

EASY-TO-USE PROGRAMS
FOR BOOTSTRAP CONFIDENCE INTERVALS

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THE STANDARD INTERVALS

$$\boxed{\hat{\theta} \pm z^{(\alpha)} \hat{\sigma}} \quad (z^{(0.975)} = 1.96)$$

- $\hat{\theta}$ a point estimate of θ
- $\hat{\sigma}$ an estimate of its standard error
(Taylor series, jackknife, bootstrap)
- Automatic!
- Used millions of times every year

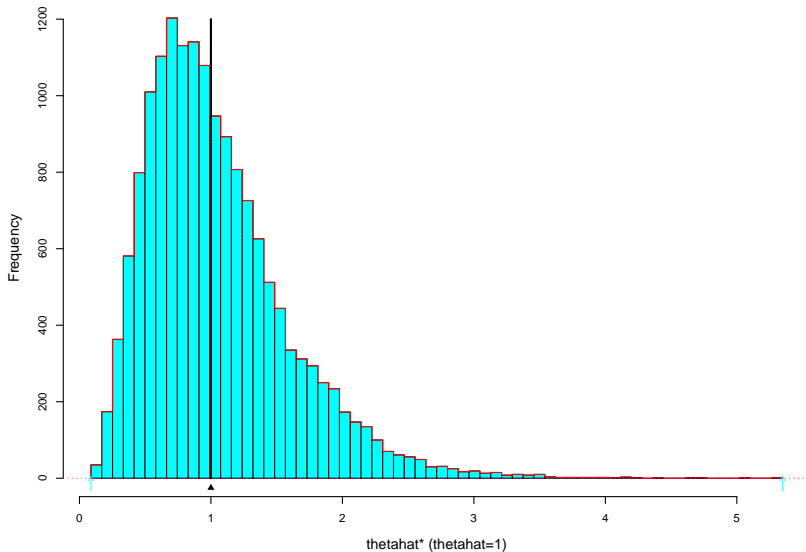
BETTER APPROXIMATE CONFIDENCE INTERVALS

- Standard intervals can be quite inaccurate
- *Two systems of better intervals* (~ 1985)
 - (A) “adjusted” likelihoods (Barndorff-Nielsen. . .)
 - (B) BCa bootstrap (← today)
- Order of magnitude improved accuracy:
coverage $0.95 \pm c/n$ rather than $0.95 \pm c/\sqrt{n}$
- Not automatic enough!
- **New package bcaboot**

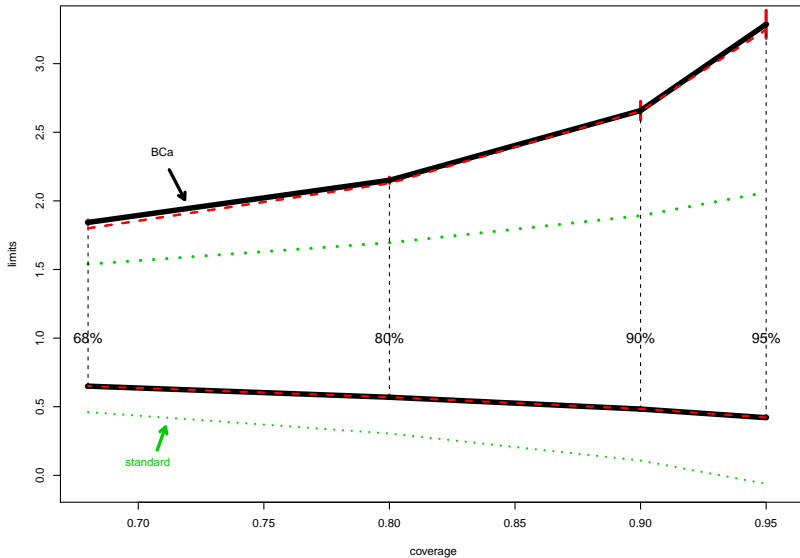
RATIO OF TWO NORMAL VARIANCE ESTIMATES

- Observe $\hat{\sigma}_1^2 \sim \sigma_1^2 \left(\frac{\chi_{10}^2}{10} \right)$ and $\hat{\sigma}_2^2 = \sigma_2^2 \left(\frac{\chi_{42}^2}{42} \right)$ (independent)
- Parameter of interest: $\theta = \frac{\sigma_1^2}{\sigma_2^2}$ so $\hat{\theta} = \frac{\hat{\sigma}_1^2}{\hat{\sigma}_2^2}$
- Exact confidence limits $\hat{\theta}_{\text{exact}}(\alpha) = \hat{\theta} / F_{10,42}^{(1-\alpha)}$
- $B = 16,000$ parametric bootstrap gave...

16,000 Parametric Bootstrap Replications for the Variance Ratio statistic



Black bca, Red exact Green standard



THE DIABETES DATA

- $n = 442$ patients
- $x_i = (c_i, y_i)$ $\begin{cases} c_i \text{ vector of 10 baseline predictors} \\ y_i \text{ measure of disease progression, 1 year} \end{cases}$
- Data matrix \mathbf{x} 442×11
- $\hat{\theta} =$ adjusted R^2 of y regressed on c

$$\hat{\theta} = \text{lm}(y \sim c)\$ \text{adj.r.squared} = 0.507$$

DIABETES DATA

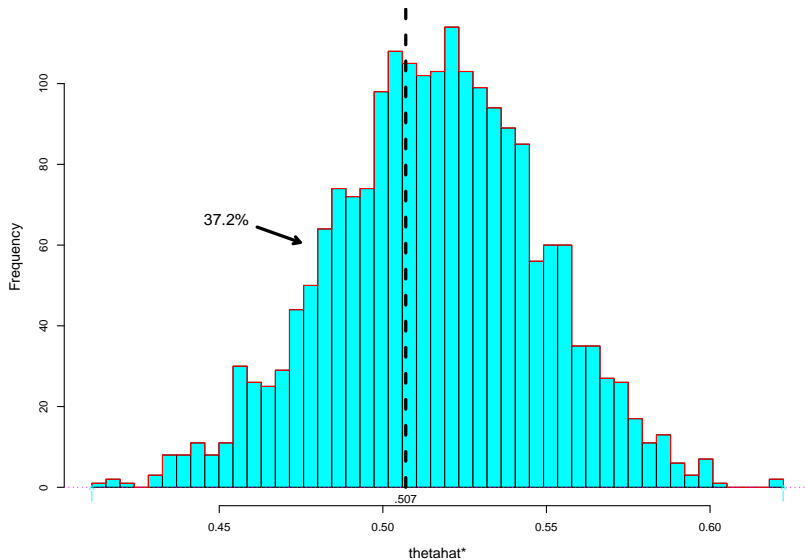
$n = 442$ SUBJECTS, 10 PREDICTORS, RESPONSE y "PROGRESSION".

age	sex	bmi	map	tc	ldl	hdl	tch	ltg	glu	spg	y
59	1	32.1	101	157	93.2	38	4	2.11	87	151	-1.13
48	0	21.6	87	183	103.2	70	3	1.69	69	75	-77.13
72	1	30.5	93	156	93.6	41	4	2.03	85	141	-11.13
24	0	25.3	84	198	131.4	40	5	2.12	89	206	53.87
50	0	23.0	101	192	125.4	52	4	1.86	80	135	-17.13
23	0	22.6	89	139	64.8	61	2	1.82	68	97	-55.13
36	1	22.0	90	160	99.6	50	3	1.72	82	138	-14.13
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮

NONPARAMETRIC BOOTSTRAPPING: BCAJACK

- Data matrix $\mathbf{x}_{n \times p}$ e.g., $x_i = (c_i, y_i)$
- $\hat{\theta} = t(\mathbf{x})$ estimates parameter of interest θ
- Bootstrap data matrix \mathbf{x}^* : randomly choose n rows from \mathbf{x} *with replacement*
- Gives $\hat{\theta}^* = t(\mathbf{x}^*)$
- $\{\hat{\theta}^*(1), \hat{\theta}^*(2), \dots, \hat{\theta}^*(B)\}$ provides inferences for θ
($\hat{\sigma}_{\text{boot}}$ = standard deviation of $\hat{\theta}^*$)

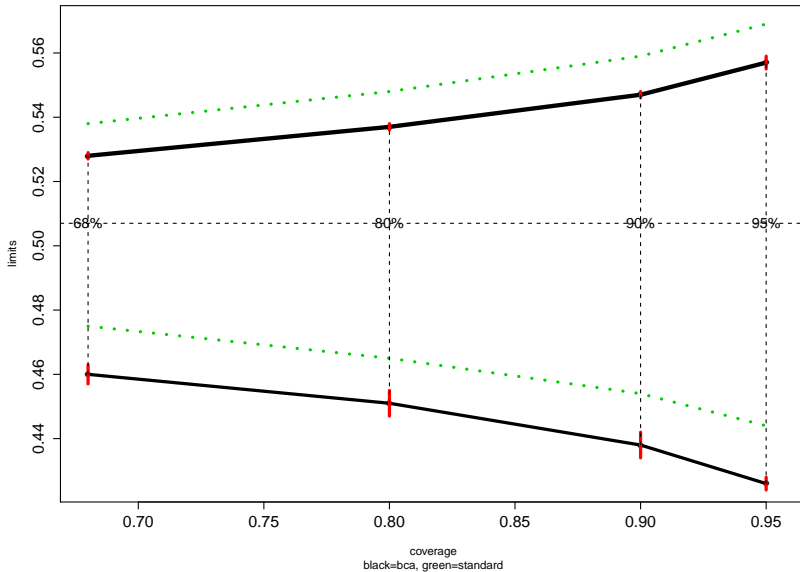
B=2000 nonparametric bootstrap reps for adj.r.squared;
Only 37.2% of the boots are less than .507



CORRECTING THE STANDARD INTERVALS, CONTINUED

- Standard intervals assume $\hat{\theta} \sim \mathcal{N}(\theta, \sigma^2)$
- BCa makes three corrections:
 - 1 For normality using boot cdf \widehat{G}
 - 2 For bias using $\widehat{G}(\hat{\theta})$ (proportion of $\hat{\theta}^*$ s less than $\hat{\theta}$)
 - 3 For “acceleration” (i.e., nonconstant σ^2) using jackknife

Bca and standard two-sided intervals: adjusted R2 statistic (from bcajack; red bars indicate monte carlo error)



THE BCA LEVEL α ENDPOINT

- Let Φ be standard normal cdf and $z^{(\alpha)} = \Phi^{-1}(\alpha)$

$$\hat{\theta}_{\text{bca}}(\alpha) = \widehat{G}^{-1} \Phi \left(\hat{z}_0 + \frac{z^{(\alpha)} + \hat{z}_0}{1 - \hat{a}(z^{(\alpha)} + \hat{z}_0)} \right)$$

- \widehat{G} bootstrap cdf
- $\hat{z}_0 = \Phi^{-1} \widehat{G}(\hat{\theta})$ “bias corrector”
- \hat{a} “acceleration” estimate

- **Transformation invariant**

if $\lambda = m(\theta)$ then $\hat{\lambda}_{\text{bca}}(\alpha) = m(\hat{\theta}_{\text{bca}}(\alpha))$

- *Exact* if $\hat{\lambda} = m(\hat{\theta})$ normal translation family

($\hat{\lambda} = \frac{1}{2} \log \frac{1+\hat{\theta}}{1-\hat{\theta}}$ for normal correlation coefficients)

- **Second-order accurate** Claimed coverage accurate to $O(1/n)$

- Reduces to standard intervals if \widehat{G} normal, $\hat{z}_0 = 0$, $\hat{a} = 0$

JACKKNIFE CALCULATION OF ACCELERATION a

- $\mathbf{x}_{(i)}$ is \mathbf{x} with i th row removed
- $\hat{\theta}_{(i)} = t(\mathbf{x}_{(i)})$ and $\hat{\theta}_{(\cdot)} = \sum_1^n \hat{\theta}_{(i)} / n$
- $D_i = \hat{\theta}_{(i)} - \hat{\theta}_{(\cdot)}$

- Acceleration $\hat{a} = \frac{1}{6} \sum_1^n D_i^3 / \left(\sum_1^n D_i^2 \right)^{3/2}$

- Jackknife standard error $\left(\frac{n-1}{n} \sum_1^n D_i^2 \right)^{1/2}$

GROUPED JACKKNIFE

- n can be enormous these days
- partition \mathbf{x} into m groups of size $g = n/m$:

$$X_k = \{x_{i_1}, x_{i_2}, \dots, x_{i_g}\} \quad (k = 1, 2, \dots, m)$$

- Now $\mathbf{X} = (X_1, X_2, \dots, X_m)$ has just m “points”
- Diabetes $m = 40, g = 11$ (2 left over)

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bcajack(x, 2000, rfun, m = 40)
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PARTIAL OUTPUT OF BCAJACK(x , 2000, RFUN, $m=40$)

x = DIABETES DATA, RFUN = ADJUSTED R^2

α	bcalims	jacksd	standard
.025	.424	.004	.443
.16	.465	.001	.474
.5	.497	.001	.507
.84	.529	.001	.539
.975	.560	.002	.570

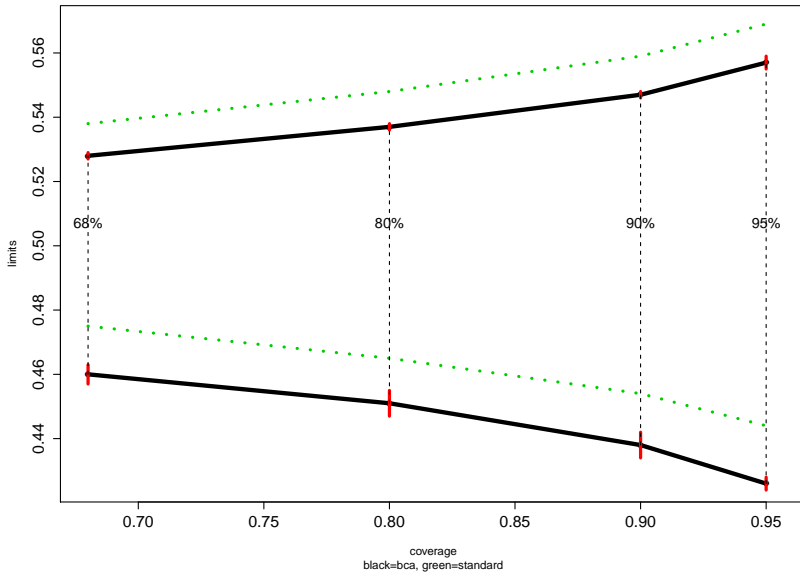
Monte Carlo Error

- *Two types of error* “sampling” and “Monte Carlo”
- $\hat{\sigma}_{\text{boot}}$ concerns sampling error of $\hat{\theta}$
- Was $B = 2000$ enough bootstrap replications?
- **Answer** Jackknife the bootstrap replications.

JACKKNIFE ESTIMATES OF MONTE CARLO ERROR

- Randomly partition bootstrap replications $\{\hat{\theta}_{(1)}^*, \hat{\theta}_{(2)}^*, \dots, \hat{\theta}_{(2000)}^*\}$ into 10 groups of 200 each
- Remove one group at a time, and rerun `bcajack`
- Use jackknife formula to get “jacksd”
- No new bootstrapping required

Monte Carlo error is small for upper limits, not so small for lower limits



MORE OUTPUT OF BCAJACK(x , 2000, RFUN, $M=40$)

	$\hat{\theta}$	sdboot	\hat{z}_0	\hat{a}	sdjack
estimate	.507	.033	-.327	-.004	.034
jacksd	.000	.001	.027	.000	.000

PARAMETRIC EXAMPLE: THE PEDIATRIC DEATH DATA

- 800 cases African facility for very sick babies
- 600 survived, 200 died
- 11 predictors $\mathbf{x}_i = (\text{respiration, heart rate, weight, } \dots)$
- *Logistic regression model*

π_i death probability ($i = 1, 2, \dots, 800$)

$$y_i = \begin{cases} 1 & \text{probability } \pi_i \\ 0 & \text{probability } 1 - \pi_i \end{cases} \quad \text{where } \pi_i = \frac{1}{1 + e^{-\mathbf{x}_i' \boldsymbol{\alpha}}}$$

$\theta = \text{"resp" coefficient } \alpha_1$

PARAMETRIC BOOTSTRAPPING

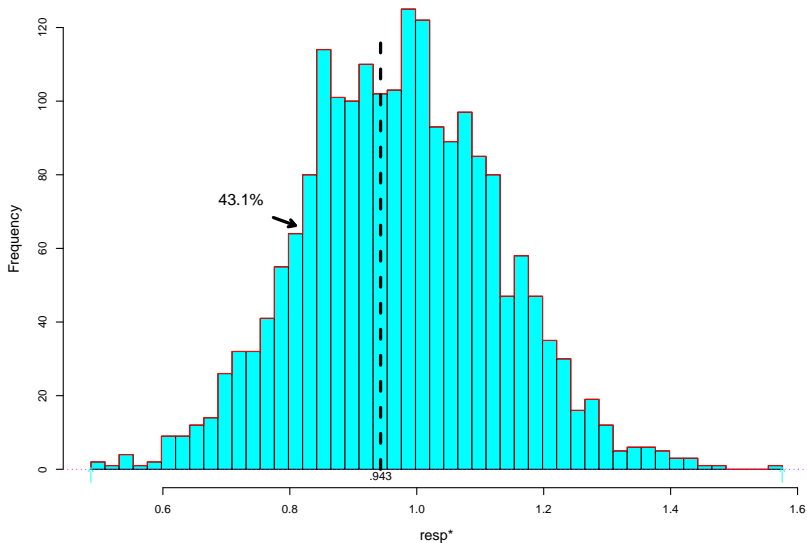
- $\text{glm}(\mathbf{y} \sim_{800 \times 11} \mathbf{X}, \text{binomial})$: MLE $\hat{\alpha}$; $\hat{\theta} = \hat{\alpha}_1 = 0.943$
- $\hat{\pi}_i = 1 / (1 + e^{-\mathbf{x}'_i \hat{\alpha}})$
- $y_i^* = 1$ or 0 prob $\hat{\pi}_i$ or $1 - \hat{\pi}_i$
- $\text{glm}(\mathbf{y}^* \sim \mathbf{X}, \text{binomial})$ gives $\hat{\alpha}^*$ and $\hat{\theta}^* = \hat{\alpha}_1^*$
- Also need $b^* = \mathbf{X}' \mathbf{y}^*$ for $\hat{\alpha}$.

- B bootstrap samples give

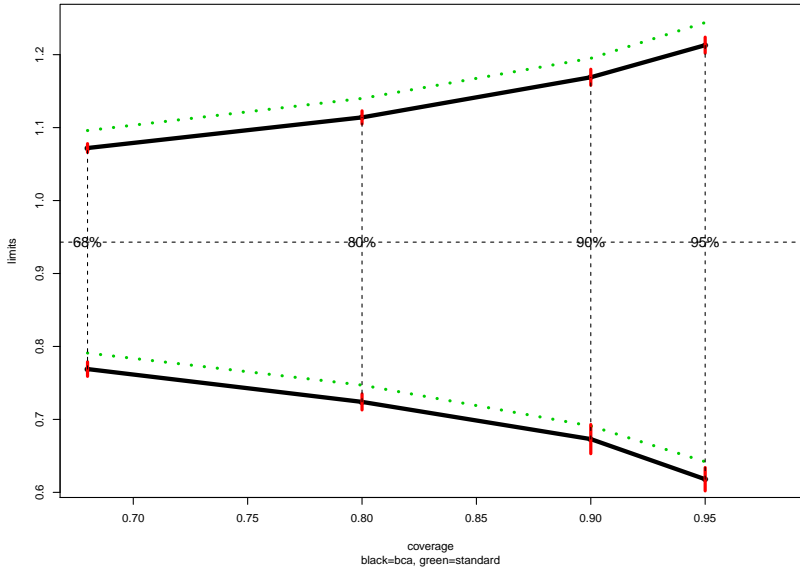
$$\hat{\theta}^* = (\hat{\theta}^*(1), \hat{\theta}^*(2), \dots, \hat{\theta}^*(B)) \text{ and } \mathbf{b}_{11 \times B}^* = (b^*(1), b^*(2), \dots, b^*(B))$$

- $\text{bcapar}(\hat{\theta}, \hat{\theta}^*, \mathbf{b}^*)$ yields bca limits
- $\hat{\theta}$ and $\hat{\theta}^*$ give \widehat{G} and \hat{z}_0
- \mathbf{b}^* gives acceleration \hat{a}

2000 parametric bootstrap replications, ped death data;
coef 'resp', logistic regression, 11 covariates



confidence intervals for resp, using bcapar
(resphat = .943)

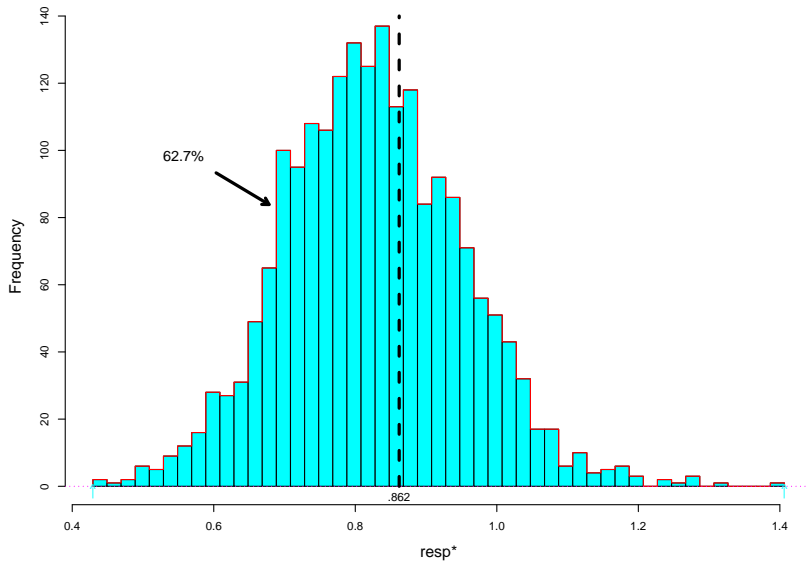


GLMNET ESTIMATE OF α

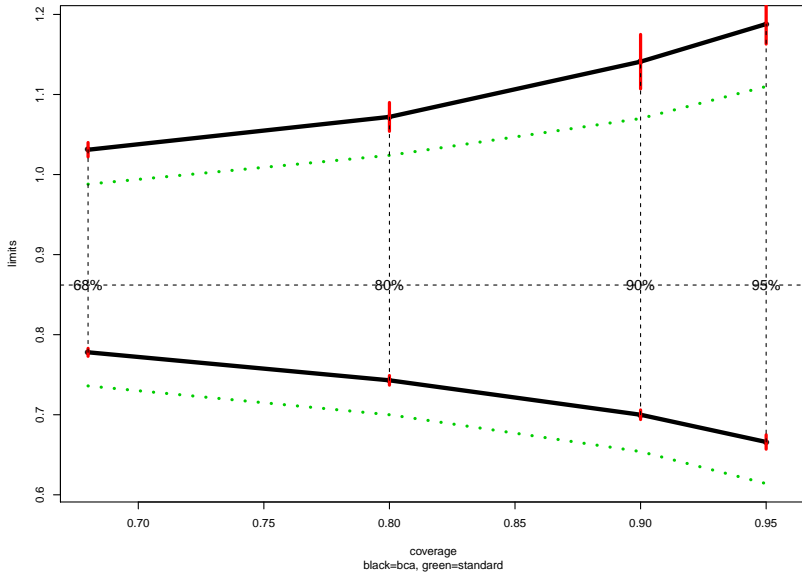
(INSTEAD OF MLE)

- `glmnet(\mathbf{X}, \mathbf{y})` fits increasing succession of logistic regressions; cross-validation used to choose “best” one (*shrinkage*)
- `glmnet` gave $\hat{\alpha}$ and $\hat{\theta} = \hat{\alpha}_1 = 0.862$ (cf 0.943 for MLE)
- **Bootstrapping** $\hat{\alpha} \rightarrow \hat{\pi} \rightarrow \mathbf{y}^*$ and then `glmnet(\mathbf{X}, \mathbf{y}^*)` gives $\hat{\theta}^*$ and $\mathbf{b}^* = \mathbf{X}'\mathbf{y}^*$
- Confidence limits from `bcapar($\hat{\theta}, \hat{\theta}^*, \mathbf{b}^*$)`

2000 boot estimates of 'resp' using glmnet estimation
(point estimate .862)



bcapar confidence limits for 'resp' based on glmnet ;
(glmnet point estimate = .862)



COMPARING MLE AND GLMNET ESTIMATES OF “RESP”

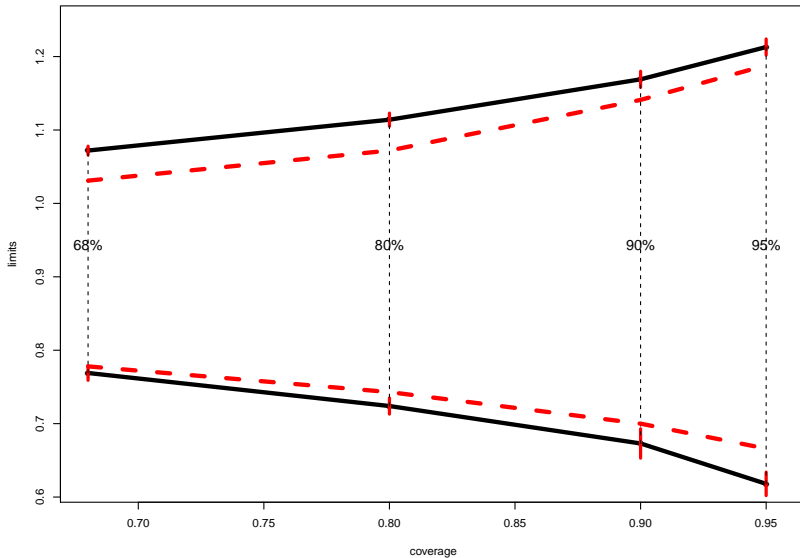
- glmnet estimate $\hat{\theta}$ is smaller than MLE:

glmnet .86 ± .13

MLE .94 ± .15

- However bcapar confidence limits have almost the same centering (but glmnet intervals shorter)

Compare logistic regression limits (black) with glmnet limits (red)



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