

# Efficient modelling of complex responder endpoints to improve trial power

James Wason

[www.newcastle-biostatistics.com/staff/james\\_wason](http://www.newcastle-biostatistics.com/staff/james_wason)

SUPPORTED BY

**NIHR** | National Institute for  
Health and Care Research

---

## Responder endpoints

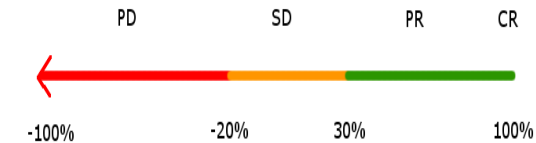
---

- In many conditions, especially ones with heterogeneous symptoms, specifying a single primary endpoint is difficult.
- One approach to this is combining multiple distinct endpoints (components) into a single **composite endpoint**.
- One type of composite divides patients into **responders** and **non-responders**; responders have to meet specified criteria on the components.

# Responder endpoints - examples

---

1. Oncology: 30% decrease in target tumour lesions length and no new lesions.
2. Rheumatology: 20% decrease in number of tender and swollen joints and three other continuous components.
3. Type II Diabetes: 1. Glycated haemoglobin A<sub>1c</sub> concentration  $\leq 6.5$ ; Fasting glucose concentration  $\leq 5.6$  mmol/L; No non-study pharmacological treatment given



## MEASUREMENTS OF RESPONSE

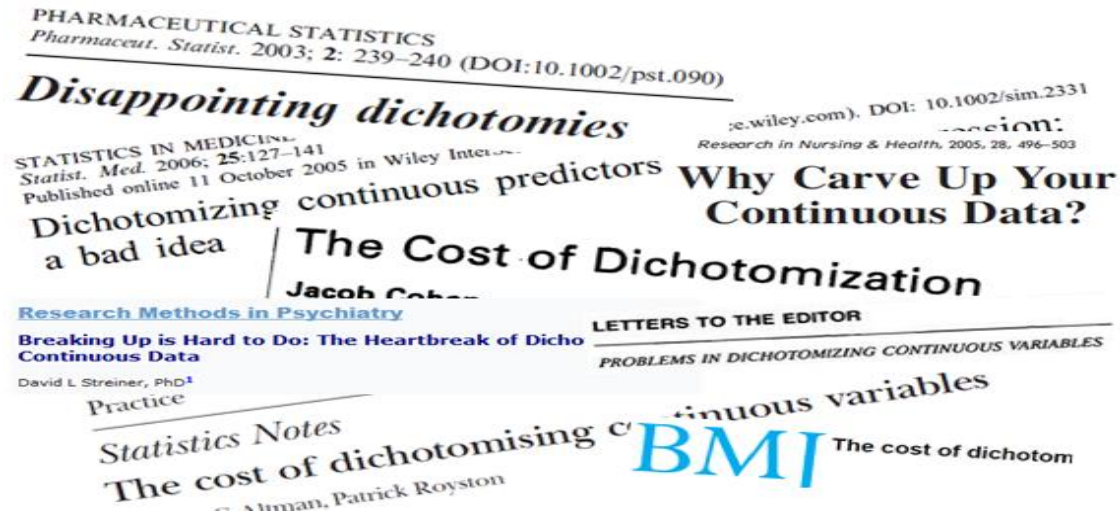
### ACR 20 Response :

A decrease of at least 20% in both the number of tender and swollen joints along with 20% reduction in at least three of the following:

- Patient's assessment of disease status
- Patient's assessment of pain
- Patient's assessment of physical function
- Physician's assessment of disease status
- C-reactive protein level

# Responder endpoints

- These endpoints all involve continuous components being dichotomised.
- Usual analysis would treat response/non-response as binary outcome.
- Dichotomisation loses substantial statistical efficiency but difficult to avoid if combining continuous and binary components.



## Alternative approaches

---

1. Pick a single (continuous) primary outcome and analyse that;
  2. If response has >2 levels then using ordinal approaches can reclaim some lost efficiency;
  3. Approaches for analysing composite endpoints (e.g. Win ratio<sup>1</sup>) could be used.
- However, assuming there's a good reason to use responder outcomes:
  - How can we make inference about proportion of responders with maximum efficiency?

---

<sup>1</sup>Pocock SJ, Ariti CA, Collier TJ, Wang D. The win ratio: a new approach to the analysis of composite endpoints in clinical trials based on clinical priorities. *European heart journal*. 2012 Jan 1;33(2):176-82.

# Augmented binary method

- Methods I've previously proposed (with others) retain the responder endpoint but use the continuous component to improve precision.

Research Article

Statistics  
in Medicine

Received 7 January 2013, Accepted 9 May 2013, Published online 18 June 2013 in Wiley Online Library  
(wileyonlinelibrary.com) DOI: 10.1002/sim.5867

## Using continuous data on tumour measurements to improve inference in phase II cancer studies

James M. S. Wason<sup>\*†</sup> and Shaun R. Seaman

Wason et al. *Trials* (2020) 21:427  
<https://doi.org/10.1186/s13063-020-04353-8>

Trials

RESEARCH

Open Access

## Analysis of responder-based endpoints: improving power through utilising continuous components

James Wason<sup>1,2\*</sup>, Martina McMenamini<sup>2</sup> and Susanna Dodd<sup>3</sup>



RHEUMATOLOGY

Rheumatology 2016;55:1796–1802  
doi:10.1093/rheumatology/kew263  
Advance Access publication 23 June 2016

Original article

## Improving the power of clinical trials of rheumatoid arthritis by using data on continuous scales when analysing response rates: an application of the augmented binary method

James M. S. Wason<sup>1</sup> and Martin Jenkins<sup>2</sup>

Article

**SMMR**  
STATISTICAL METHODS IN MEDICAL RESEARCH

## Employing a latent variable framework to improve efficiency in composite endpoint analysis

Martina McMenamini<sup>1</sup>, Jessica K Barrett<sup>1</sup>, Anna Berglind<sup>2</sup> and James MS Wason<sup>1,3</sup>

Statistical Methods in Medical Research  
2021, Vol. 30(3) 702–716  
© The Author(s) 2020



Article reuse guidelines:  
[sagepub.com/journals-permissions](https://sagepub.com/journals-permissions)  
DOI: 10.1177/0962280220970986  
[journals.sagepub.com/home/smm](https://journals.sagepub.com/home/smm)

**SAGE**

- Randomised trial comparing extracorporeal photopheresis (ECP) vs standard of care for treatment of chronic lung allograft dysfunction (CLAD) following lung transplant.
- Primary endpoint is ‘lung function stabilisation’ which consists of the following criteria:
  1. Lower than 10% loss in FEV1\* from baseline to 24 weeks
  2. Lower than 10% loss in FVC† from baseline to 24 weeks
  3. No rapid decline confirmed being due to progressive CLAD at 12 weeks.
- Target sample size of 90 patients to be enrolled.

---

\*Forced Expiratory Volume in 1 second

† Forced Vital Capacity

## How does it work?

---

- Let  $R_i$  be response indicator for participant  $i$  and  $T_i$  be treatment indicator.
- Of interest to make inference on  $R_i$ , e.g.

$$P(R_i = 1 | T_i = 1) - P(R_i = 1 | T_i = 0)$$

- $R_i$  defined by:
  1.  $Y_{i1}$  percentage reduction in FEV1
  2.  $Y_{i2}$  percentage reduction in FVC
  3.  $Y_{i3}$  a binary indicator as to whether there was rapid decline due to progressive CLAD.
- $R_i = 1$  if:  $Y_{i1} \leq 10\%$ ,  $Y_{i2} \leq 10\%$ ,  $Y_{i3} = 0$

## How does it work?

---

- Instead of making inference on  $R_i$ , the augmented binary method involves two steps:

1) Fit a suitable joint model to  $Y_{i1}, Y_{i2}, Y_{i3}$

2a) Use the parameter estimates from this model to estimate the quantity of interest

$$P(R_i = 1 | T_i = 1) - P(R_i = 1 | T_i = 0)$$

2b) Use the covariance of the parameter estimates and the delta method to estimate the standard error of the quantity of interest and get a confidence interval + Wald test.

## How does it work?

---

- Latent variable model can be used for step 1: allows modelling correlation between continuous and binary components.

$$Y_{i1} = \mu_1 + \alpha_1 X_{i1} + \beta_1 T_i + \varepsilon_{i1}$$

$$Y_{i2} = \mu_2 + \alpha_2 X_{i2} + \beta_2 T_i + \varepsilon_{i2}$$

$$Y_{i3}^* = \mu_3 + \beta_3 T_i + \varepsilon_{i3}$$

- $Y_{i3} = 1$  if  $Y_{i3}^* > 0$ ;  $Y_{i3} = 0$  if  $Y_{i3}^* \leq 0$  (latent variable)
- $X_{i1}$  and  $X_{i2}$  are baseline measurements of FEV1 and FVC.
- $(\varepsilon_{i1}, \varepsilon_{i2}, \varepsilon_{i3})$  distributed as  $N(0, \Sigma)$ ,

## How does it work?

---

- Step 2a involves a multidimensional integration over a multivariate normal distribution – computationally efficient to evaluate, e.g. with pmvnorm in R.

$$p_{ij} = P(R_i = 1 | T_i = j) = \int_{-\infty}^{10} \int_{-\infty}^{10} \int_{-\infty}^0 f_{Y_1, Y_2, Y_3}(y_1, y_2, y_3 | T_i = j, \boldsymbol{\theta}) dy_1 dy_2 dy_3,$$

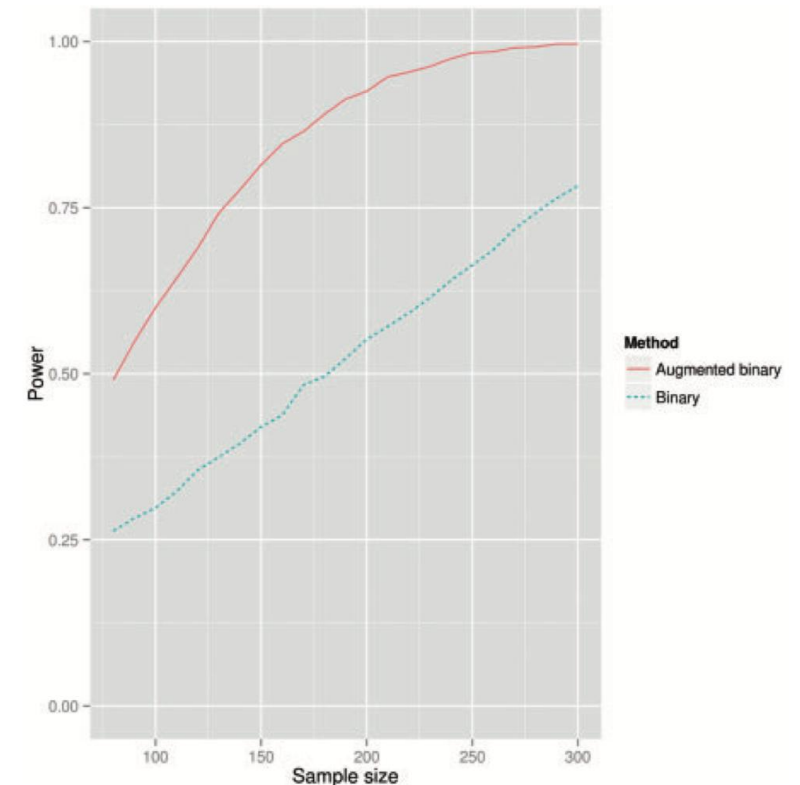
where  $\boldsymbol{\theta}$  is the vector of latent variable model parameters.

- Step 2b uses the delta method and  $\text{Cov}(\hat{\boldsymbol{\theta}})$  to get variance of between-group difference in response probability.

# Augmented binary method

- The method has been tested on oncology<sup>1</sup>, rheumatoid arthritis<sup>2</sup> and SLE datasets<sup>3</sup>.
- Compared to analysing as binary variable, using the method is equivalent to increasing the sample size by >30%.
- ...without type I error rate inflation or extra data being required.
- Power gain achieved varies between an effective increase in sample size between 30% and 1000%<sup>3</sup>!

Fig. 2 Power of standard and augmented binary methods for different sample sizes



<sup>1</sup>Wason J. and Seaman S. (2013) *Statistics in Medicine*, 32: 4639-4650

<sup>2</sup>Wason J, Jenkins M. (2016) *Rheumatology* 55:1796-1802

<sup>3</sup>McMenamin et al (2021) *Statistical Methods in Medical Research* 30(3) 702–716

## Case studies

---

- In Newcastle we are now running four trials that are utilising the augmented binary method prospectively as the primary analysis.
- Three are CTIMPs and one is an ATIMP, all regulated by MHRA\*.

<b>Participants</b>	People with Chronic Lung Allograft Dysfunction following lung transplant
<b>Intervention</b>	Extracorporeal photopheresis (ECP)
<b>Comparator</b>	Standard of care
<b>Outcome</b>	Lung function stabilisation at 24 weeks: 1) $\leq 10\%$ decrease in FEV1; 2) $\leq 10\%$ decrease in FVC; 2) No progressive CLAD at 12 weeks
<b>Augmented binary effect</b>	Trial was powered for 80% power using Binary endpoint (n=90); we argued that power using augmented approach would be $>90\%$ as per funder requirement.

<b>Participants</b>	People with Primary Biliary Cholangitis with non-response risk score > 50%*
<b>Intervention</b>	Obeticholic acid
<b>Comparator</b>	Ursodeoxycholic acid (standard first-line therapy)
<b>Outcome</b>	Biochemical remission, defined as normalisation of liver biochemistry (ALP and bilirubin) at 6 months.
<b>Augmented binary effect</b>	Used registry data to simulate efficiency gain achieved, allowing reduction of sample size from 156 to 106.

\*this is a risk score that was derived to predict the probability of not responding to first-line therapy

---

<b>Participants</b>	Young people (12-24 years old) with newly diagnosed Graves Disease
<b>Intervention</b>	Standard antithyroid drug treatment (ATD) + 1 dose of 500mg rituximab
<b>Comparator</b>	Standard ATD + placebo
<b>Outcome</b>	Remission at 36 months (not requiring ATD, receiving thyroidectomy), non-suppressed TSH concentration and FT3 below laboratory reference range.
<b>Augmented binary effect</b>	Used data from previous (single-arm) phase II to investigate efficiency increase: allowed reduction in sample size from 180 to 124

---

<b>Participants</b>	People with moderate psoriasis (PASI score 5-10)
<b>Intervention</b>	Adalimumab
<b>Comparator</b>	Methotrexate
<b>Outcome</b>	Reduction of 75% in PASI score at 16 weeks with no topical steroid use
<b>Augmented binary effect</b>	Funding panel was concerned by optimistic effect size so we said that we would switch to using augmented binary method as primary analysis to allow us adequate power to detect smaller differences.

McMenamin et al. *BMC Rheumatol* (2021) 5:54  
<https://doi.org/10.1186/s41927-021-00224-0>

BMC Rheumatology

SOFTWARE

Open Access

## Increasing power in the analysis of responder endpoints in rheumatology: a software tutorial

Martina McMenamin<sup>1,2\*</sup>, Michael J. Grayling<sup>3</sup>, Anna Berglind<sup>4</sup> and James M. S. Wason<sup>1,3</sup>



Home

- Sample size
- Co-primary
- Multiple Primary
- Composite
- Source code

### Endpoint

Number of continuous components

Number of binary components

Y<sub>1</sub> responder threshold

Y<sub>2</sub> responder threshold

### Model Summary

#### Latent Variable Model

Let  $\mathbf{Y}_i = (Y_{i1}, Y_{i2}, Y_{i3})^T$  represent the vector of observed outcomes for patient  $i \in N$  and  $\mathbf{Y} = (\mathbf{Y}_1, \dots, \mathbf{Y}_N)^T$  represent the observed outcomes for all patients.  $Y_{i1}$  and  $Y_{i2}$  are the observed continuous measure and  $Y_{i3}$  denotes the observed binary variable for latent  $Y_{i3}^*$ . Let  $\mathbf{Y}_i^* = (Y_{i1}, Y_{i2}, Y_{i3}^*)^T$  denote the vector of observed and latent continuous measures for patient  $i$ ,  $\mathbf{Y}^* = (\mathbf{Y}_1^*, \dots, \mathbf{Y}_N^*)^T$  and  $T_i$  represents the treatment indicator for patient  $i$ .

The observed binary variable is related to its latent continuous variable by partitioning the latent variable space.

$$Y_{i3} = \begin{cases} 0, & \text{if } Y_{i3}^* < 0, \\ 1, & \text{if } Y_{i3}^* \geq 0 \end{cases}$$

The error terms are assumed to be distributed as multivariate normal with zero mean and variance-covariance matrix  $\Sigma_{123}$ . Note that the error variances for  $\epsilon_3^*$  is  $\sigma_3 = 1$ .

$$(\epsilon_{i1}, \epsilon_{i2}, \epsilon_{i3}^*) \sim N(\mathbf{0}, \Sigma_{123}) \quad \Sigma = \begin{pmatrix} \sigma_1^2 & \rho_{12}\sigma_1\sigma_2 & \rho_{13}\sigma_1 \\ \rho_{12}\sigma_1\sigma_2 & \sigma_2^2 & \rho_{23}\sigma_2 \\ \rho_{13}\sigma_1 & \rho_{23}\sigma_2 & 1 \end{pmatrix}$$

#### Probability of response

In the case of composite endpoints, the required quantity is some function of the probability of response in the treatment group  $p_T$  and in the control group  $p_C$ . In this case the overall responder index  $S_i$  can be formed for patient  $i$ , where  $S_i = 1$  if  $Y_{i1} \leq \eta_1, Y_{i2} \leq \eta_2, Y_{i3}^* \leq \eta_3$  and 0 otherwise, where  $\eta_1, \eta_2$  are predefined responder thresholds and  $\eta_3$  is set to zero for identifiability. The probability of response for patient  $i$  in the treatment arm  $p_{iT}$  and the control arm  $p_{iC}$ , are as shown

$$p_{iT} = P(S_i = 1 | T_i = 1) = \int_{-\infty}^{\eta_1} \int_{-\infty}^{\eta_2} \int_{-\infty}^0 f_{Y_1, Y_2, Y_3^*}(y_{i1}, y_{i2}, y_{i3}^* | T_i = 1, \theta) dy_3^* dy_2 dy_1$$

$$p_{iC} = P(S_i = 1 | T_i = 0) = \int_{-\infty}^{\eta_1} \int_{-\infty}^{\eta_2} \int_{-\infty}^0 f_{Y_1, Y_2, Y_3^*}(y_{i1}, y_{i2}, y_{i3}^* | T_i = 0, \theta) dy_3^* dy_2 dy_1$$

where  $\theta$  is the vector of model parameters and we assume that  $p_T \sim N(\delta_T^*, \sigma^2/n)$ ,  $p_C \sim N(\delta_C^*, \sigma^2/n)$  and  $\delta^* \sim N(\delta_T^* - \delta_C^*, 2\sigma^2/n)$ .

#### Power Function

$$1 - \beta = \Phi\left(\frac{\delta^*}{\sqrt{\frac{2\sigma^2}{n}}} - z_\alpha\right)$$

$1 - \beta$  is the required power,  $n$  is the number of patients per group and  $z_\alpha$  is the  $(1 - \alpha)100^{\text{th}}$  standard normal percentile.

<https://martinamcm.shinyapps.io/multsampsize/>

- Several diseases use time-to-event outcomes where the event includes a continuous component, e.g.:
  1. Multiple Sclerosis: time to progression on EDSS
  2. Lupus: time to flare (although depends on definition of flare)
  3. Rheumatoid arthritis: time to sustained remission.
- Further work on extending methods to analyse these types of endpoints would be valuable.
- Use of sample size re-estimation approaches when no pilot data is available to choose  $\hat{\sigma}^2$ .