

Conducting trial-based cost-effectiveness analyses: A tutorial

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Section 1

Introduction & Modelling in HTA

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 - Prof. Bosmans (Health Sciences @VU) & El Alili (@ZIN)

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- **Personal goal** to facilitate uptake of methods in HTA via software:
 - I am a bit of a **R** enthusiast
 - I am a bit of a **Excel** hater (for statistical analyses)

Before I begin:

- **Statistics** is an all-encompassing discipline: *Statisticians are unified not by the subject matter they work in, but the methodology used to address problems that arise in diverse fields*

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- So I probably will be very annoying throughout the presentation¹

¹But luckily no non-Statistician has been harmed in the making of these slides

Health technology assessment (HTA)

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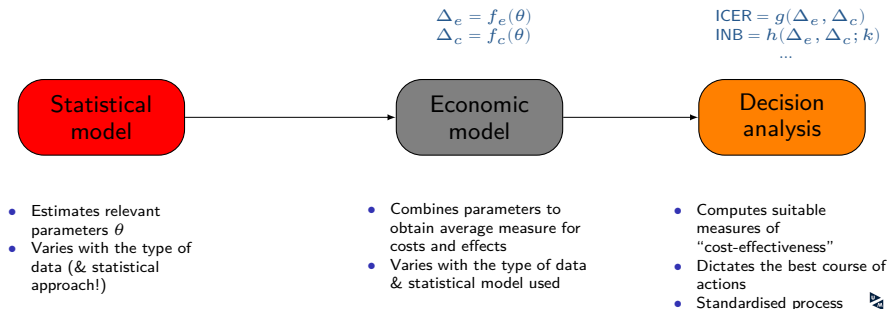
Statistical
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Economic
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- Estimates relevant parameters θ
 - Varies with the type of data (& statistical approach!)
- Combines parameters to obtain average measure for costs and effects
 - Varies with the type of data & statistical model used

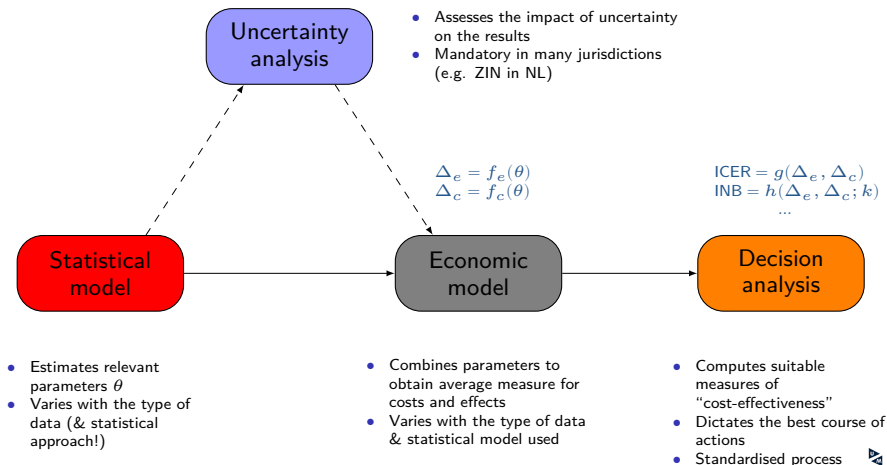
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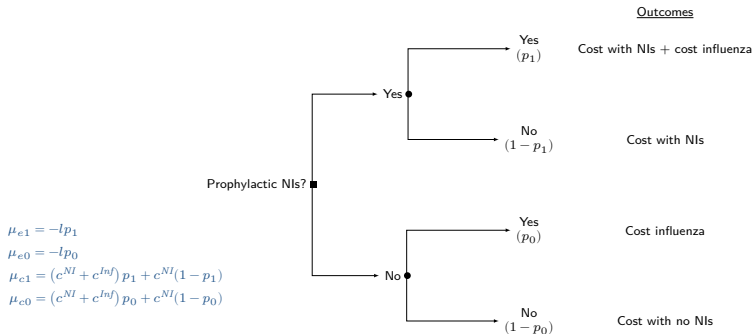
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Statistical modelling for model-based analyses

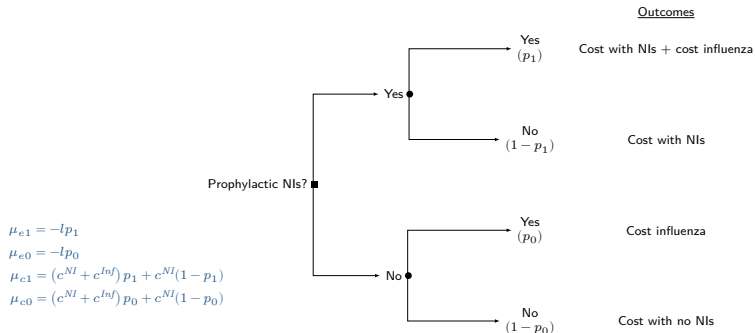
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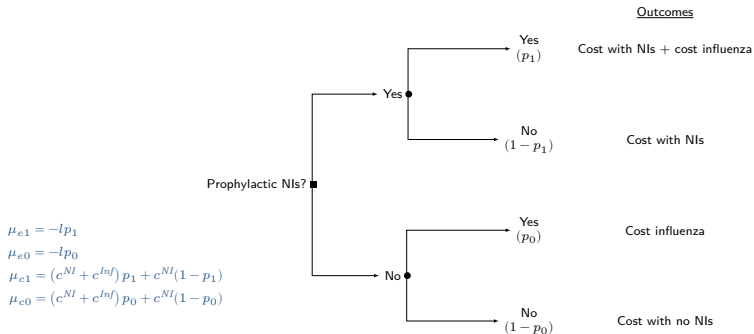


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- 2 Use point estimates for the parameters to build the “base-case” (average) evaluation
- 3 Use resampling methods (eg bootstrap) to propagate uncertainty in the point estimates and perform uncertainty analysis

Statistical modelling for empirical analyses

ID	Trt	Demographics			HRQL data				Resource use data				Clinical outcome			
		Sex	Age	...	u_0	u_1	...	u_J	c_0	c_1	...	c_J	y_0	y_1	...	y_J
1	1	M	23	...	0.32	0.66	...	0.44	103	241	...	80	y_{10}	y_{11}	...	y_{1J}
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y_{ij} = Survival time, event indicator (eg CVD), number of events, continuous measurement (eg blood pressure), ...

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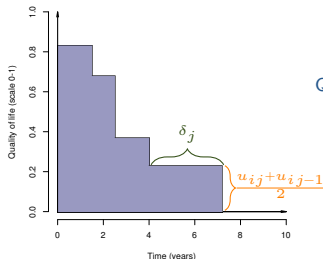
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$$e_i = \sum_{j=1}^J (u_{ij} + u_{i,j-1}) \frac{\delta_j}{2} \quad \text{and} \quad c_i = \sum_{j=1}^J c_{ij}, \quad \left[\text{with: } \delta_j = \frac{\text{Time}_j - \text{Time}_{j-1}}{\text{Unit of time}} \right]$$



QALY_i = "Area under the curve"

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- 2 (Often implicitly) assume normality and linearity and model **independently** individual QALYs and total costs by controlling for baseline values

$$e_i = \alpha_{e0} + \alpha_{e1}u_{0i} + \alpha_{e2}\text{Trt}_i + \varepsilon_{ei} [+ \dots], \quad \varepsilon_{ei} \sim \text{Normal}(0, \sigma_e)$$

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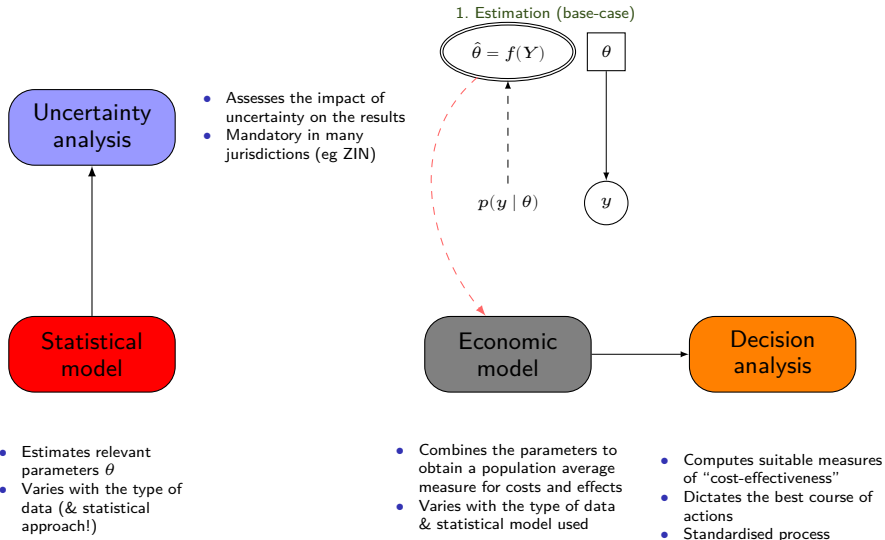
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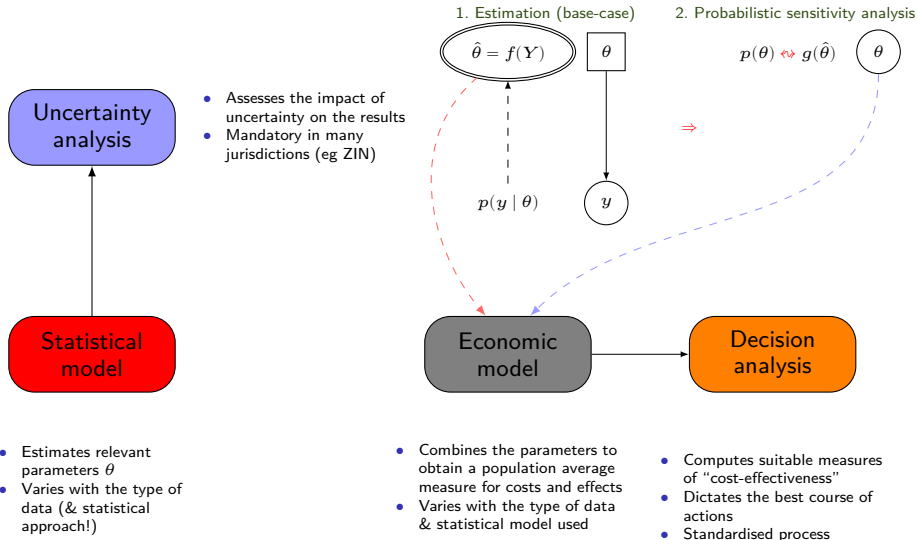
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- 3 Estimate population average cost and effectiveness differentials and use **bootstrap** to quantify uncertainty

“Two-stage” approach to HTA



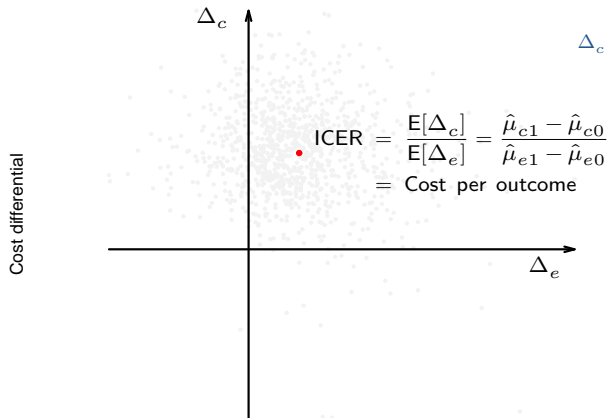
“Two-stage” approach to HTA



“Two-stage approach” (Spiegelhalter, Abrams & Myles, 2004)

Decision + Uncertainty* analysis

Cost-effectiveness plane

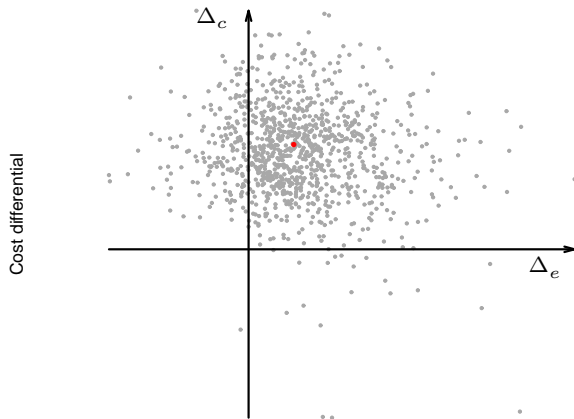


$$\Delta_e = \underbrace{E[e | \hat{\theta}_1]}_{\hat{\mu}_{e1}} - \underbrace{E[e | \hat{\theta}_0]}_{\hat{\mu}_{e0}}$$

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*Induced by $g(\hat{\theta}_0), g(\hat{\theta}_1)$

Effectiveness differential

Section 2

Zorginstituut Nederland (ZIN) 2024 guidelines

ZIN 2024 guidelines: summary

- Cost-effectiveness in the Netherlands has become more and more important in reimbursement decisions of the *National Health Care Institute* over the years
- **Standardise** analyses to improve comparability and enhance quality
- Revision of elements for the “**Reference Case**” to which all economic evaluations *have to comply with*

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 - ① **Perspective** of the analysis
 - Default: **Societal** - *all societal costs and benefits irrespective of who are the beneficiaries/payers*
 - Alternative perspectives may be presented as **scenario analyses**

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 - 1 **Perspective** of the analysis
 - 2 **PICOTS** criteria
 - Patient, Intervention, Comparison & Setting: **Dutch practice** - *relevant to current clinical practice at the time*
 - Outcomes: **Costs** (healthcare, P&F, other sectors) & **QALYs** (EQ-5D-5L)
 - Time horizon: **lifelong** (if possible)

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 - 1 **Perspective** of the analysis
 - 2 **PICOTS** criteria
 - 3 **Type** of evaluation
 - Default: **CUA** - *allows comparison across populations and interventions*
 - A **CEA** may also be conducted in addition

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 - ③ **Type** of evaluation
 - ④ **Data** (effectiveness, costs and QoL)
 - Literature data assessed via **systematic literature review**
 - Costs = volume (unit) × price (per unit) → **Costing Manual**
 - QoL as “utilities” via EQ-5D-5L → **QALY and QoL Manual**

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 - ④ **Data** (effectiveness, costs and QoL)
 - ⑤ **Methods**
 - MB: Discount, Extrapolation, Subgroup, Uncertainty, Validation
 - **EMP**: Missingness, Adjustment, Uncertainty

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 - 5 **Methods**
 - 6 **Reporting**

– **Data, Methods, Results**

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- Focus on **recommended methods** in the context of a *RCT with a 1-year follow-up and homogeneous population*:

- No *selection bias* due to lack of randomisation
- No *discounting* for costs & effects
- No *extrapolation* of results beyond end of trial
- No *subgroup* or *Value of Information* analysis
- No *validation* of source data

Statistical “issues” in analyses (El Alili et al. 2022)

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- **Missing** effects/costs during follow-up are common and may introduce bias. Methods that appropriately account for missing data uncertainty and assess the sensitivity of results are needed (Gabrio et al. 2017, Leurent et al. 2018)

How do we deal with all of this?



Section 3

Methods to handle statistical issues in CEA

Baseline imbalances

- Randomisation ensures that baseline variables are *balanced* between arms but **SOME** differences will inevitably occur

Baseline imbalances

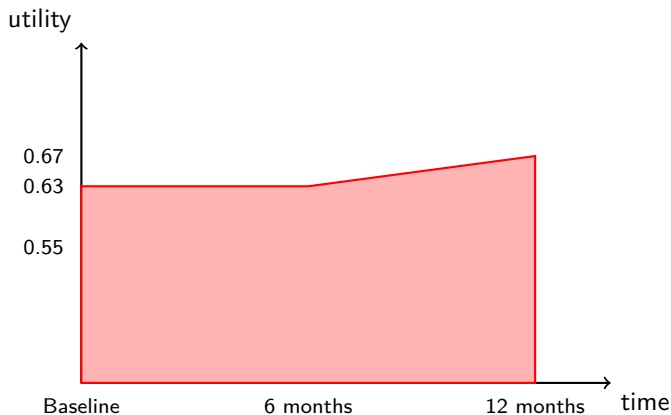
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- This is particularly an issue for **baseline utilities** because:
 - they are used in the *computation of QALYs* through AUC method
 - they are likely to be *predictive* of utilities during follow-up
- Even small changes in Δ_e have consequences on *ICER* and *CE results*
- This is true **regardless** of whether the difference in baseline values is statistically significant or not
- This is also true for any baseline variable that is **strongly predictive** of follow-up outcome values (eg **baseline costs**)

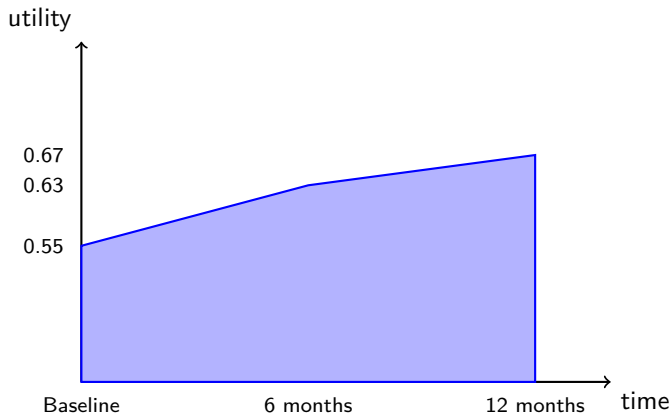
Baseline imbalances - an example

- Old : $QALY_{old} = \left[\frac{0.63+0.63}{2} \times \frac{6}{12} + \frac{0.63+0.67}{2} \times \frac{6}{12} \right] = \mathbf{0.64}$



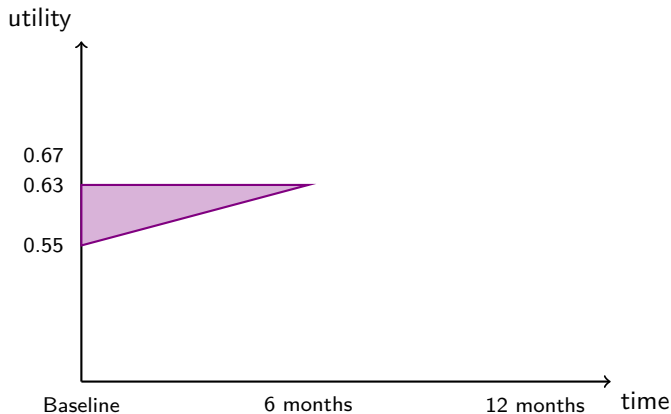
Baseline imbalances - an example

- New : $QALY_{\text{new}} = \left[\frac{0.55+0.63}{2} \times \frac{6}{12} + \frac{0.63+0.67}{2} \times \frac{6}{12} \right] = \mathbf{0.62}$



Baseline imbalances - an example

- $\Delta_e = \text{New} - \text{Old} : QALY_{\text{new}} - QALY_{\text{old}} = 0.62 - 0.64 = -0.02$



Baseline imbalances - unadjusted estimates

- **Unadjusted mean difference** can be obtained from the estimated *slope* ($\hat{\beta}_1$) of the linear regression

$$\text{QALY}_i = \beta_0 + \beta_1 \times \text{arm}_i + \varepsilon_i$$

- **Unadjusted means** in each arm can be obtained as *functions* of the estimated regression coefficients

$$E[\text{QALY} \mid \text{arm} = \text{old}] = \hat{\beta}_0$$

$$E[\text{QALY} \mid \text{arm} = \text{new}] = \hat{\beta}_0 + \hat{\beta}_1$$

Baseline imbalances - adjusted estimates

- Recommended approach is to *include the imbalanced baseline variable into the regression*

$$\text{QALY}_i = \beta_0 + \beta_1 \times \text{arm}_i + \beta_2 \times u_{i0} + \varepsilon_i$$

- Adjusted** estimates for Δ_e and mean QALYs in each arm can be obtained exactly as in the unadjusted case **BUT** with the *inclusion* of u_0 into the model

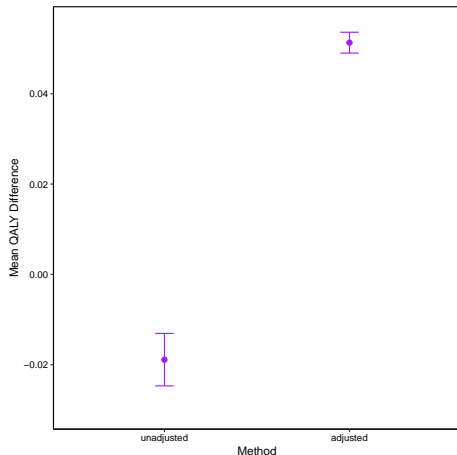
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- Adjusted** estimates for Δ_e and mean QALYs in each arm can be obtained exactly as in the unadjusted case **BUT** with the *inclusion* of u_0 into the model
- In the presence of baseline imbalances, the **adjusted model** allows to:
 - Retrieve through $\hat{\beta}_1$ an **unbiased estimate** of Δ_e and $E[\text{QALY} \mid \text{arm}]$
 - Increase the **precision** of these estimates (ie *lower SEs & narrower CIs*)

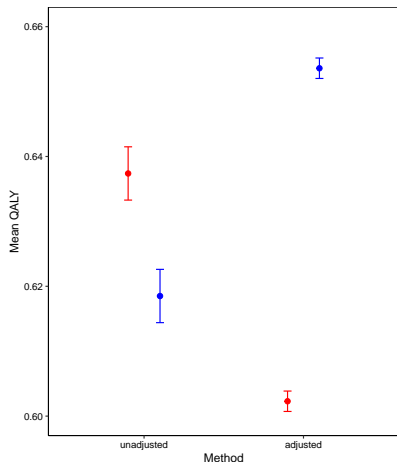
Baseline imbalances - unadjusted vs adjusted estimates



- Mean QALY difference Δ_e

Estimate	CI.low	CI.high	method
<i>-0.019</i>	<i>-0.025</i>	<i>-0.013</i>	<i>unadjusted</i>
<i>0.051</i>	<i>0.049</i>	<i>0.054</i>	<i>adjusted</i>

Baseline imbalances - unadjusted vs adjusted estimates



- **Mean QALY** for arm = “Old”

Estimate	CI.low	CI.high	method
<i>0.637</i>	<i>0.633</i>	<i>0.641</i>	<i>unadjusted</i>
<i>0.602</i>	<i>0.601</i>	<i>0.604</i>	<i>adjusted</i>

Arm
• Old
• New

- **Mean QALY** for arm = “New”

Estimate	CI.low	CI.high	method
<i>0.619</i>	<i>0.614</i>	<i>0.623</i>	<i>unadjusted</i>
<i>0.654</i>	<i>0.652</i>	<i>0.655</i>	<i>adjusted</i>

Baseline imbalances - regression adjustment

- **Advantages:**

- Easy to implement
- Allow to control for multiple variables
- Assess impact of specific variables on marginal CE outcomes (eg via interaction terms)

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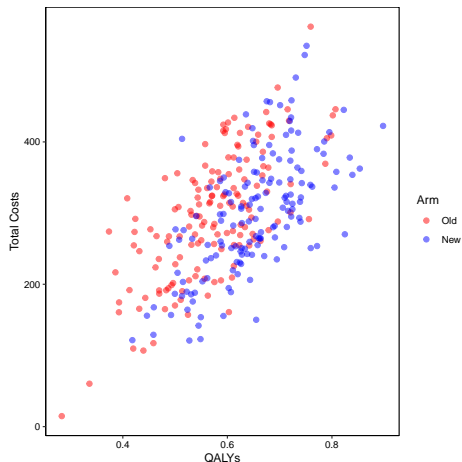
- **Other approaches:**

- *Propensity score adjustment* (Indurkha et al. 2006)
- *Propensity score matching* (Sekhon et al. 2012)
- *Genetic matching* (Sekhon et al. 2012)

Correlation between CE outcomes

- Possible types of associations:
 - Treatments come from intensive research and are **(+)** associated with higher unit costs
 - Treatments **(-)** reduce care pathway costs (eg fewer hospitalisations, side effects, etc.)
- If the outcomes are **sufficiently correlated**:
 - **Joint modelling** of costs & effects is needed to properly characterise uncertainty around parameter estimates and CE results
 - There is additional benefit from *borrowing information* across outcomes to estimate variance components and standard errors *more efficiently* than in separate univariate analyses

Correlation between CE outcomes - an example



- Means and (Pearson's) **correlations** between costs & effects

QALY	TC	corr	arm
<i>0.57</i>	<i>298</i>	<i>0.694</i>	<i>Old</i>
<i>0.65</i>	<i>299</i>	<i>0.648</i>	<i>New</i>

- We could run **separate analyses** for each outcome using the models

$$\text{QALY}_i = \beta_0 + \beta_1 \times \text{arm}_i + \beta_2 \times u_{i0} + \varepsilon_{ie}$$

$$\text{TC}_i = \alpha_0 + \alpha_1 \times \text{arm}_i + \alpha_2 \times c_{i0} + \varepsilon_{ic}$$

- Get the estimates $\hat{\beta} = (\hat{\beta}_0, \hat{\beta}_1)$ and $\hat{\alpha} = (\hat{\alpha}_0, \hat{\alpha}_1)$, then derive:
 - **Incremental**(Δ_e, Δ_c) and **marginal**($E[\text{QALY} \mid \text{arm}], E[\text{TC} \mid \text{arm}]$) quantities of interest
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 - Associated *measures of uncertainty* (eg SEs or CIs)
- **Important:** by doing so, we are assuming **independence** between the outcomes!

CE correlation - “joint” analyses

- **Seemingly Unrelated Regression** (SUR) equations
 - Same models but with **error terms linked** through the parameter ρ :

$$\begin{pmatrix} \varepsilon_{ie} \\ \varepsilon_{ic} \end{pmatrix} \sim \text{Normal} \left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_e^2 & \rho\sigma_e\sigma_c \\ \rho\sigma_c\sigma_e & \sigma_c^2 \end{pmatrix} \right]$$

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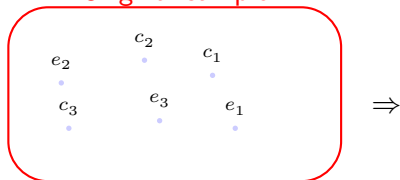
$$\begin{pmatrix} \varepsilon_{ie} \\ \varepsilon_{ic} \end{pmatrix} \sim \text{Normal} \left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_e^2 & \rho\sigma_e\sigma_c \\ \rho\sigma_c\sigma_e & \sigma_c^2 \end{pmatrix} \right]$$

- **Bootstrapping** costs & effects “in pairs”

- Generate a “bootstrap” sample by **sampling with replacement** CE values for each individual from the observed data
- Analyse CE outcomes and derive $(\hat{\beta}, \hat{\alpha})^b \rightarrow (\Delta_e, \Delta_c)^b$
- Iterate the process a *sufficiently large number of times* (B)
- Use $(\Delta_e, \Delta_c)^b$ to approximate the sampling distribution of (Δ_e, Δ_c)
- Use this distribution to quantify uncertainty (eg obtain CIs)

What is bootstrapping?

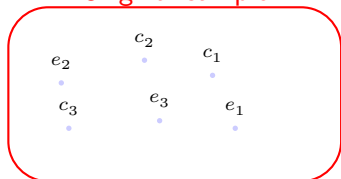
Original sample



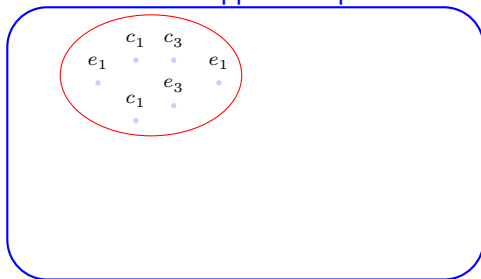
- Original sample \approx population
- Original sample size $n = 6$
- Mean $\bar{e} = 0.5$ & $\bar{c} = 150$
- Sd $s_e = 0.25$ & $s_c = 50$
- Coeff $\hat{\beta}_1 = 0.15$ & $\hat{\alpha}_1 = 35$

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Bootstrapped samples

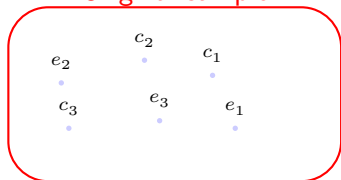


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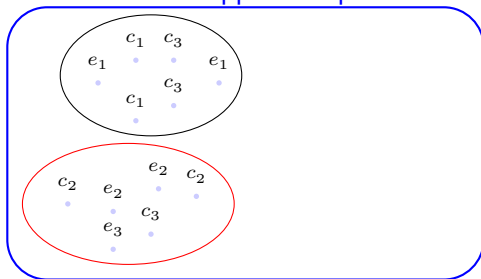
- Bootstrap sample number $b = 1$
- Bootstrapped sample size $n^b = 6$
- Bootstrapped Mean $\bar{e}^b = 0.4$ & $\bar{c}^b = 160$
- Bootstrapped Sd $s_e^b = 0.2$ & $s_c^b = 50$
- Bootstrapped Coeff $\hat{\beta}_1^b = 0.2$ & $\hat{\alpha}_1^b = 40$

What is bootstrapping?

Original sample



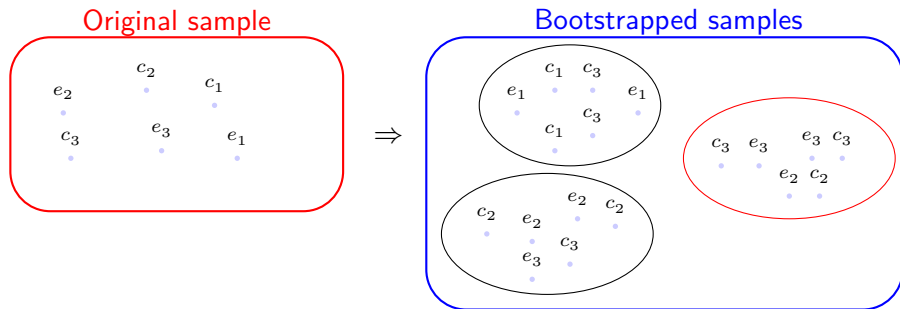
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- Coeff $\hat{\beta}_1 = 0.15$ & $\hat{\alpha}_1 = 35$

- Bootstrap sample number $b = 2$
- Bootstrapped sample size $n^b = 6$
- Bootstrapped Mean $\bar{e}^b = 0.37$ & $\bar{c}^b = 130$
- Bootstrapped Sd $s_e^b = 0.13$ & $s_c^b = 42$
- Bootstrapped Coeff $\hat{\beta}_1^b = 0.18$ & $\hat{\alpha}_1^b = 25$

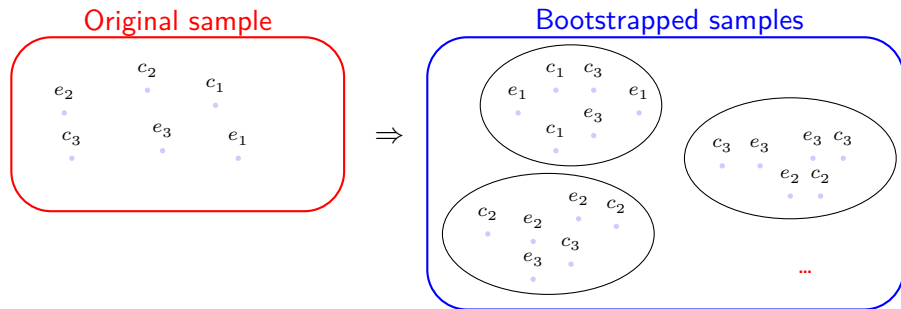
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- Bootstrap sample number $b = 3$
- Bootstrapped sample size $n^b = 6$
- Bootstrapped Mean $\bar{e}^b = 0.5$ & $\bar{c}^b = 155$
- Bootstrapped Sd $s_e^b = 0.14$ & $s_c^b = 32$
- Bootstrapped Coeff $\hat{\beta}_1^b = 0.15$ & $\hat{\alpha}_1^b = 33$

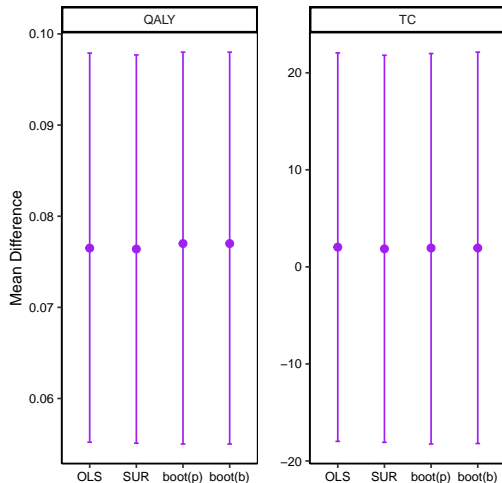
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- Iterate the process $b = 4, \dots, B$ times
- Quantify uncertainty of the estimators (eg CIs) using all bootstrapped samples

Correlation - comparison of approaches



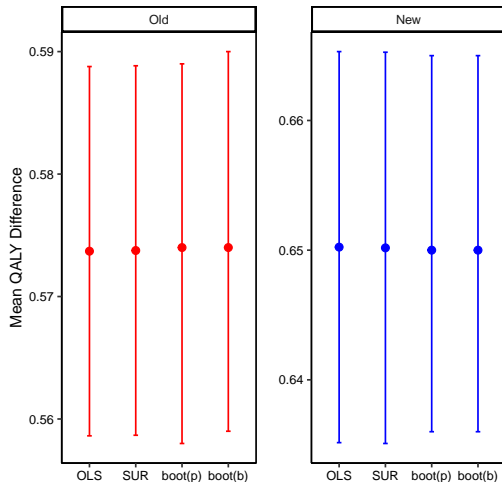
- Mean QALY difference Δ_e

Estimate	CI.low	CI.high	method
0.0765	0.0552	0.0979	OLS
0.0764	0.0551	0.0977	SUR
0.0770	0.0550	0.0980	boot(p)
0.0770	0.0550	0.0980	boot(b)

- Mean TC difference Δ_c

Estimate	CI.low	CI.high	method
2.033	-17.984	22.051	OLS
1.862	-18.080	21.805	SUR
1.943	-18.258	21.983	boot(p)
1.943	-18.204	22.125	boot(b)

Correlation - comparison of approaches



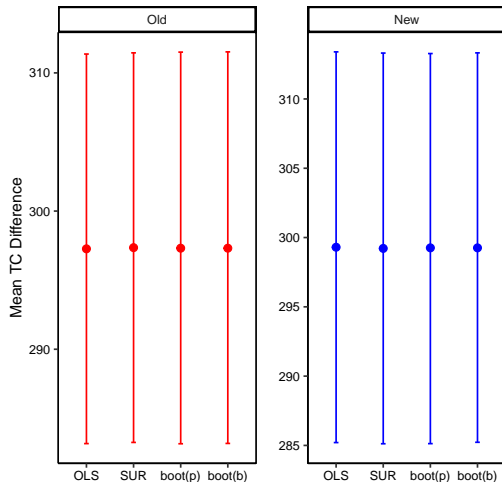
- Mean **QALY** for arm = “Old”

Estimate	CI.low	CI.high	method
0.5737	0.5586	0.5888	OLS
0.5738	0.5587	0.5888	SUR
0.5740	0.5580	0.5890	boot(p)
0.5740	0.5590	0.5900	boot(b)

- Mean **QALY** for arm = “New”

Estimate	CI.low	CI.high	method
0.6502	0.6352	0.6653	OLS
0.6502	0.6351	0.6653	SUR
0.6500	0.6360	0.6650	boot(p)
0.6500	0.6360	0.6650	boot(b)

Correlation - comparison of approaches



- Mean TC for arm = "Old"

Estimate	CI.low	CI.high	method
297.268	283.172	311.364	OLS
297.353	283.257	311.449	SUR
297.313	283.160	311.503	boot(p)
297.313	283.184	311.520	boot(b)

- Mean TC for arm = "New"

Estimate	CI.low	CI.high	method
299.301	285.205	313.397	OLS
299.215	285.119	313.312	SUR
299.256	285.129	313.276	boot(p)
299.256	285.226	313.325	boot(b)

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- Allow inclusion of outcome-specific variables into the regressions
- Similar **limitations** of standard regression

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- **Other approaches:**

- *Bayesian joint models* (Gabrio et al. 2019)

Skewness in CE outcomes

- Costs are typically **right-skewed** while utilities tend to be **left-skewed**:
 - Costs are bound at 0 with few participants with very high costs
 - Utilities are bound at 1 with few participants with very low (also negative) values

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 - In “large” samples, **CLT** ensures that estimates are unbiased but *efficiency* may not be achieved
 - In “small” samples, *unbiasdness* is no longer guaranteed

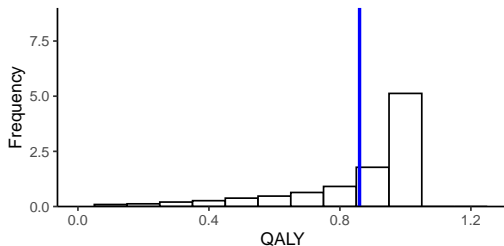
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Skewness in CE outcomes

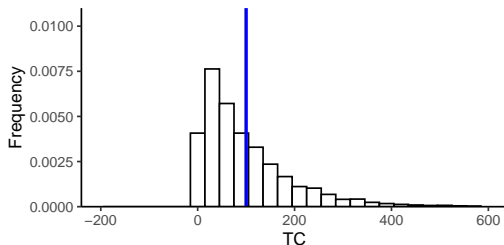
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- **No general consensus** at which point:
 - The degree of skewness is “too high”
 - The size of the sample is “too small”
- Data *transformations* (eg log) are **not appropriate** as they do not provide inferences about population means of interest

Skewness in CE outcomes - an example



- QALYs in **large** samples

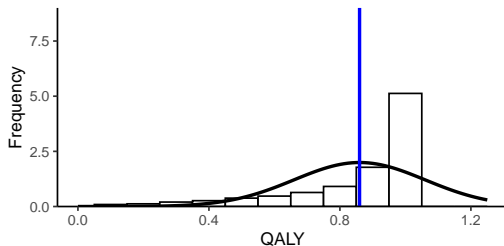
Mean	Sd	CI(low)	CI(high)	size
<i>0.86</i>	<i>0.2</i>	<i>0.266</i>	<i>1</i>	<i>5000</i>



- TC in **large** samples

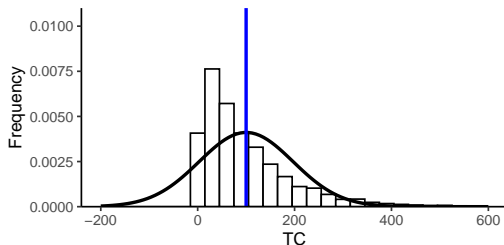
Mean	Sd	CI(low)	CI(high)	size
<i>100</i>	<i>97</i>	<i>2.67</i>	<i>350.153</i>	<i>5000</i>

Skewness in CE outcomes - an example



- CLT in **large** samples

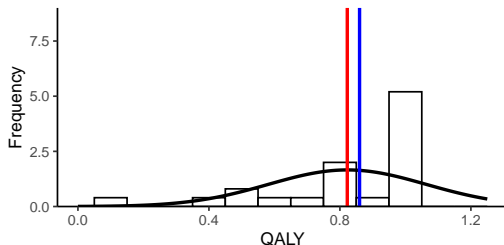
Mean	Sd	CI(low)	CI(high)	size
<i>0.86</i>	<i>0.200</i>	<i>0.266</i>	<i>1.00</i>	5000
0.86	0.003	0.860	0.86	5000



- CLT **large** samples

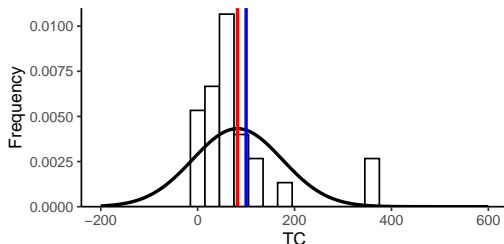
Mean	Sd	CI(low)	CI(high)	size
<i>100.000</i>	<i>97.000</i>	<i>2.67</i>	<i>350.153</i>	5000
99.999	1.372	99.96	100.034	5000

Skewness in CE outcomes - an example



- CLT in **small** samples

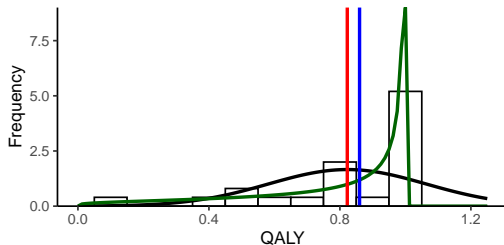
Mean	Sd	CI(low)	CI(high)	size
<i>0.860</i>	<i>0.200</i>	<i>0.266</i>	<i>1.000</i>	5000
<i>0.822</i>	<i>0.241</i>	<i>0.266</i>	<i>1.000</i>	25
0.822	0.040	0.822	0.823	25



- CLT in **small** samples

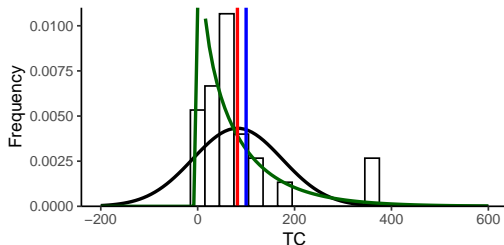
Mean	Sd	CI(low)	CI(high)	size
<i>100.000</i>	<i>97.000</i>	<i>2.670</i>	<i>350.153</i>	5000
<i>82.062</i>	<i>92.265</i>	<i>6.047</i>	<i>356.448</i>	25
82.063	19.400	82.025	82.098	25

Skewness in CE outcomes - an example



- Other distribution (**Beta**) in **small** samples

Mean	Sd	CI(low)	CI(high)	size
0.860	0.200	0.266	1.000	5000
0.822	0.241	0.266	1.000	25
0.813	0.238	0.362	1.295	25
0.818	0.245	0.157	1.000	25



- Other distribution (**Gamma**) in **small** samples

Mean	Sd	CI(low)	CI(high)	size
100.000	97.000	2.670	350.153	5000
82.062	92.265	6.047	356.448	25
84.503	89.313	-89.825	263.089	25
84.592	98.106	0.886	351.883	25

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- **Generalised Linear Model** (GLM):

$$E[QALY_i] = g_e(\beta_0 + \beta_1 \times \text{arm}_i + \beta_2 \times u_{i0})^{-1}$$

$$E[TC_i] = g_c(\alpha_0 + \alpha_1 \times \text{arm}_i + \alpha_2 \times c_{i0})^{-1}$$

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- Choose **link functions** to model the *expected values*:
 - $g_e(\cdot)^{-1} = \text{logit}()$ & $g_c(\cdot)^{-1} = \log()$

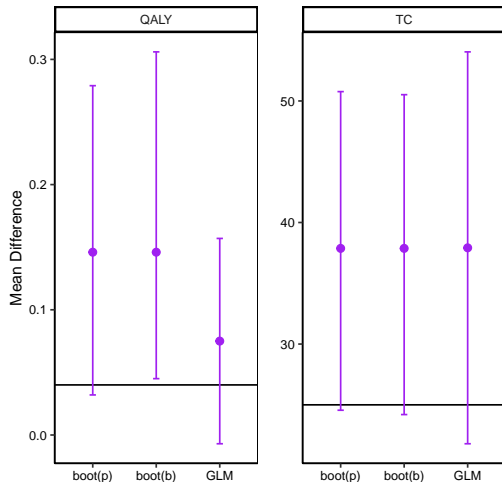
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- Choose **link functions** to model the *expected values*:
 - $g_e(\cdot)^{-1} = \text{logit}()$ & $g_c(\cdot)^{-1} = \text{log}()$
- Choose **alternative distributions** for the *error terms*:
 - $\varepsilon_{ie} \sim \text{Beta}()$ & $\varepsilon_{ic} \sim \text{Gamma}()$

Skewness - alternative methods



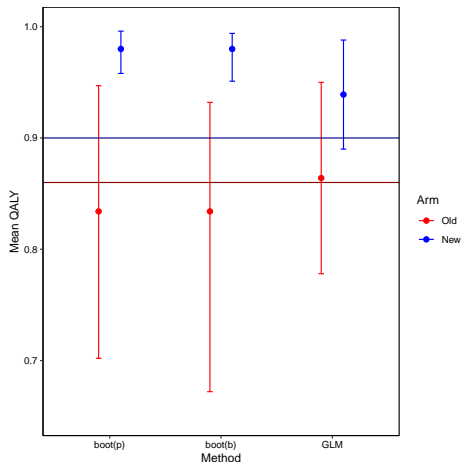
- Mean QALY difference Δ_e

Estimate	CI.low	CI.high	method
<i>0.146</i>	<i>0.032</i>	<i>0.279</i>	<i>boot(p)</i>
<i>0.146</i>	<i>0.045</i>	<i>0.306</i>	<i>boot(b)</i>
<i>0.075</i>	<i>-0.007</i>	<i>0.157</i>	<i>GLM</i>

- Mean TC difference Δ_c

Estimate	CI.low	CI.high	method
<i>37.872</i>	<i>24.555</i>	<i>50.768</i>	<i>boot(p)</i>
<i>37.872</i>	<i>24.198</i>	<i>50.517</i>	<i>boot(b)</i>
<i>37.918</i>	<i>21.797</i>	<i>54.038</i>	<i>GLM</i>

Skewness - alternative methods



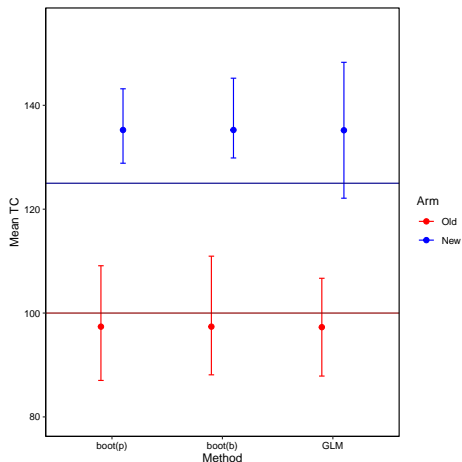
- **Mean QALY** for arm = “Old”

Estimate	CI.low	CI.high	method
<i>0.834</i>	<i>0.702</i>	<i>0.947</i>	<i>boot(p)</i>
<i>0.834</i>	<i>0.672</i>	<i>0.932</i>	<i>boot(b)</i>
<i>0.864</i>	<i>0.778</i>	<i>0.950</i>	<i>GLM</i>

- **Mean QALY** for arm = “New”

Estimate	CI.low	CI.high	method
<i>0.980</i>	<i>0.958</i>	<i>0.996</i>	<i>boot(p)</i>
<i>0.980</i>	<i>0.951</i>	<i>0.994</i>	<i>boot(b)</i>
<i>0.939</i>	<i>0.890</i>	<i>0.988</i>	<i>GLM</i>

Skewness - alternative methods



- **Mean TC for arm = "Old"**

Estimate	CI.low	CI.high	method
97.381	87.023	109.112	boot(p)
97.381	88.104	110.953	boot(b)
97.282	87.866	106.697	GLM

- **Mean TC for arm = "New"**

Estimate	CI.low	CI.high	method
135.253	128.852	143.187	boot(p)
135.253	129.866	145.226	boot(b)
135.199	122.114	148.284	GLM

Skewness - GLM/bootstrapping

- **GLM:**

- Allow comparison of means on **natural scale**
- Can handle **skewness** also in “small” samples
- The choice of **distribution** and **link function** crucial (not always easy)

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- Good performance in “**large**” samples but **poor** in “**small**” samples
- **Different ways** to compute CIs (percentile, bias-corrected and accelerated, ...)

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- **Other approaches:**

- *Bayesian joint models* (Gabrio et al. 2019,)
- *Hurdle models* (Gabrio et al. 2019, Lambert et al. 2008)

Clustering of data

- Trial participants may be **clustered** (eg practices/hospitals) and *clusters may be randomised instead of individuals*
 - Typical of **cluster RCTs** where patients in a cluster are randomised to different treatments
 - Individual effects & costs in the same cluster tend to be more *homogeneous* than those in different clusters

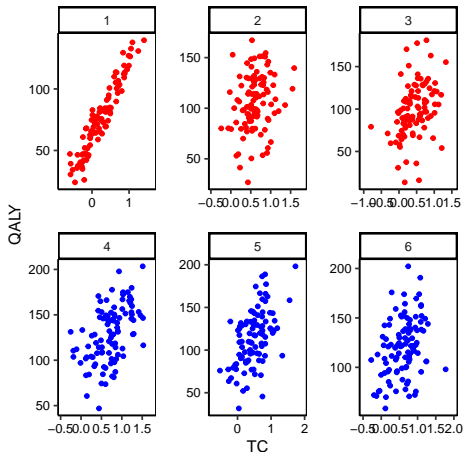
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 - Ignoring clustering **underestimates** statistical uncertainty (eg variance)
 - may lead to **incorrect** inferences and **bias** the results
- In CE studies, **additional challenges** need to be addressed:
 - Account for **correlation** between outcomes
 - Deal with **skewness** in both outcomes

Clustering of data - an example



- Costs & effects across **clusters**

mean(e)	sd(e)	mean(c)	sd(c)	arm
<i>0.433</i>	<i>0.410</i>	<i>93.959</i>	<i>31.518</i>	Old
<i>0.604</i>	<i>0.407</i>	<i>121.437</i>	<i>31.525</i>	New

- Costs & effects by **cluster**

mean(e)	sd(e)	mean(c)	sd(c)	arm
<i>0.252</i>	<i>0.450</i>	<i>77.095</i>	<i>27.742</i>	Old
<i>0.608</i>	<i>0.326</i>	<i>106.259</i>	<i>28.088</i>	Old
<i>0.438</i>	<i>0.369</i>	<i>98.524</i>	<i>31.314</i>	Old
<i>0.718</i>	<i>0.402</i>	<i>129.361</i>	<i>30.897</i>	New
<i>0.489</i>	<i>0.401</i>	<i>114.054</i>	<i>32.540</i>	New
<i>0.606</i>	<i>0.387</i>	<i>120.896</i>	<i>29.484</i>	New

Clustering - alternative methods

- **Multilevel Model (MLM):**
- ① Add **"random" terms** (u_{je}, u_{jc}) to OLS/SUR model to capture differences between j -th cluster QALY/TC means from overall means in each arm

$$\begin{aligned}\text{QALY}_{ij} &= \beta_0 + \beta_1 \times \text{arm}_j + u_{je} + \varepsilon_{ije} \\ \text{TC}_{ij} &= \alpha_0 + \alpha_1 \times \text{arm}_j + u_{jc} + \varepsilon_{ijc}\end{aligned}$$

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- ② Model cluster-specific error terms using some *distribution* (eg Normal) and **link them** through the parameter ψ (often assumed 0)

$$\begin{pmatrix} u_{je} \\ u_{jc} \end{pmatrix} \sim \text{Normal} \left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \tau_e^2 & \psi \tau_e \tau_c \\ \psi \tau_c \tau_e & \tau_c^2 \end{pmatrix} \right]$$

- (non-parametric) **Two-Stage Bootstrap** (TSB):

- 1 **Two-stage routine** to account for data clustering:

- First **sample clusters** then **individuals** within each resampled cluster
- Analyse CE outcomes and derive $(\hat{\beta}, \hat{\alpha})^b \rightarrow (\Delta_e, \Delta_c)^b$
- Iterate the process a *sufficiently* large number of times (B)
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Clustering - alternative methods

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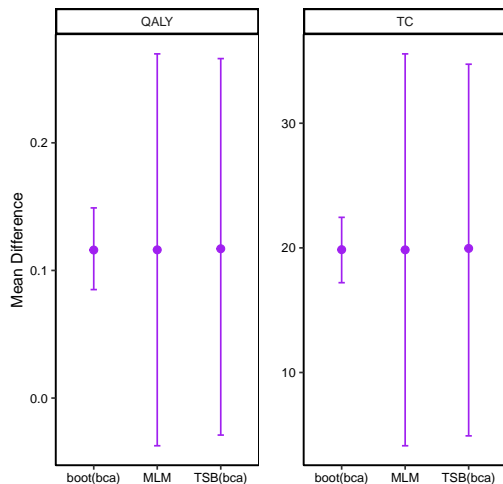
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- 2 Apply "**shrinkage**" correction to avoid **overestimation** of variance

- Before any resampling, **cluster means** are *shrunk* and **individual residuals** estimated from cluster means
- Sample **shrunk cluster means** then **individual residuals**
- Combine shrunk means and residuals to obtain bootstrap dataset

Clustering - alternative methods



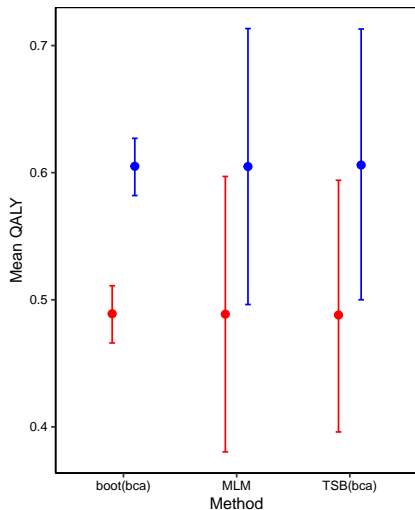
- Mean QALY difference Δ_e

Estimate	CI.low	CI.high	method
<i>0.116</i>	<i>0.085</i>	<i>0.149</i>	<i>boot(bca)</i>
<i>0.116</i>	<i>-0.037</i>	<i>0.270</i>	<i>MLM</i>
<i>0.117</i>	<i>-0.029</i>	<i>0.266</i>	<i>TSB(bca)</i>

- Mean TC difference Δ_c

Estimate	CI.low	CI.high	method
<i>19.857</i>	<i>17.205</i>	<i>22.449</i>	<i>boot(bca)</i>
<i>19.843</i>	<i>4.122</i>	<i>35.565</i>	<i>MLM</i>
<i>19.955</i>	<i>4.916</i>	<i>34.736</i>	<i>TSB(bca)</i>

Clustering - alternative methods



• Mean QALY for arm = "Old"

Estimate	CI.low	CI.high	method	arm
0.489	0.466	0.511	boot(bca)	Old
0.489	0.380	0.597	MLM	Old
0.488	0.396	0.594	TSB(bca)	Old

Arm

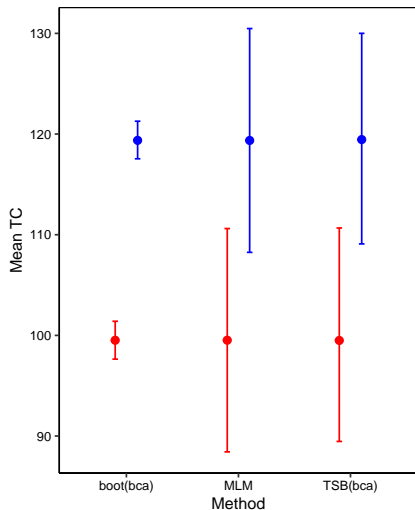
• Old

• New

• Mean QALY for arm = "New"

Estimate	CI.low	CI.high	method	arm
0.605	0.582	0.627	boot(bca)	New
0.605	0.496	0.713	MLM	New
0.606	0.500	0.713	TSB(bca)	New

Clustering - alternative methods



• Mean TC for arm = "Old"

Estimate	CI.low	CI.high	method	arm
99.516	97.642	101.403	boot(bca)	Old
99.520	88.427	110.614	MLM	Old
99.497	89.465	110.668	TSB(bca)	Old

Arm
● Old
● New

• Mean TC for arm = "New"

Estimate	CI.low	CI.high	method	arm
119.373	117.542	121.276	boot(bca)	New
119.364	108.247	130.481	MLM	New
119.451	109.087	130.005	TSB(bca)	New

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- **Other approaches:**

- *Bayesian hierarchical models* (Grieve et al. 2010, Gomes et al. 2012)

Missing data

- Missing CE values almost **inevitably** occur:
 - A single missing CE *component* leads to a missing *QALY/TC* value
 - Need to accept **inherent uncertainty** in analysis
 - Any method is based on some **untestable assumptions**

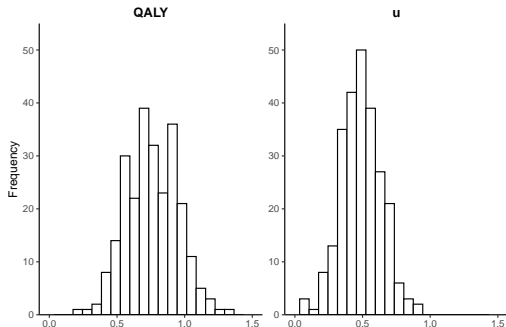
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 - **Missing Not At Random** (MNAR): due to some *unobserved variables*
- Method should be *aligned* with the **selected assumptions** :
 - Avoid methods with **unrealistic** assumptions (eg mean imputation)
 - Define a *base-case* scenario (eg MAR)
 - Assess **sensitivity** of results to some *departures*

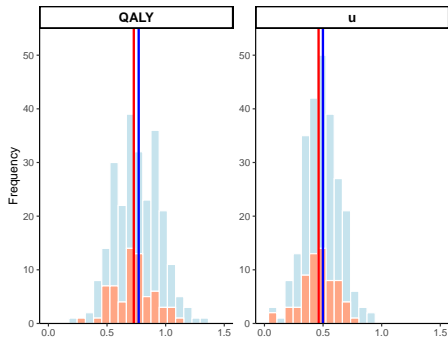
Missing data - an example



- QALYs & utilities **fully observed**

Mean(e)	Sd(e)	Mean(u)	Sd(u)	n
0.759	0.189	0.489	0.147	250

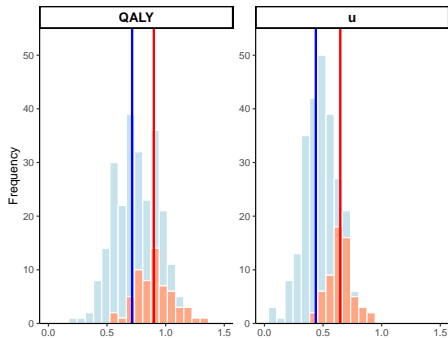
Missing data - an example



- QALYs under **MCAR** & utilities

	Mean(e)	Sd(e)	Mean(u)	Sd(u)	n
obs	0.770	0.194	0.499	0.147	185
mis	0.728	0.171	0.462	0.145	65

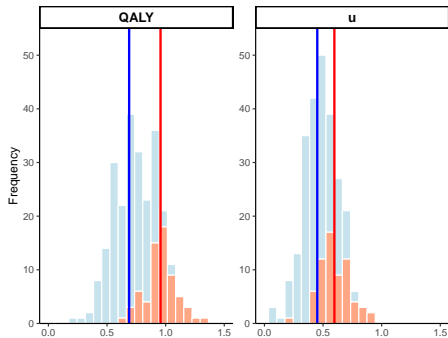
Missing data - an example



- QALYs under **MAR** & utilities

	Mean(e)	Sd(e)	Mean(u)	Sd(u)	n
obs	0.714	0.176	0.438	0.121	189
mis	0.899	0.157	0.647	0.103	61

Missing data - an example



- QALYs under **MNAR** & utilities

	Mean(e)	Sd(e)	Mean(u)	Sd(u)	n
obs	0.689	0.154	0.451	0.134	184
mis	0.956	0.129	0.596	0.129	66

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 - Reduce **efficiency** and may **bias** estimates

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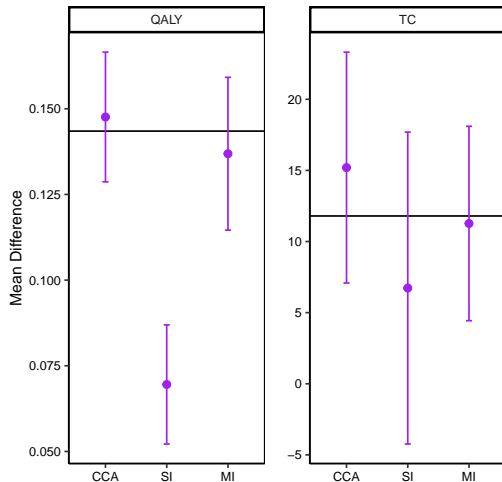
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- **Multiple Imputation (MI):**

- **Impute** y^{mis} M times with an *imputation model*
- **Analyse** each dataset and derive estimates $\hat{\beta}_m$ for $m = 1, \dots, M$
- **Combine** M estimates into a single quantity $\hat{\beta}$
- Validity relies on **correct** model specification

Missing data - alternative methods



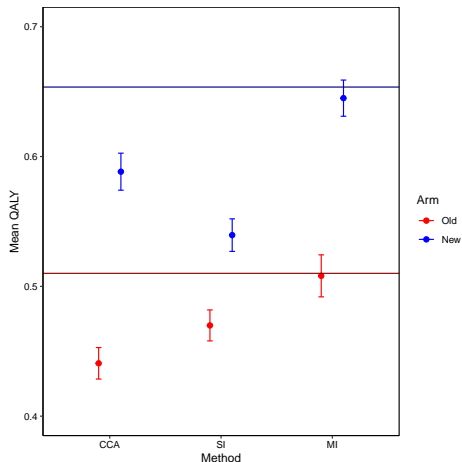
- Mean QALY difference Δ_e

Estimate	CI.low	CI.high	method
<i>0.148</i>	<i>0.129</i>	<i>0.167</i>	CCA
<i>0.070</i>	<i>0.052</i>	<i>0.087</i>	SI
<i>0.137</i>	<i>0.115</i>	<i>0.159</i>	MI

- Mean TC difference Δ_c

Estimate	CI.low	CI.high	method
<i>15.197</i>	<i>7.082</i>	<i>23.313</i>	CCA
<i>6.728</i>	<i>-4.236</i>	<i>17.691</i>	SI
<i>11.268</i>	<i>4.434</i>	<i>18.102</i>	MI

Missing data - alternative methods



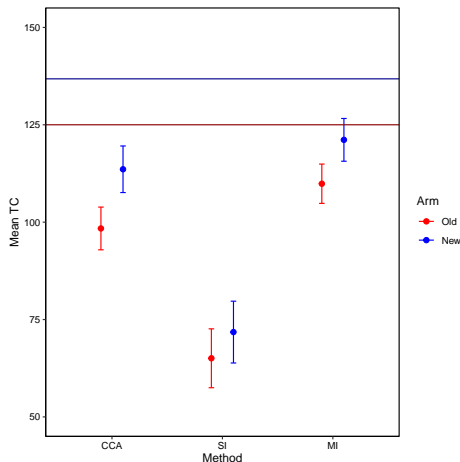
- **Mean QALY** for arm = “Old”

Estimate	CI.low	CI.high	method
<i>0.441</i>	<i>0.429</i>	<i>0.453</i>	CCA
<i>0.470</i>	<i>0.458</i>	<i>0.482</i>	SI
<i>0.508</i>	<i>0.492</i>	<i>0.524</i>	MI

- **Mean QALY** for arm = “New”

Estimate	CI.low	CI.high	method
<i>0.588</i>	<i>0.574</i>	<i>0.603</i>	CCA
<i>0.539</i>	<i>0.527</i>	<i>0.552</i>	SI
<i>0.645</i>	<i>0.631</i>	<i>0.659</i>	MI

Missing data - alternative methods



- **Mean TC for arm = "Old"**

Estimate	CI.low	CI.high	method
<i>98.389</i>	<i>92.904</i>	<i>103.874</i>	CCA
<i>65.052</i>	<i>57.490</i>	<i>72.614</i>	SI
<i>109.871</i>	<i>104.826</i>	<i>114.917</i>	MI

- **Mean TC for arm = "New"**

Estimate	CI.low	CI.high	method
<i>113.586</i>	<i>107.605</i>	<i>119.567</i>	CCA
<i>71.780</i>	<i>63.845</i>	<i>79.714</i>	SI
<i>121.139</i>	<i>115.650</i>	<i>126.628</i>	MI

Missing data - things to consider

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 - Account for missingness **uncertainty**
 - Require specification of **imputation model** for each variable (MICE)
 - Valid under *less restrictive* assumptions (eg MAR)
- **Further issues** to address:
 - Check **sensitivity** of results to departures (eg MNAR)
Use specific *MNAR approaches* (Leurent et al. 2018)
 - Imputation of **longitudinal** variables (u_{ij}, c_{ij}) challenging
Use mixed models under *MAR* (Gabrio et al. 2022)
 - “Best” way to **combine** MI/bootstrap *unclear* (Brand et al. 2019)

Are we still alive?



Section 4

Reporting of CEAs

- **Patient characteristics** (eg baseline var) & **effectiveness** by arm

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- **Costs & Quality of Life** :
 - **Prices** (with year) and **volumes** of all cost components
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- **Extrapolation & Validation** :
 - Measures for checking the validity of extrapolation (time-to-event data)
 - *AdVISHE*² checklist (validation of input data and outcomes)

²Assessment of the Validation Status of Health-Economic

- **Costs & Effects :**

- *Absolute & incremental* estimates with CIs
- *Absolute & incremental* costs by cost category and total sums
- *Absolute & incremental* QoL by health state (if applicable)

Results: base-case analysis

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- **CE quantities :**

- **Incremental Cost-Effectiveness Ratio** : $ICER = \frac{\Delta_e}{\Delta_c}$

- **Net Monetary Benefit** : $NMB = k \times \Delta_e - \Delta_c$

Use **reference CE threshold** $k \rightarrow$ **CE in practice Manual**

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- **Subgroup analyses** (if applicable):

- All CE results *presented separately* for each subgroup

Results: base-case analysis - an example

- Summary of CE results in **table** format:

	Mean	SE	CI(low)	CI(high)
<i>Old(QALY)</i>	<i>0.511</i>	<i>0.012</i>	<i>0.487</i>	<i>0.535</i>
<i>New(QALY)</i>	<i>0.557</i>	<i>0.013</i>	<i>0.532</i>	<i>0.582</i>
<i>Old(TC)</i>	<i>125.010</i>	<i>2.169</i>	<i>120.739</i>	<i>129.281</i>
<i>New(TC)</i>	<i>147.056</i>	<i>2.275</i>	<i>142.575</i>	<i>151.538</i>
Incr(QALY)	0.046	0.018	0.012	0.081
Incr(TC)	22.046	3.144	15.854	28.239
NMB(k=5000)	24.385			
ICER	474.820			

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- In **Base-Case** analysis, focus on:
 - **Point** & **CI** estimates for QALY/TC by arm (over the study period)
 - **Point** & **CI** estimates for incremental QALY/TC (New-Old)
 - **Point** estimate for *ICER* and *NMB* (assuming **reference value** for *k*)

- **Deterministic & scenario** analyses (*model-based*):
 - Chosen parameter distribution
 - ICER and incremental quantities lower/upper values
 - Always compared with base-case results

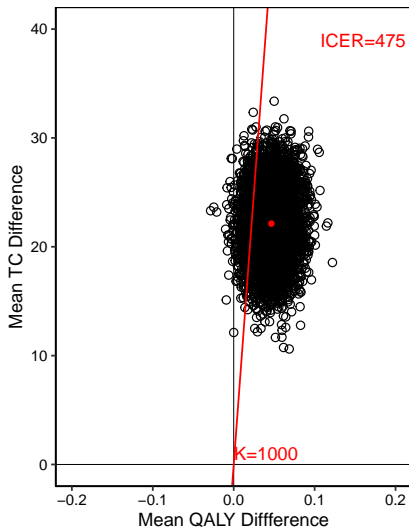
Results: sensitivity analyses

- **Deterministic & scenario** analyses (*model-based*):
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 - **Expected Value of (Partial) Perfect Information** ($EV(P)PI$) plot
 - EVSI and ENBS results may be presented → **Vol analyses Manual**

Results: probabilistic analyses - an example

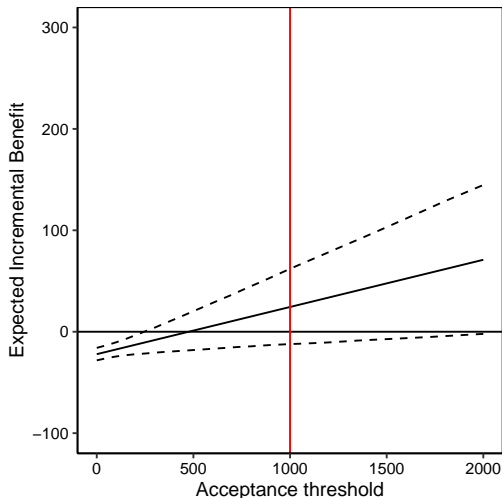


- **CE plane**

- Scatter plot of **bootstrapped** estimates (Δ_e^b, Δ_c^b)
- Red line slope equal to **reference value** for K
- $ICER = \frac{E[\Delta_c^b]}{E[\Delta_e^b]}$

	Mean	NE	NW	SE	SW	K=1000
%		0.994	0.006	0	0	0.909
QALY	0.047					
TC	22.129					
ICER	475.487					

Results: probabilistic analyses - an example

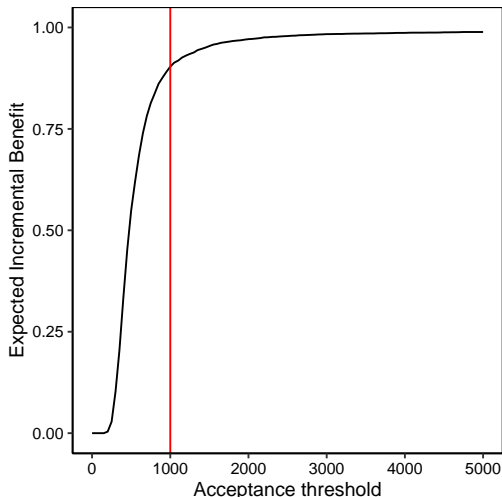


- **NMB**

- Plot of **bootstrapped** NMB^b estimates for $K \in [0, K_{\max}]$
- Red line equal to **reference value** for K
- Dashed lines are 95% interval based on **bootstrapped** estimates
- $\text{NMB}^b = K \times \Delta_e^b - \Delta_c^b$

	Mean	CI(low)	CI(high)
<i>K=1000</i>	24.41	-12.159	62.059
<i>K=475.487</i>	0.00	-18.302	18.195

Results: probabilistic analyses - an example



- **CEAC**

- Plot of % of **bootstrapped** estimates $\frac{\Delta_c^b}{\Delta_e^b}$ below K for $K \in [0, K_{\max}]$
- Often interpreted as **"probability"** that New is CE compared to Old
- Red line equal to **reference value** for K

	K=500	K=1000	K=2000
% CE	0.549	0.903	0.971

Section 5

Conclusions

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 - Randomisation & ITT analysis minimises chance of **bias**
 - Provide *prospective* patient-level cost and effect data

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 - Require a **combination** of different statistical methods use
- Important to identify **barriers** and **facilitators** of methods

R you still using Excel/SPSS?



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- Historically, HTAs conducted with **commercial software** (eg SPSS) or **spreadsheet software** (eg Excel) which:
 - Are sufficient for simple analyses **BUT**
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 - Transparent and reproducible
 - Reusable and adaptable
- **R** user/developer communities well suited to:
 - Develop/implement HTA models in a **single software environment**
 - Catch up with **methodological advances**
 - Spot and correct code errors via **open-source** nature of packages

A path forward for HTA

- Still a general lack of **software experience** in the HTA community:
 - *Insufficient* training in script-based prog software
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- Critical to **train** the next generation of health economists in *state of the art* methods and *software* to implement them
- **How to do this?**
 - Developing university *courses & workshops*
 - Writing *tutorial papers*
 - Making code *freely available* on repositories (eg *GitHub*)
 - *Encouraging* the use of programming languages among researchers

Key references

- El Alili, M., Dongen, J. M. van, Esser, J. L., Heymans, M. W., Tulder, M. W. van, & Bosmans, J. E. (2022). A scoping review of statistical methods for trial-based economic evaluations: The current state of play. *Health Economics*, 31(12), 2680–2699.
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- Leurent, B., Gomes, M., Faria, R., Morris, S., Grieve, R., & Carpenter, J. R. (2018). Sensitivity analysis for not-at-random missing data in trial-based cost-effectiveness analysis: A tutorial. *Pharmacoeconomics*, 36(8), 889–901.
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- Nederland, Z. (2024). Guideline for economic evaluations in healthcare (2024 version). *Zorginstituut Nederland: Diemen*.

Section 6

Appendix - R code

Appendix - R code - Baseline adjustment

- Full code available [@AnGabrio GitHub](#)

```
> #fit QALY OLS model adjusting for baseline utilities
> lm2 <- lm(QALY ~ trt + u, data = dataset)
> #get mean QALY in each trt group
> lm2em <- emmeans(lm2, ~ trt)
> #get mean difference between groups
> contrast2_1vs0 <- list("New vs Old" = c(-1, 1))
> #summarise estimates
> confint(contrast(lm2em, contrast2_1vs0))
```

contrast	estimate	SE	df	lower.CL	upper.CL
New vs Old	0.0765	0.0108	297	0.0552	0.0979

Confidence level used: 0.95

Appendix - R code - Dealing with correlation

- Full code available [@AnGabrio GitHub](#)

```
> #fit SUR model to QALY and TC
> sur <- systemfit(list(QALYreg = QALY ~ trt + u,
+   TCreg = TC ~ trt + c), method="SUR", data=dataset)
> #get mean QALY difference CI
> sur_e.trt.ci <- confint(sur, level=0.95)[2,]
> #summarise mean QALY difference between groups
> sur_e.trt.sum <- c(coef(summary(sur))[2,
+   c("Estimate", "Std. Error")],sur_e.trt.ci)
> sur_e.trt.sum
```

Estimate	Std. Error	2.5 %	97.5 %
0.07641998	0.01083463	0.05509761	0.09774235

Appendix - R code - Dealing with correlation

- Full code available [@AnGabrio GitHub](#)

```
> #fit OLS/SUR model and get bootstrap estimates
> boot_res <- boot_ec(dataset, QALYreg = QALY ~ trt + u,
+   TCreg = TC ~ trt + c, method = "OLS", B=200)
> summary(boot_res$QALY_boot$Delta_e)
```

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
	0.04894	0.06982	0.07790	0.07711	0.08325	0.10448

```
> #compute percentile or BCa CIs
> boot_ci_bca <- boot_ci(x = boot_res, method = "BCa")
> boot_ci_bca$Delta_e
```

1.638952%	96.28698%
0.05464895	0.09617978

Appendix - R code - Dealing with skewness

- Full code available [@AnGabrio GitHub](#)

```
> #fit GLM model for TC
> glm_c <- glm(TC ~ trt + c, data = dataset_sam_skew.df,
+   family = Gamma(link = "identity"))
> #get mean TC in each trt group
> glm_c.em <- emmeans(glm_c, ~ trt)
> #get mean difference between groups
> contrast1_1vs0 <- list("New vs Old" = c(-1, 1))
> #summarise estimates
> confint(contrast(glm_c.em, contrast1_1vs0))
```

contrast	estimate	SE	df	lower.CL	upper.CL
New vs Old	35.6	6.65	17	21.6	49.6

Confidence level used: 0.95

Appendix - R code - Dealing with clustering

- Full code available [@AnGabrio GitHub](#)

```
> #fit MLM model for QALY
> mlm_e <- lme(QALY ~ trt, random = ~1|cluster,
+ data = data.clus.df)
> #get mean QALY in each trt group
> mlm1em_e <- emmeans(mlm_e, ~ trt)
> #get mean difference between groups
> contrast1_1vs0 <- list("New vs Old" = c(-1, 1))
> confint(contrast(mlm1em_e, contrast1_1vs0))
```

contrast	estimate	SE	df	lower.CL	upper.CL
New vs Old	0.116	0.0744	24	-0.0374	0.27

Degrees-of-freedom method: containment

Confidence level used: 0.95

Appendix - R code - Dealing with clustering

- Full code available [@AnGabrio GitHub](#)

```
> #fit OLS/SUR model and get TSB estimates
> tsboot_res <- tsboot_ec(data = data.clus.df,
+   QALYreg = QALY ~ trt, TCreg = TC ~ trt,
+   cluster = "cluster", B=200)
> summary(tsboot_res$QALY_boot$Delta_e)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-0.08989	0.06294	0.11181	0.11045	0.15426	0.32714

```
> #compute percentile or BCa CIs
> tsboot_ci_bca <- boot_ci(x = tsboot_res, method = "BCa")
> tsboot_ci_bca$Delta_e
```

2.971331%	97.90686%
-0.05569824	0.27476579

Appendix - R code - Dealing with missing data

- Full code available [@AnGabrio GitHub](#)

```
> #impute data using MICE with pmm
> mice_data <- mice(full.mar.MI, predictorMatrix = pM,
+   method='pmm', m = 20, print = FALSE)
> #analyse imputed data with OLS for QALY
> lme_mice_data <- with(mice_data, lm(QALY_obs ~ trt + u))
> #get pooled mean QALY per group
> em_lme_mu_data.mi <- emmeans(lme_mice_data, ~ trt)
> #get pooled mean difference between groups
> contrast1_1vs0 <- list("New vs Old" = c(-1, 1))
> confint(contrast(em_lme_mu_data.mi, contrast1_1vs0))
```

contrast	estimate	SE	df	lower.CL	upper.CL
New vs Old	0.138	0.00948	41.8	0.119	0.157

Confidence level used: 0.95

Appendix - R code - probabilistic analysis

```
> #get CEA output from bootstrapped estimates
> library(BCEA)
> cea_res <- bcea(eff = boo.mu.e, cost = boo.mu.c,
+   Kmax = 25000, ref = 2)
> summary(cea_res)
```

Cost-effectiveness analysis summary

Reference intervention: intervention 2

Comparator intervention: intervention 1

Optimal decision: choose intervention 1 for $k < 500$ and intervention 2 for $k \geq 500$

Analysis for willingness to pay parameter $k = 25000$

	Expected net benefit
intervention 1	12642
intervention 2	13783

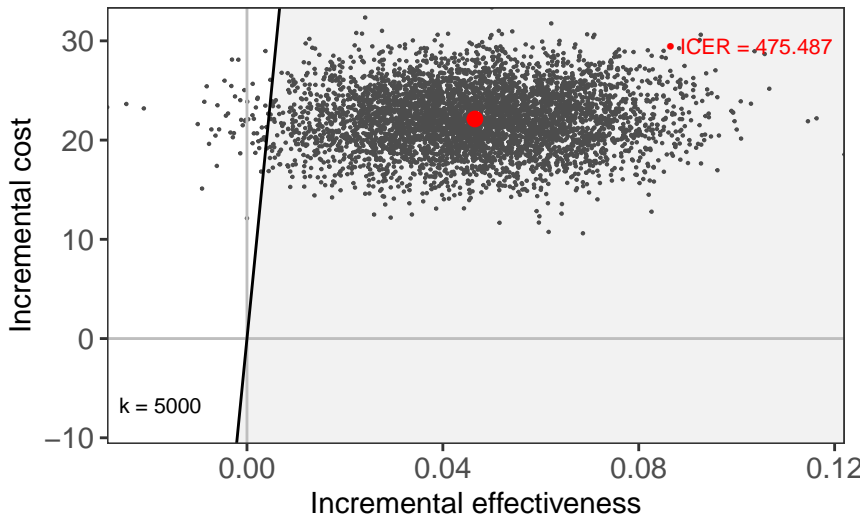
	EIB	CEAC	ICER
intervention 2 vs intervention 1	1141.3	0.9934	475.49

Optimal intervention (max expected net benefit) for $k = 25000$: intervention 2

EVPI 1.0828

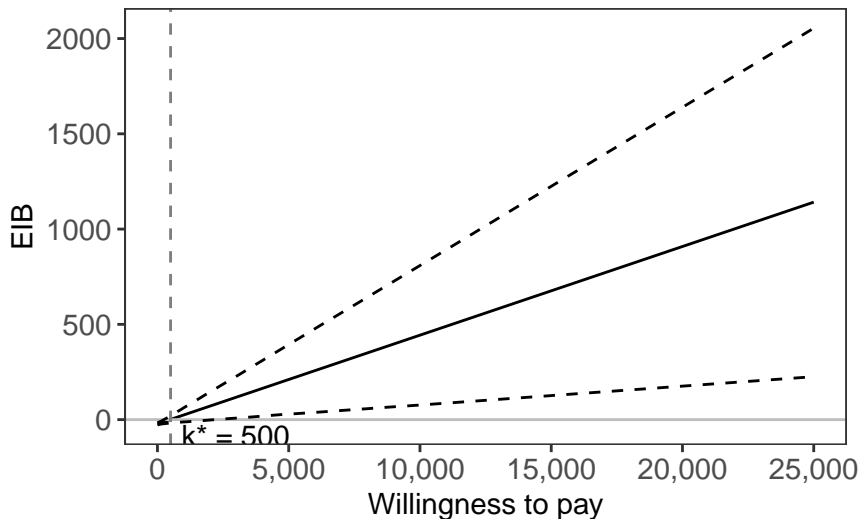
Appendix - R code - probabilistic analysis

```
> ceplane.plot(cea_res, graph = "ggplot2", wtp = 5000) + labs(title="")
```



Appendix - R code - probabilistic analysis

```
> eib.plot(cea_res, graph = "ggplot2", plot.cri = TRUE) + labs(title="")
```



Appendix - R code - probabilistic analysis

```
> ceac.plot(cea_res, graph = "ggplot2") + labs(title="")
```

