



# 2016 PSI Conference

The Pullman Hotel, Berlin 22 - 25 May 2016

# Welcome to the 2016 PSI Conference







39th Annual PSI Conference  
The Pullman Hotel, Berlin, 22-25 May 2016

ence  
y 2016

ence  
2016

ual PSI Conferenc  
22-25 Ma

patientslikeme'



Not Just Another Statistic:  
How Patients are Taking  
Control of Data & Research



Promoting  
Statistical  
Insight

Wicks, PhD  
of Innovation









22 - 25 May 2016

Welcome to the  
2016 PSI  
Confere

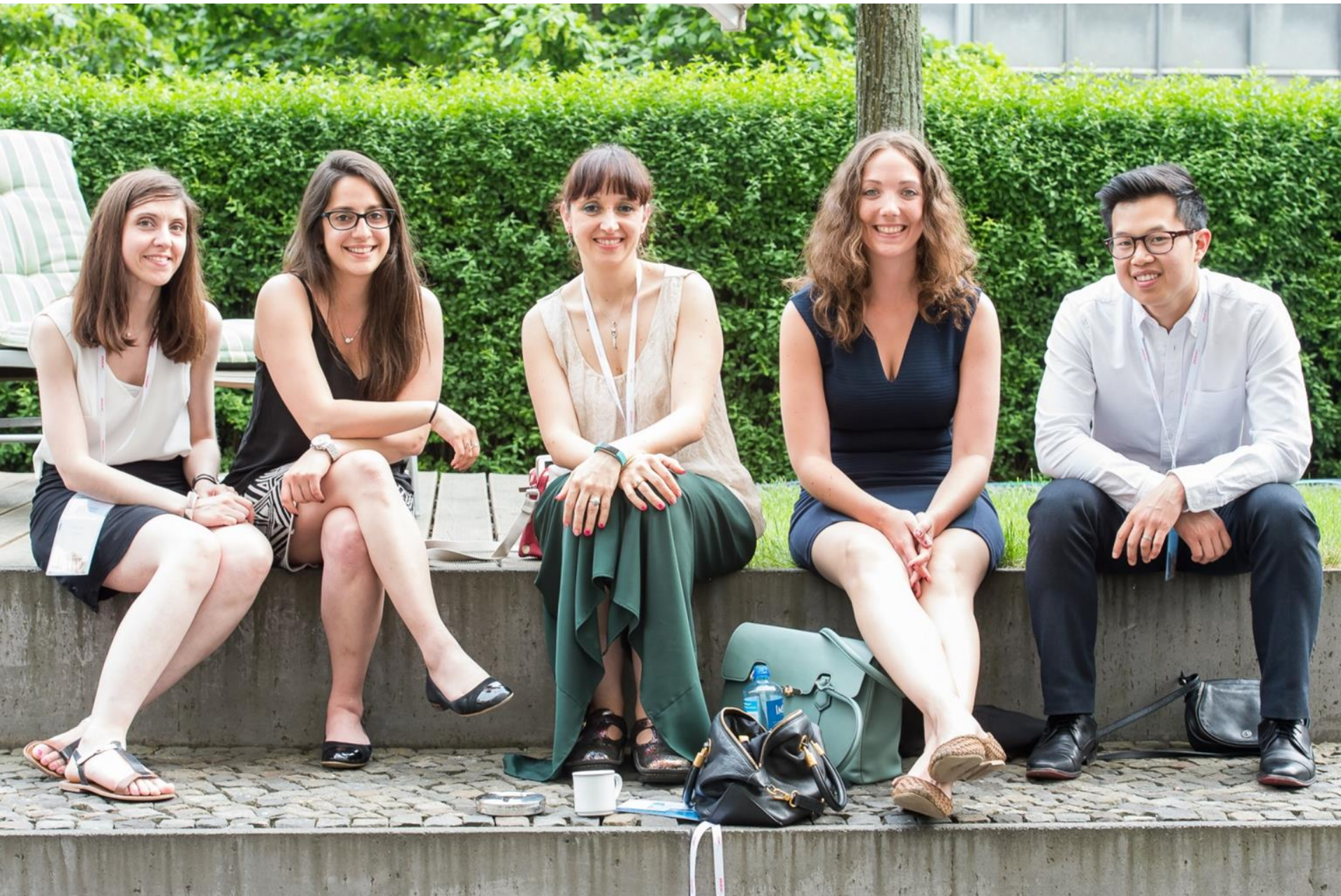


















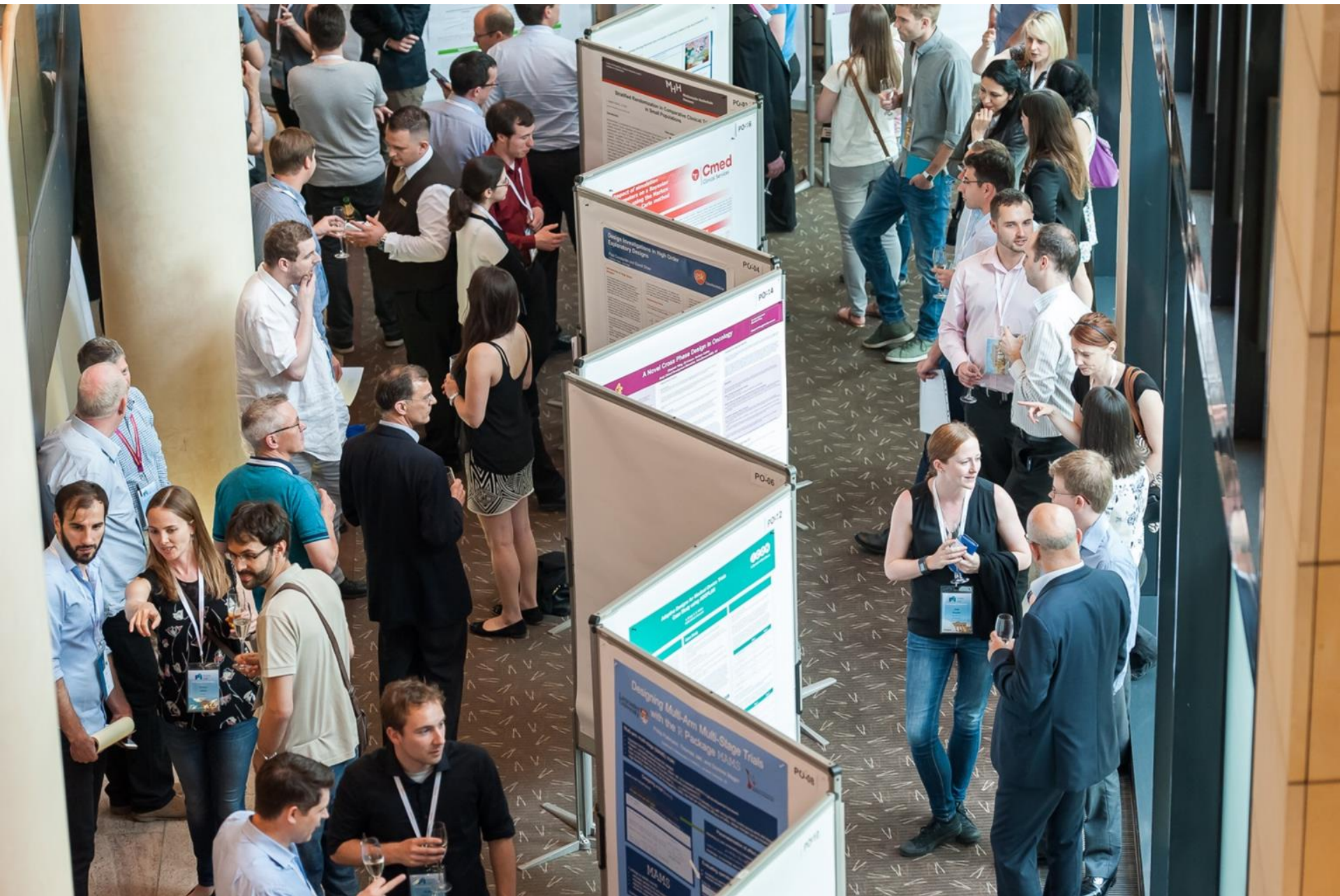


















PO-38

**Estimating marginal distributions at endpoint when only baseline and relative improvement is available: a two-dimensional probability model for the Psoriasis Area and Severity Index (PASI) to transform relative PASI improvements of  $\geq 75\%$ ,  $\geq 90\%$  and  $\geq 100\%$  (PASI75, PASI90 and PASI100) into proportions of patients reaching absolute PASI  $\leq 1, 3$  or  $5$**

Helmut Pottel<sup>1</sup>, Alexander Schachl<sup>2</sup>

<sup>1</sup>Medical Department I, University Hospital Bonn, Bonn, Germany; <sup>2</sup>Department of Biostatistics, University of Bonn, Bonn, Germany

**Introduction**

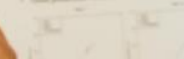
The PSM model is a two-dimensional probability model for the Psoriasis Area and Severity Index (PASI) to transform relative PASI improvements of  $\geq 75\%$ ,  $\geq 90\%$  and  $\geq 100\%$  (PASI75, PASI90 and PASI100) into proportions of patients reaching absolute PASI  $\leq 1, 3$  or  $5$ . The model is based on the assumption that the relative improvement is normally distributed and the absolute PASI is exponentially distributed. The model is applied to the data of the phase III trial of the treatment of psoriasis with the drug Xelvalto.

**Parameter estimation**

Parameter estimation is used for finding estimates regarding their relative accuracy. The relative improvement  $R$  is assumed to be normally distributed with mean  $\mu$  and standard deviation  $\sigma$ . The absolute PASI  $A$  is assumed to be exponentially distributed with rate  $\lambda$ . The joint distribution of  $R$  and  $A$  is given by  $f(r, a) = \frac{1}{\sigma \sqrt{2\pi}} \frac{\lambda}{a} \exp\left(-\frac{(r-\mu)^2}{2\sigma^2} - \frac{\lambda a}{a}\right)$ . The parameters  $\mu, \sigma, \lambda$  are estimated by maximum likelihood estimation (MLE). The MLE estimates are  $\hat{\mu} = \frac{\sum_{i=1}^n r_i}{n}$ ,  $\hat{\sigma} = \sqrt{\frac{\sum_{i=1}^n (r_i - \hat{\mu})^2}{n-1}}$ , and  $\hat{\lambda} = \frac{n}{\sum_{i=1}^n a_i}$ .

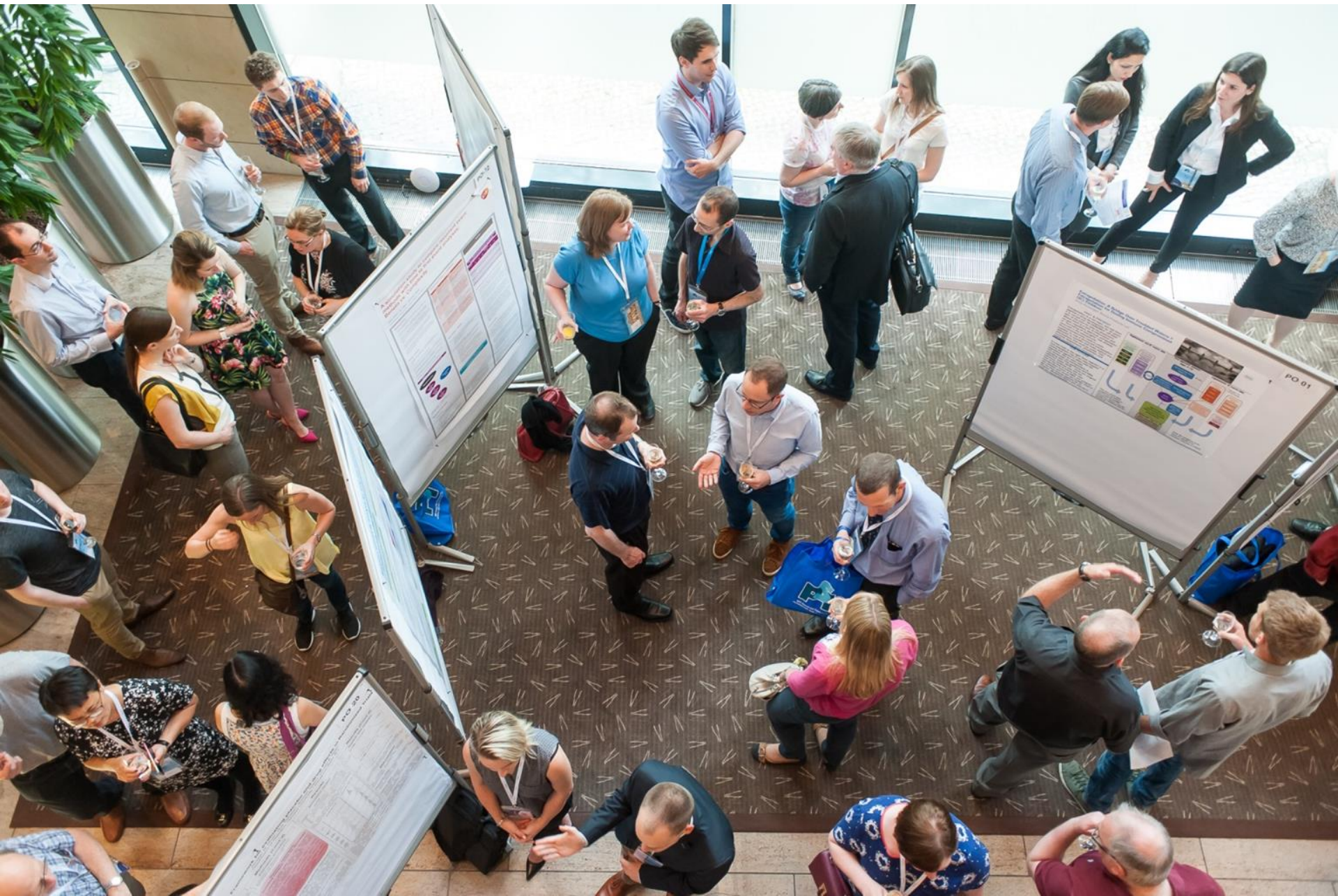
**Application of the PSM Model**

The PSM model was used to estimate the proportions of patients reaching absolute PASI  $\leq 1, 3$  or  $5$  from the relative improvements  $\geq 75\%$ ,  $\geq 90\%$  and  $\geq 100\%$ . The model was applied to the data of the phase III trial of the treatment of psoriasis with the drug Xelvalto. The results are shown in the following table:



Medical Department I  
University Hospital Bonn  
Bonn, Germany  
Annual Conference  
POT-38











### A BAYESIAN NETWORK APPROACH TO ANALYSE 16S rRNA BACTERIA INTERACTIONS IN INFANTS PARTICIPATING IN A NUTRITIONAL INTERVENTION STUDY

A case-study on the application of Bayesian models for integrative data research  
in collaboration with Danone Nutricia Research

#### LEARN

The first step in this analysis was to identify the key interactions between the 16S rRNA sequences. This was achieved by using a Bayesian Network (BN) approach. The BN is a probabilistic graphical model that represents a set of variables and their conditional dependencies. In this case, the variables are the 16S rRNA sequences and the interactions between them. The BN approach allows for the identification of key interactions between the 16S rRNA sequences, even in the presence of missing data. The BN approach is a powerful tool for integrative data research, and it has been used successfully in a number of other studies. The BN approach is a powerful tool for integrative data research, and it has been used successfully in a number of other studies.

#### PER

The results of the BN analysis show that there are several key interactions between the 16S rRNA sequences. These interactions are important for understanding the microbial community structure and function. The BN approach is a powerful tool for integrative data research, and it has been used successfully in a number of other studies. The BN approach is a powerful tool for integrative data research, and it has been used successfully in a number of other studies.



Promoting  
Professional  
Insight  
PSJ Annual Conference  
**Evian  
Fernandez Garcia**  
PCS Consulting  
Southbank

PO-17































Promoting  
Statistical  
Insight



Thank you  
Cytel for  
Sponsoring  
the 2016 PSI





Promoting  
Statistical  
Insight

Thank you  
to Cytel for  
sponsoring  
the 2016 PSI  
Gala Dinner

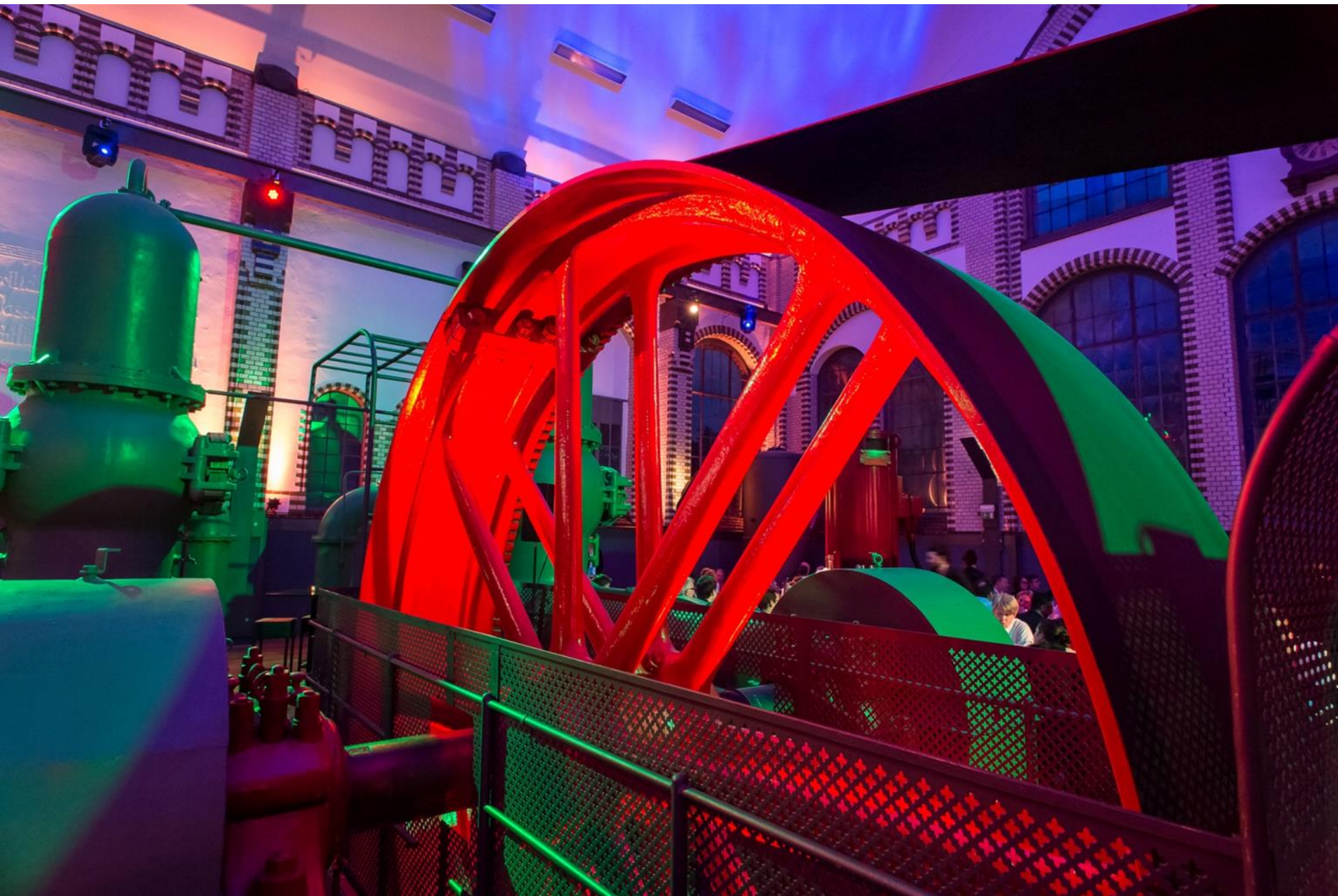


















# 2017 PSI Conference

Grange Tower Bridge Hotel, London

14 – 17 May 2017

