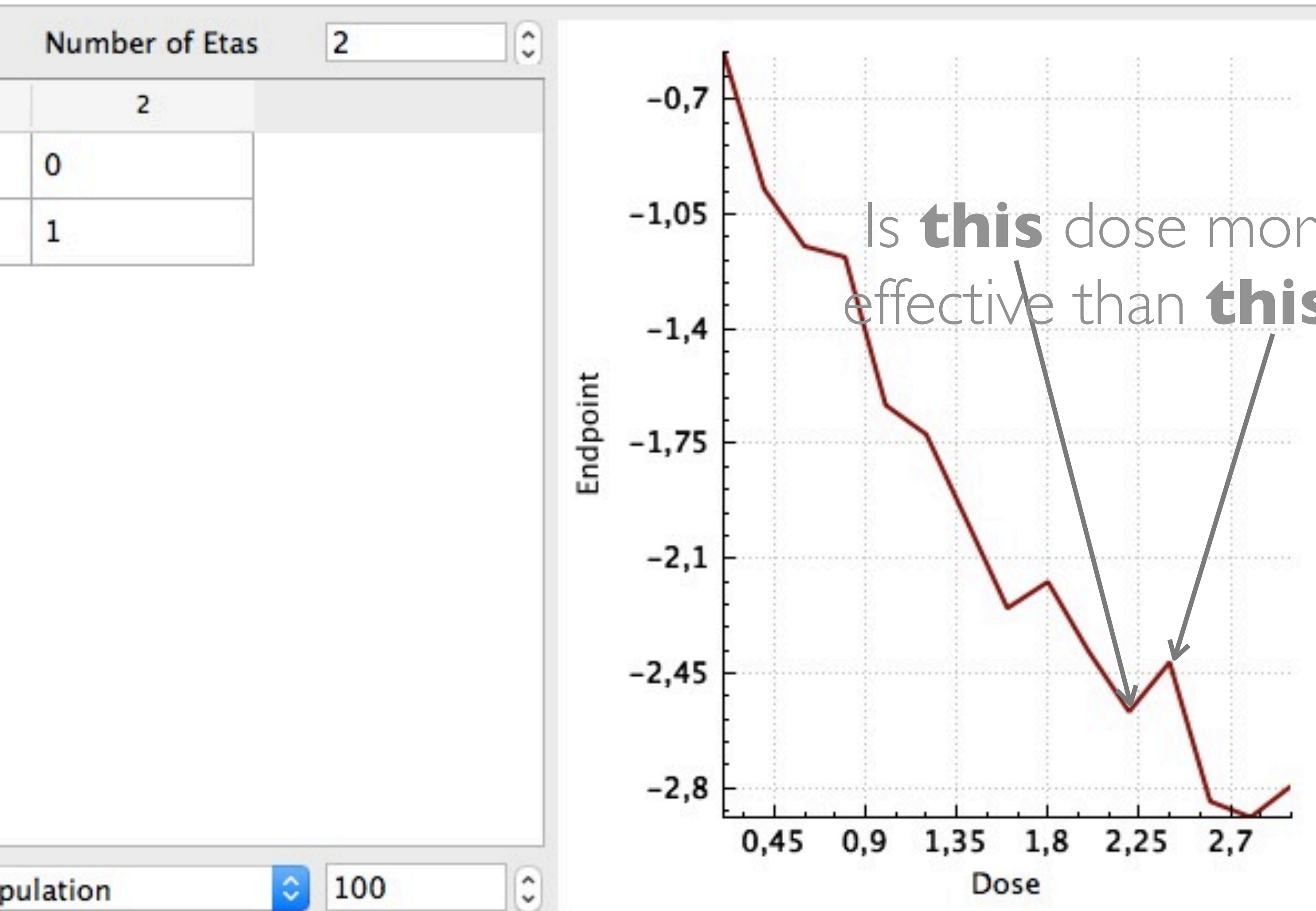
Raw Results Column Labels:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	"model"	"problem"	"subproblem"	"covariance..."	"minimizati..."	"covariance..."	"covariance..."	"estimate_n..."	"rounding..."	"zero_gradi..."	"final_zero..."	"hessian_re..."	"s_matrix_s..."	"significant"

3: Probability of Achieving the Target Value

4: Dose Selection

5: Compare with Truth (For simulation studies)



No this “zig-zag” is just an artifact of how we calculate the average (stochastic noise).

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/modelAverage_Handson

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

Possible doses (independent variables) (e.g., 1,2,3,4,5 or 0:1:10 => 0,1,2,3,4,5,6,7,8,9,10)

0.2:0.2:3

Endpoint Definitions

EndPoint Definition	
model0_placebo	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + 0) - 1)$
model1_linear	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose}) - 1)$
model2_loglinear	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \log(\text{Dose} + 1))) \dots$
model3_emax	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose} / (\text{Dose} \dots$
model4_sigmoidal	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose}^{\text{THETA} \dots$

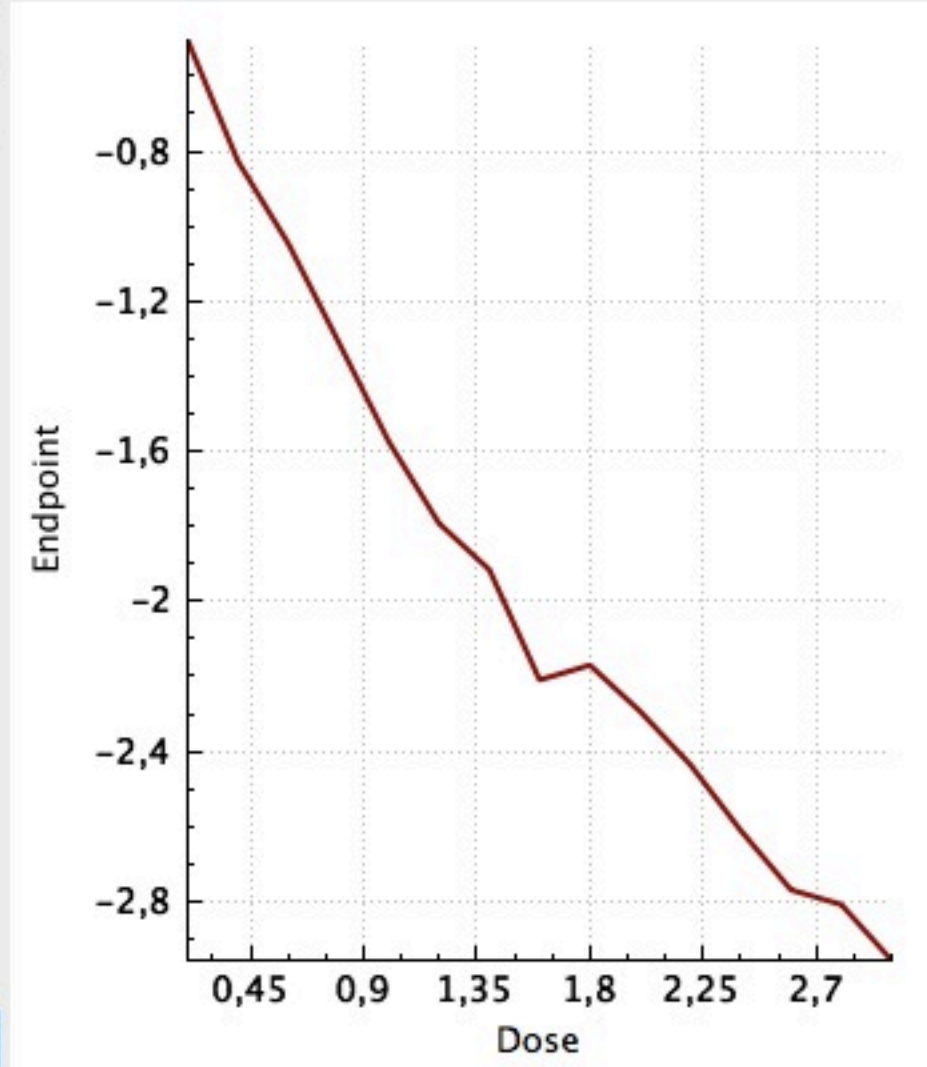
OmegaBlock

Number of Etas

2

1		2	
1	1	0	
2	0	1	

Mean of the Population 200



Note: THETA(1) ETA(1) need to be written as THETA1 ETA1, can also use COL1 for 1st column of raw results file

Raw Results Column Labels:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	"model"	"problem"	"subproblem"	"covariance..."	"minimizati..."	"covariance..."	"covariance..."	"estimate_n..."	"rounding_..."	"zero_gradi..."	"final_zero_..."	"hessian_re..."	"s_matrix_s..."	"significant"

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

4: Dose Selection

5: Compare with Truth (For simulation studies)

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/modelAverage_Handson

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

Possible doses (independent variables) (e.g., 1,2,3,4,5 or 0:1:10 => 0,1,2,3,4,5,6,7,8,9,10)

0.2:0.2:3

Endpoint Definitions

EndPoint Definition	
model0_placebo	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + 0) - 1)$
model1_linear	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose}) - 1)$
model2_loglinear	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \log(\text{Dose} + 1))) \dots$
model3_emax	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose} / (\text{Dose} \dots$
model4_sigmoidal	$\text{THETA1} \cdot \exp(\text{THETA8} \cdot \text{ETA1}) \cdot ((\text{THETA7} + 1 + \text{THETA9} \cdot \text{ETA2}) / (1 + \text{THETA3} \cdot \text{Dose}^{\text{THETA} \dots$

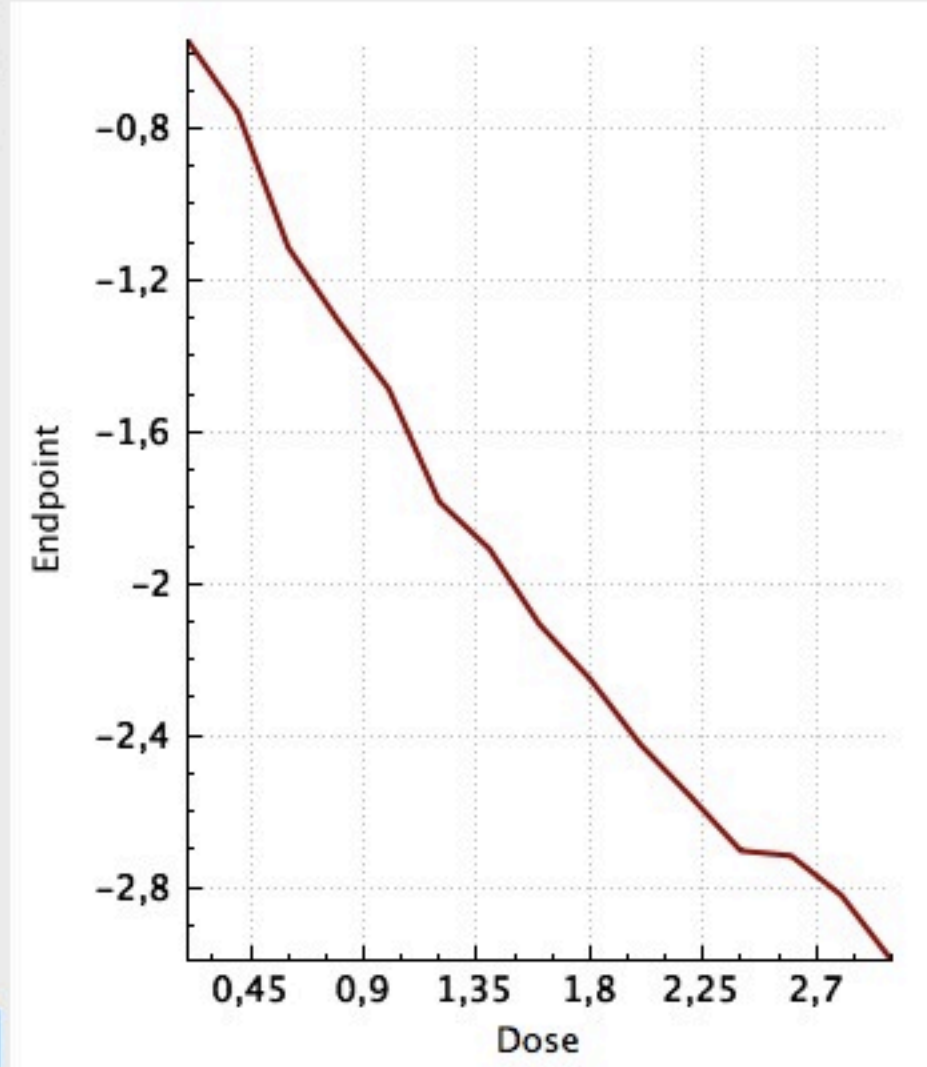
OmegaBlock

Number of Etas

2

1		2	
1	1	0	
2	0	1	

Mean of the Population 400



Note: THETA(1) ETA(1) need to be written as THETA1 ETA1, can also use COL1 for 1st column of raw results file

Raw Results Column Labels:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	"model"	"problem"	"subproblem"	"covariance..."	"minimizati..."	"covariance..."	"covariance..."	"estimate_n..."	"rounding_..."	"zero_gradi..."	"final_zero_..."	"hessian_re..."	"s_matrix_s..."	"significant"

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

4: Dose Selection

5: Compare with Truth (For simulation studies)

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/modelAverage_Handson

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

Possible doses (independent variables) (e.g., 1,2,3,4,5 or 0:1:10 => 0,1,2,3,4,5,6,7,8,9,10)

0.2:0.2:3

Endpoint Definitions

EndPoint Definition	
model0_placebo	THETA1*exp(THETA8*ETA1)*((THETA7+1+THETA9*ETA2)/(1+0)-1)
model1_linear	THETA1*exp(THETA8*ETA1)*((THETA7+1+THETA9*ETA2)/(1+THETA3*Dose)-1)
model2_loglinear	THETA1*exp(THETA8*ETA1)*((THETA7+1+THETA9*ETA2)/(1+THETA3*log(Dose+1))...
model3_emax	THETA1*exp(THETA8*ETA1)*((THETA7+1+THETA9*ETA2)/(1+THETA3*Dose/(Dose...
model4_sigmoidal	THETA1*exp(THETA8*ETA1)*((THETA7+1+THETA9*ETA2)/(1+THETA3*Dose^THETA...

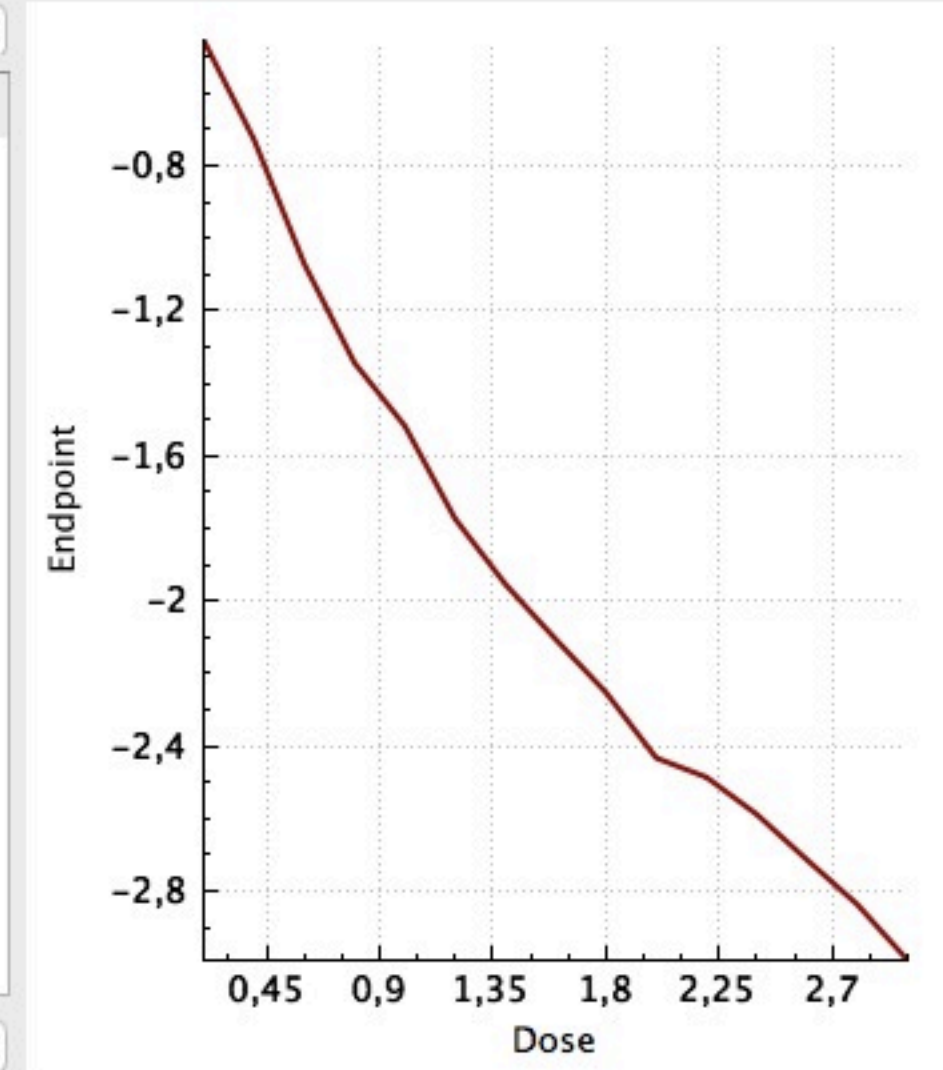
OmegaBlock

Number of Etas

2

	1	2
1	1	0
2	0	1

Mean of the Population 1000



Note: THETA(1) ETA(1) need to be written as THETA1 ETA1, can also use COL1 for 1st column of raw results file

Raw Results Column Labels:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	"model"	"problem"	"subproblem"	"covariance..."	"minimizati..."	"covariance..."	"covariance..."	"estimate_n..."	"rounding_..."	"zero_gradi..."	"final_zero_..."	"hessian_re..."	"s_matrix_s..."	"significant"

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

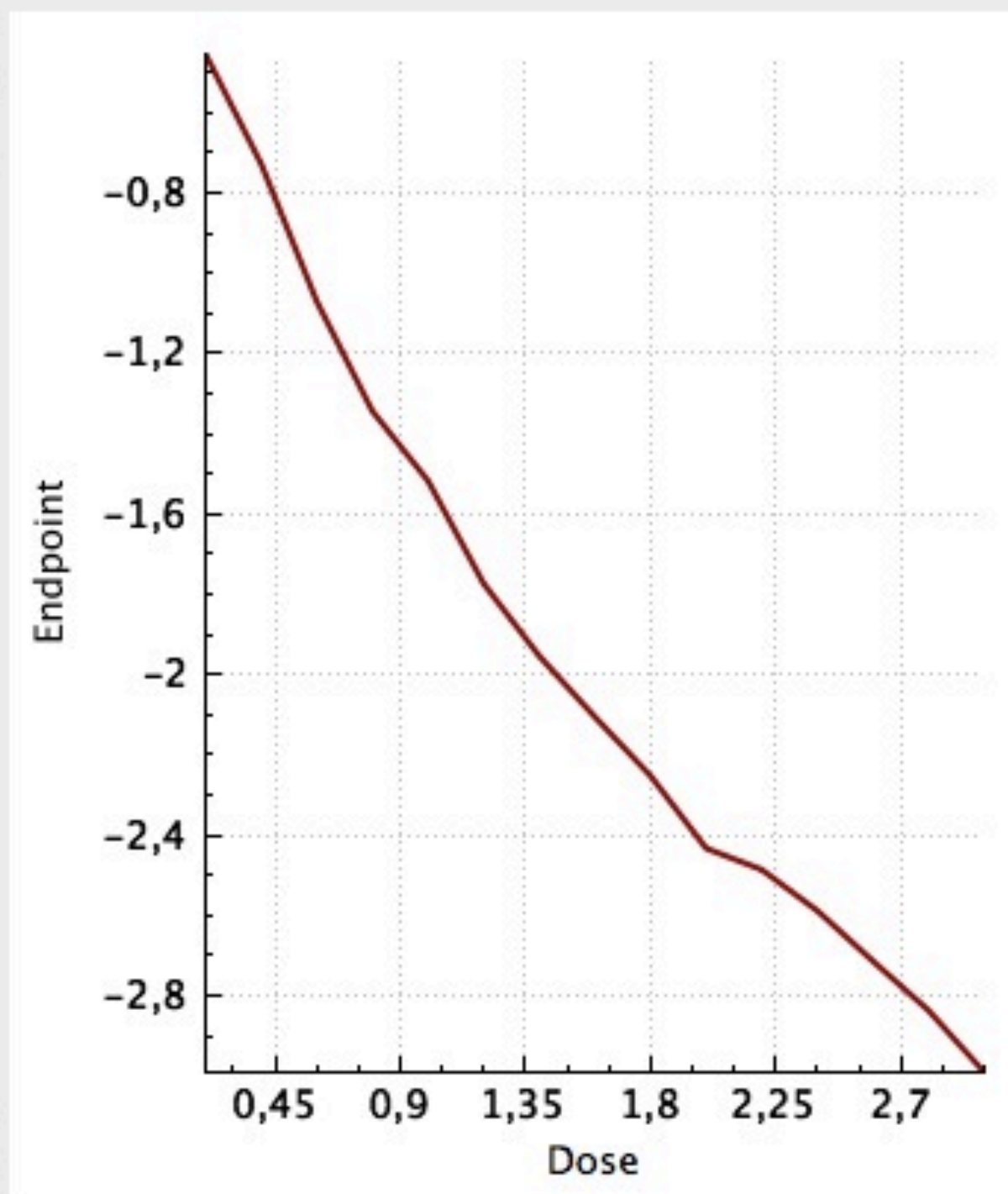
4: Dose Selection

5: Compare with Truth (For simulation studies)

OmegaBlock Number of Etas 2

	1	2
1	1	0
2	0	1

Mean of the Population 1000



With 1000 simulations we stop seeing the “zig-zag” due to the stochastic noise, hence the dose choice will not likely to be influenced by the stochastic noise.

file

	8	9	10	11	12	13	14
e...	"estimate_n...	"rounding_...	"zero_gradi...	"final_zero_...	"hessian_re...	"s_matrix_s...	"significant

exercise 4

Defining Weights

$$\text{Weight}_{\text{model1}} = \exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right)$$

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/modelAverage_Handson

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

2: Define Weight and Selection Criterion

Weight expression (assumes ofv is at 20th column, leave blank to exclude the model)

☐ in log scale

Weight Definition	
model0_placebo	$\exp((\text{ofv}+0)/(0-2))$
model1_linear	$\exp((\text{ofv}+2)/(0-2))$
model2_loglinear	$\exp((\text{ofv}+2)/(0-2))$
model3_emax	$\exp((\text{ofv}+4)/(0-2))$
model4_sigmoidal	$\exp((\text{ofv}+6)/(0-2))$

Relative weight

	model0_placebo	model1_linear	model2_loglinear	model3_emax	model4_sigmoida	
1	nan	nan	nan	nan	nan	
2	nan	nan	nan	nan	nan	
3	nan	nan	nan	nan	nan	
4	nan	nan	nan	nan	nan	
5	nan	nan	nan	nan	nan	
6	nan	nan	nan	nan	nan	
7	nan	nan	nan	nan	nan	
8	nan	nan	nan	nan	nan	

3: Probability of Achieving the Target Value

4: Dose Selection

5: Compare with Truth (For simulation studies)

1: Define Endpoint

2: Define Weight and Selection Criterion

Weight expression (assumes ofv is at 20th column, leave blank to exclude the model)

model0_placebo	$\exp((\text{ofv}+0)/(0-2))$
model1_linear	$\exp((\text{ofv}+2)/(0-2))$
model2_loglinear	$\exp((\text{ofv}+2)/(0-2))$
model3_emax	$\exp((\text{ofv}+4)/(0-2))$
model4_sigmoidal	$\exp((\text{ofv}+6)/(0-2))$

Relative weight

	model0_placebo	model1_linear	model2_loglinear	model3_emax	model4_sigmoida
1	nan	nan	nan	nan	nan
2	nan	nan	nan	nan	nan
3	nan	nan	nan	nan	nan
4	nan	nan	nan	nan	nan
5	nan	nan	nan	nan	nan

Weights cannot be calculated as is!
(nan=Not A Number)

$$\text{Weight}_{\text{model1}} = \exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right)$$

$$\text{Weight}_{\text{model1}} = \exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right)$$

$$\log (\text{Weight}_{\text{model1}}) = \log \left(\exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right) \right)$$

$$\text{Weight}_{\text{model1}} = \exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right)$$

$$\log (\text{Weight}_{\text{model1}}) = \log \left(\exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right) \right)$$

$$\log (\text{Weight}_{\text{model1}}) = \frac{\text{AIC}_{\text{model1}}}{-2}$$

$$\text{Weight}_{\text{model1}} = \exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right)$$

$$\log (\text{Weight}_{\text{model1}}) = \log \left(\exp \left(\frac{\text{AIC}_{\text{model1}}}{-2} \right) \right)$$

$$\log (\text{Weight}_{\text{model1}}) = \frac{\text{AIC}_{\text{model1}}}{-2}$$

$$\log (\text{Weight}_{\text{model1}}) = \frac{\text{NumPara}_{\text{model1}} + \text{ofv}_{\text{model1}}}{-2}$$

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/modelAverage_Handson

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

2: Define Weight and Selection Criterion

Weight expression (assumes ofv is at 20th column, leave blank to exclude the model)

☒ in log scale

Weight Definition in log scale	
model0_placebo	(ofv+0)/(0-2)
model1_linear	(ofv+2)/(0-2)
model2_loglinear	(ofv+2)/(0-2)
model3_emax	(ofv+4)/(0-2)
model4_sigmoidal	(ofv+6)/(0-2)

Relative weight

	model0_placebo	model1_linear	model2_loglinear	model3_emax	model4_sigmoidal
1	2.61348e-77	0.316755	0.0997088	0.412692	0.170844
2	1.02462e-81	0.54941	0.0148203	0.292098	0.143672
3	3.75444e-87	0.459451	0.0405881	0.361205	0.138755
4	4.05529e-72	0.539819	0.0257539	0.31174	0.122687
5	9.61023e-87	0.305135	0.151493	0.389274	0.154098
6	8.73824e-79	0.592775	0.0174443	0.281039	0.108742
7	7.22762e-69	0.580501	0.0268703	0.279099	0.113531
8	9.29944e-82	0.488208	5.90094e-06	0.1796	0.332186

3: Probability of Achieving the Target Value

4: Dose Selection

5: Compare with Truth (For simulation studies)

1: Define Endpoint

2: Define Weight and Selection Criterion

Weight expression (assumes ofv is at 20th column, leave blank to exclude the model)

☒ in log scale

Weight Definition in log scale	
model0_placebo	(ofv+0)/(0-2)
model1_linear	(ofv+2)/(0-2)
model2_loglinear	(ofv+2)/(0-2)
model3_emax	(ofv+4)/(0-2)
model4_sigmoidal	(ofv+6)/(0-2)

Now with the log scale weights can be calculated.

Relative weight

	model0_placebo	model1_linear	model2_loglinear	model3_emax	model4_sigmoida
1	2.61348e-77	0.316755	0.0997088	0.412692	0.170844
2	1.02462e-81	0.54941	0.0148203	0.292098	0.143672
3	3.75444e-87	0.459451	0.0405881	0.361205	0.138755
4	4.05529e-72	0.539819	0.0257539	0.31174	0.122687
5	9.61023e-87	0.305135	0.151493	0.389274	0.154098
6	8.73824e-79	0.592775	0.0174443	0.281039	0.108742

(bonus question)

$$\text{Normalized Weight}_{\text{model1}} = \frac{\exp\left(\frac{\text{AIC}_{\text{model1}}}{-2}\right)}{\sum_{i=0}^4 \exp\left(\frac{\text{AIC}_{\text{model}i}}{-2}\right)}$$

(bonus question)

$$\text{Normalized Weight}_{\text{model1}} = \frac{\exp\left(\frac{\text{AIC}_{\text{model1}}}{-2}\right)}{\sum_{i=0}^4 \exp\left(\frac{\text{AIC}_{\text{model}i}}{-2}\right)}$$



In double precision computation this is $\frac{\infty}{\infty}$ because $\exp(1000) > 2^{53} \approx 10^{16}$.

(bonus question)

$$\text{Normalized Weight}_{\text{model1}} = \frac{\exp\left(\frac{\text{AIC}_{\text{model1}}}{-2}\right)}{\sum_{i=0}^4 \exp\left(\frac{\text{AIC}_{\text{model}i}}{-2}\right)} = \frac{\exp\left(\frac{\text{AIC}_{\text{model1}} - \text{AIC}_{\text{model0}}}{-2}\right)}{\sum_{i=0}^4 \exp\left(\frac{\text{AIC}_{\text{model}i} - \text{AIC}_{\text{model0}}}{-2}\right)}$$



In double precision computation this is $\frac{\infty}{\infty}$ because $\exp(1000) > 2^{53} \approx 10^{16}$.

exercise 5

Plotting PoS!

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/mod

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

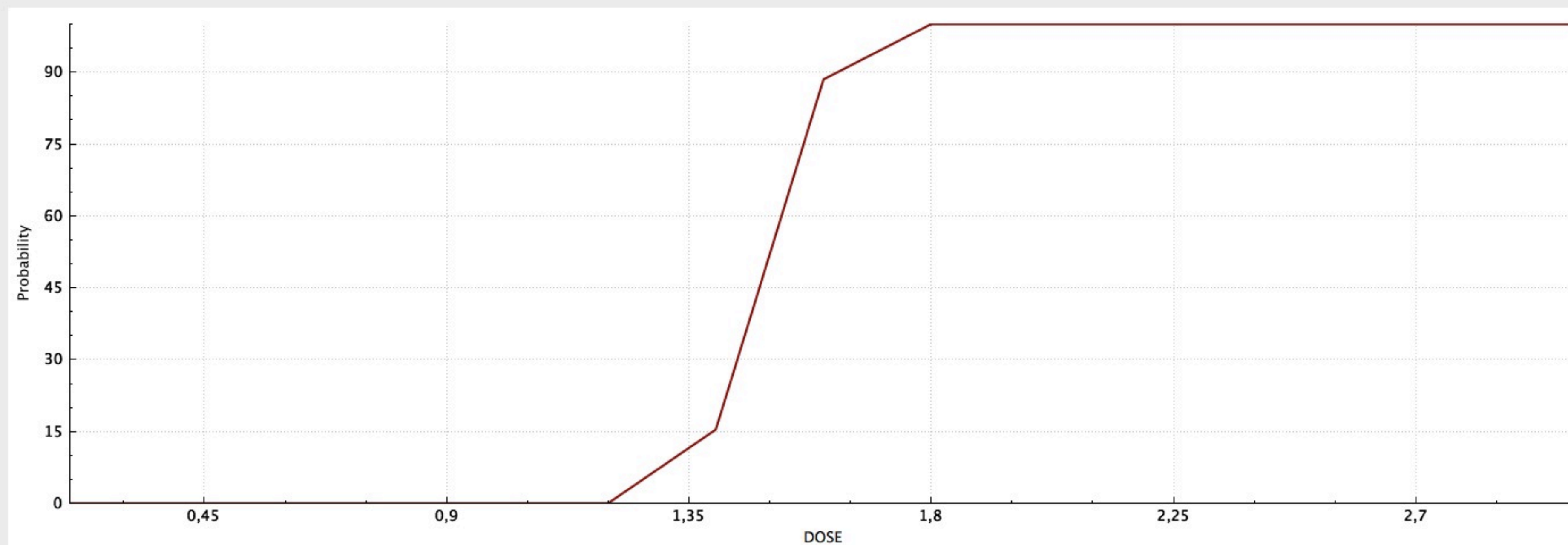
Model Selection

using

using one ofv per model

Probability of (< EndPoint <)

reCalculate



4: Dose Selection

5: Compare with Truth (For simulation studies)

Calculating probability of success using bootstrap samples 0-50.

Abort Calculation

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/mod

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

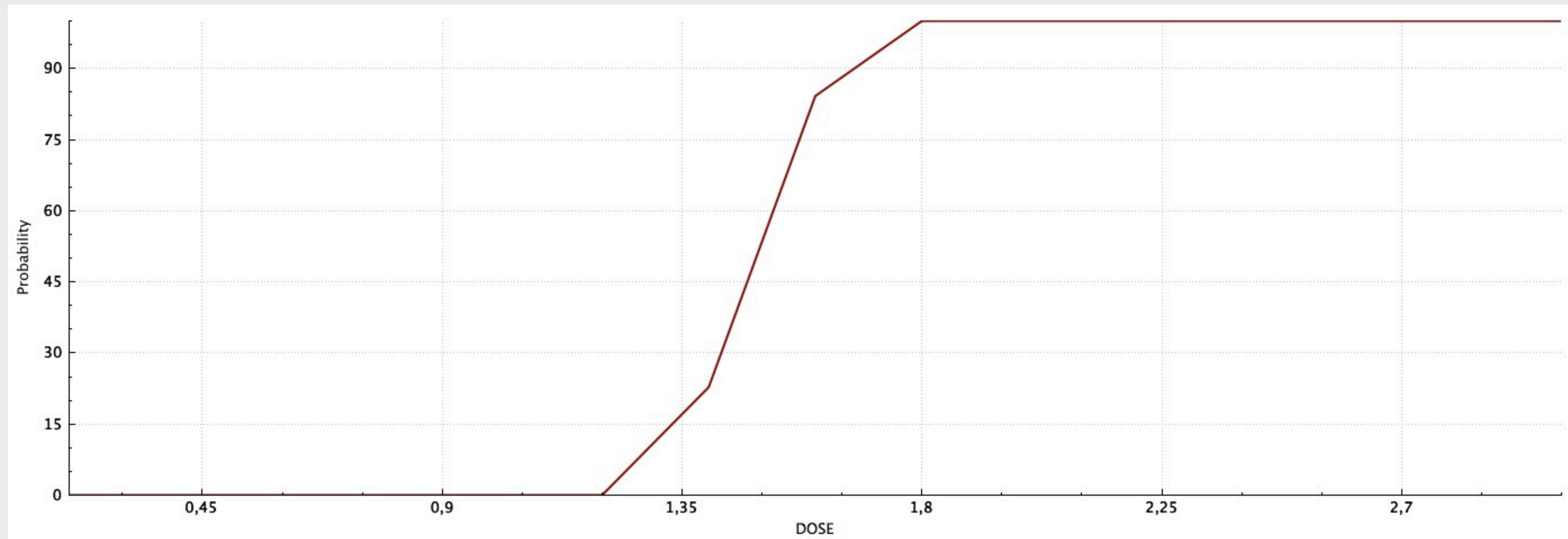
Model Selection

using

using one ofv per model

Probability of (< EndPoint <)

reCalculate



4: Dose Selection

5: Compare with Truth (For simulation studies)

Calculating probability of success using bootstrap samples 0-100.

Abort Calculation

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/mod

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

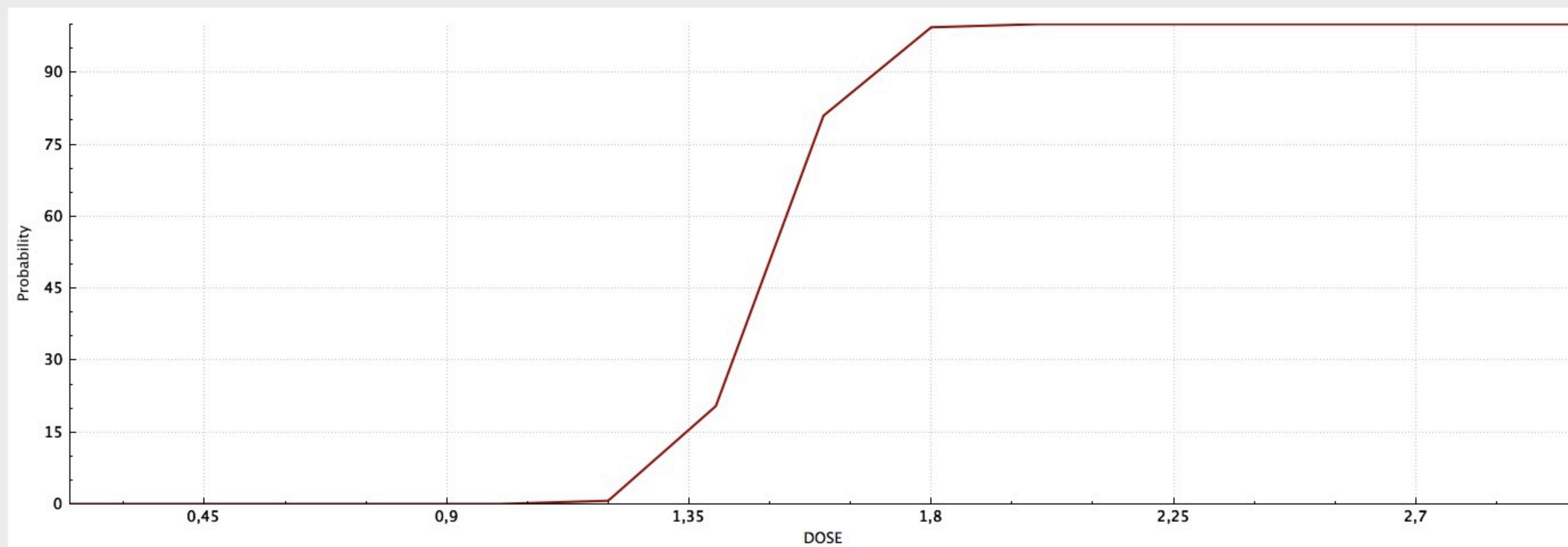
Model Selection

using

using one ofv per model

Probability of (< EndPoint <)

reCalculate



4: Dose Selection

5: Compare with Truth (For simulation studies)

Calculating probability of success using bootstrap samples 0-150.

Abort Calculation

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/mod

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

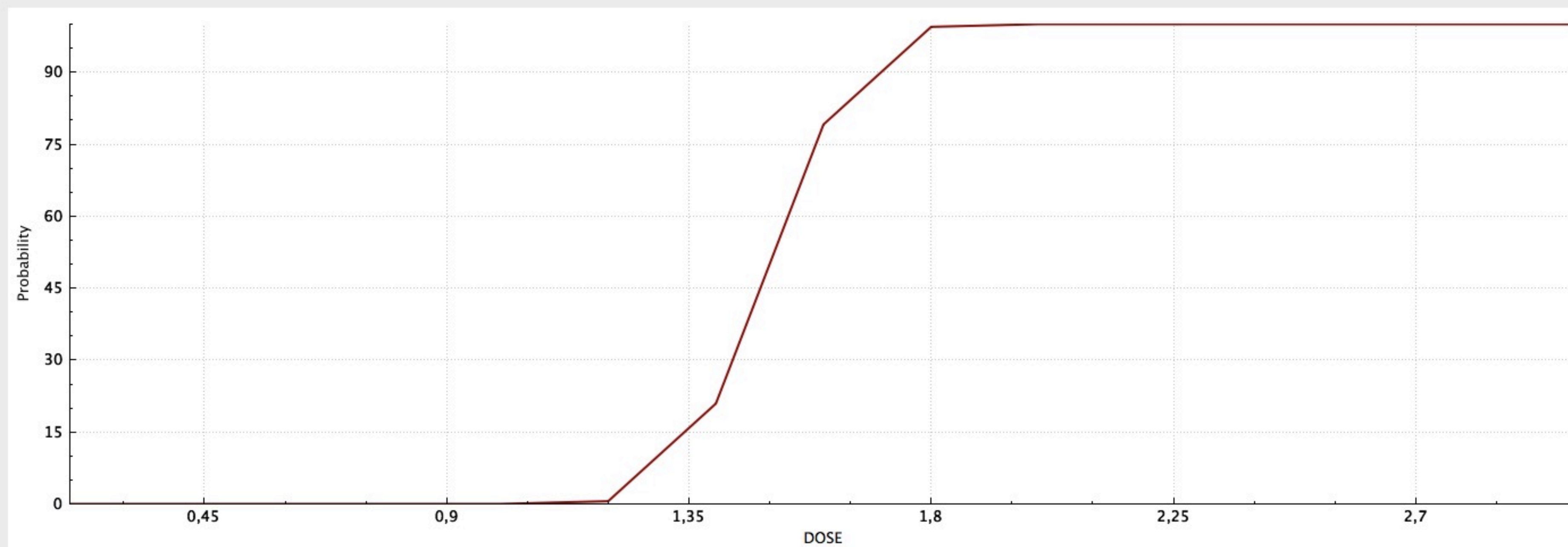
Model Selection

using

using one ofv per model

Probability of (< EndPoint <)

reCalculate



4: Dose Selection

5: Compare with Truth (For simulation studies)

Calculating probability of success using bootstrap samples 0-175.

Abort Calculation

/Volumes/macbook_air/Users/yaoki/Documents/140810_modelAverage/modelAverage_Handson

-1: Import PsN Bootstrap Raw Results Files

0: View Bootstrap Results

1: Define Endpoint

2: Define Weight and Selection Criterion

3: Probability of Achieving the Target Value

Model Selection



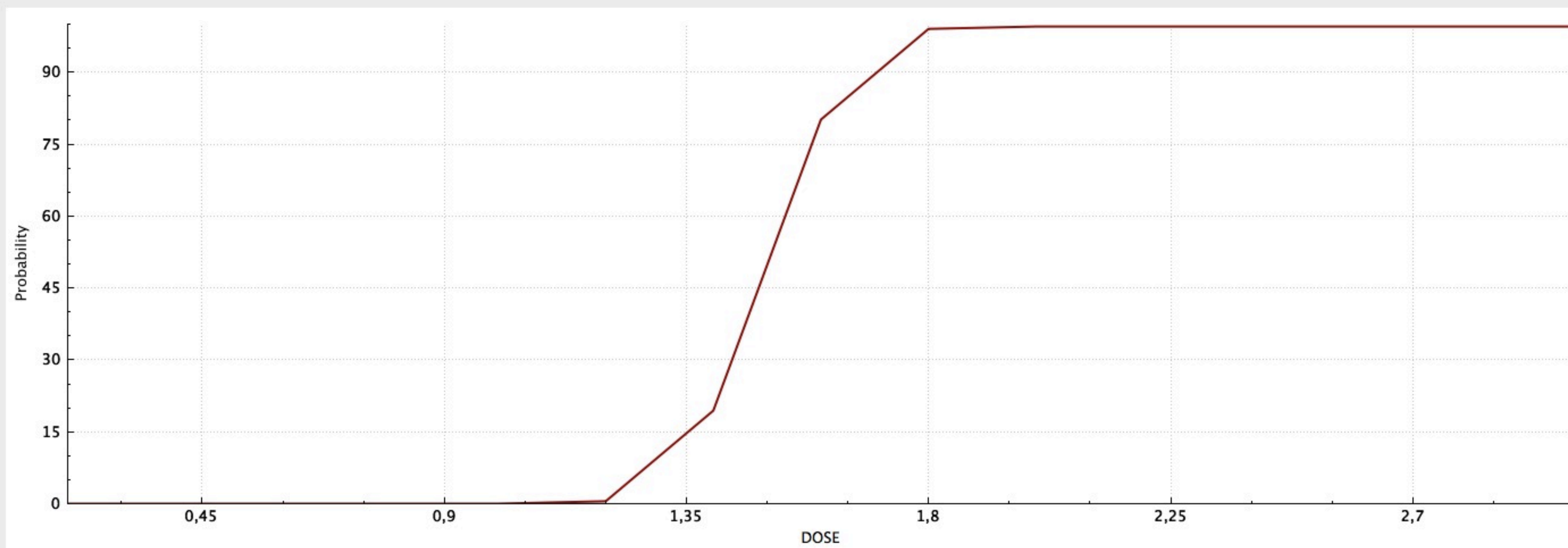
using

using one ofv per model



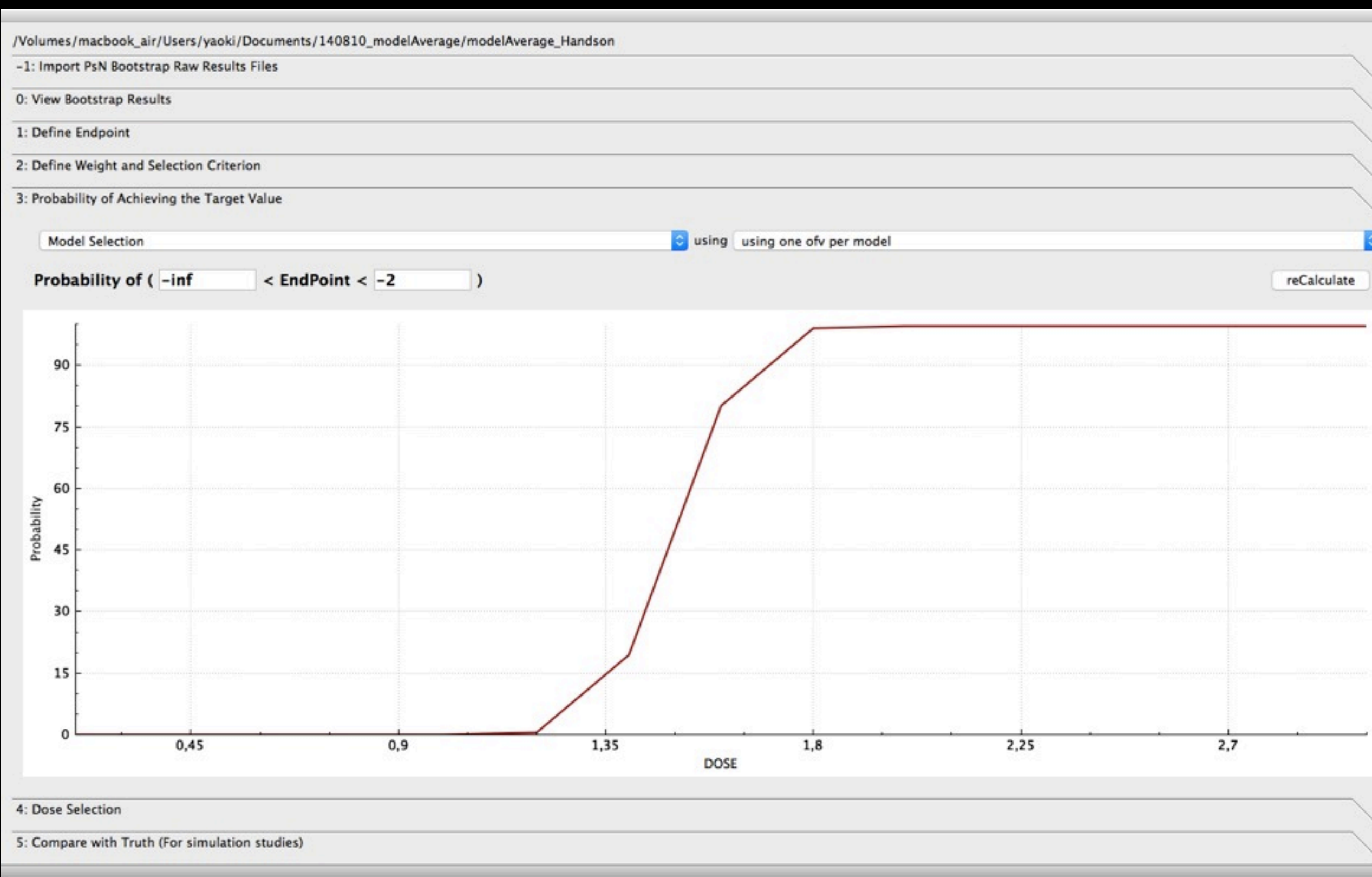
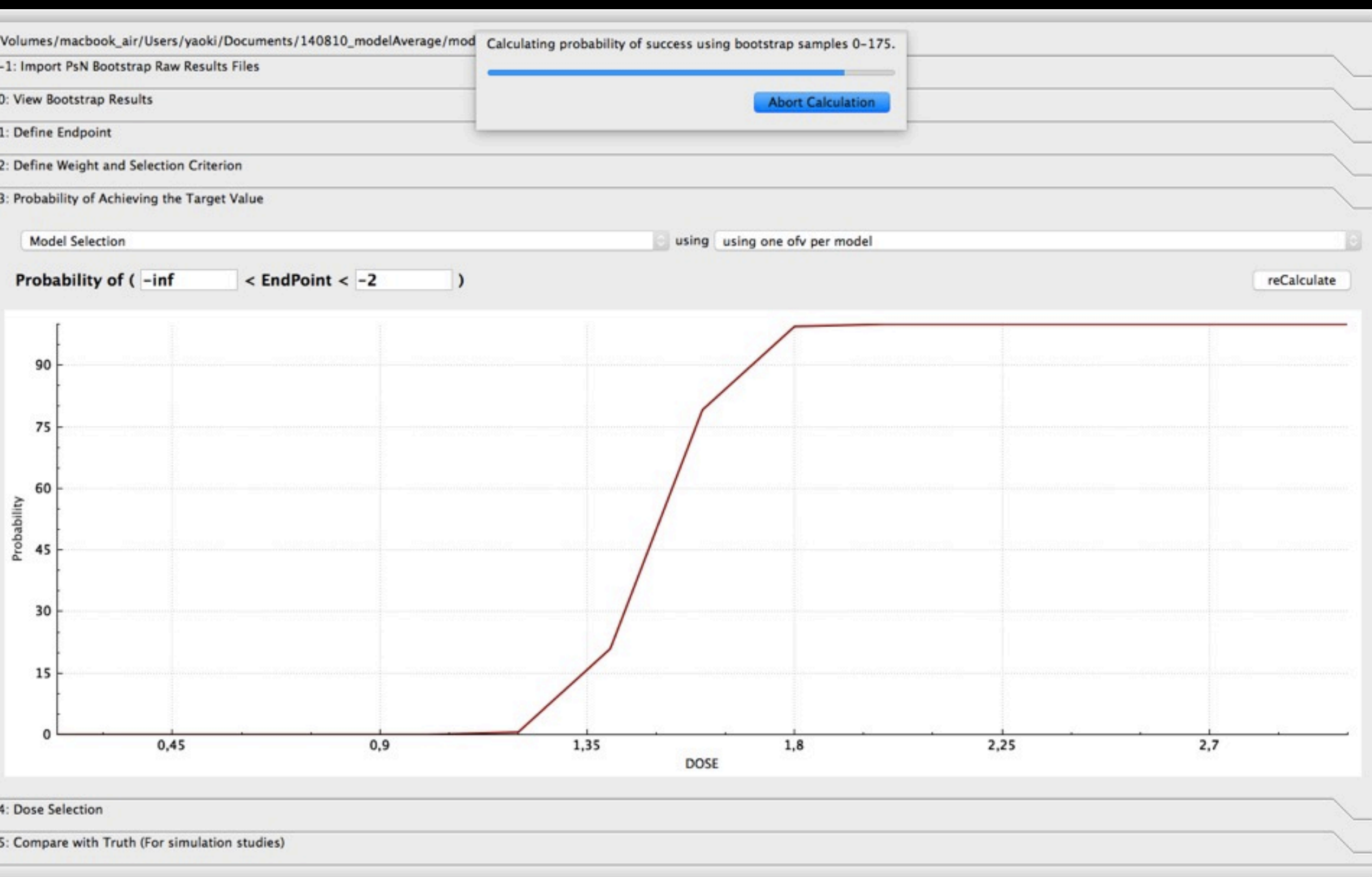
Probability of (< EndPoint <)

reCalculate



4: Dose Selection

5: Compare with Truth (For simulation studies)



The PoS plots look very similar between the one generated using bootstrap data 0-175 and 0-200 hence 200 bootstrap samples should be sufficient to reliably compute the PoS plot.