



Predictive Evidence Threshold Scaling: does the evidence meet a confirmatory standard?

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Abstract

Making better use of evidence is one of the tenets of modern drug development. This calls for an understanding of the evidential strength of non-confirmatory evidence relative to a confirmatory standard. *Predictive evidence threshold scaling (PETS)* provides a framework to do so. Under *PETS*, the evidence meets a confirmatory standard if the predictive probability of a positive effect reaches the predictive evidence threshold from hypothetical confirmatory data. Obtaining these probabilities requires hierarchical models with plausible heterogeneity and bias assumptions. After introducing the methodology, I will discuss two examples. The first is childhood Guillain-Barré syndrome, with sparse children data enriched with adult data. The second is breakthrough designation, illustrated by a recent FDA approval of Crizotinib for non-small-cell-lung-cancer based on phase I and II data. The examples suggest that the evidential strength of non-confirmatory data can meet a confirmatory standard. This is reassuring for modern drug development, which exploits various types of evidence to inform licensing decisions.

Outline

- Scope & Objective
- Predictive Evidence Threshold Scaling (PETS)
 - Idea
 - Methodology
- Examples
 - 1) Crizotinib for NSCLC
 - 2) Plasmapheresis for childhood Guillain-Barré syndrome
- Conclusions

Scope and Objective

Scope & Objective

Problem statement

■ Problem

- For a treatment effect parameter θ , we want to compare the evidential strength of two data sources Y_E and Y_C
- Which one provides more evidence for a treatment effect?

■ Question:

- Why? If we have two relevant data sources, why don't we combine them to inform θ ?

■ Answer:

- Only one is observed (Y_E), the other (Y_C) is hypothetical

Scope & Objective

Example 1: breakthrough therapy designation

- Breakthrough therapy
 - an FDA designation that expedites drug development (FDA Safety and Innovation Act, July 9, 2012)
 - unmet clinical
 - *real world evidence (RWE)*, data outside well-controlled clinical trials, can be used
 - effect sizes are large
- How does RWE (Y_E) compare to a confirmatory standard (Y_C)?

Scope & Objective

Example 1: Crizotinib in non-small-cell lung cancer (NSCLC)

- Promising NSCLC progression-free survival (PFS) data: median 8-9 months

Trial	median (95%-CI)	y (s)*
PROFILE 1001	9.7 (7.7, 12.8)	2.272 (0.130)
PROFILE 1005	8.1 (6.8, 9.7)	2.092 (0.091)

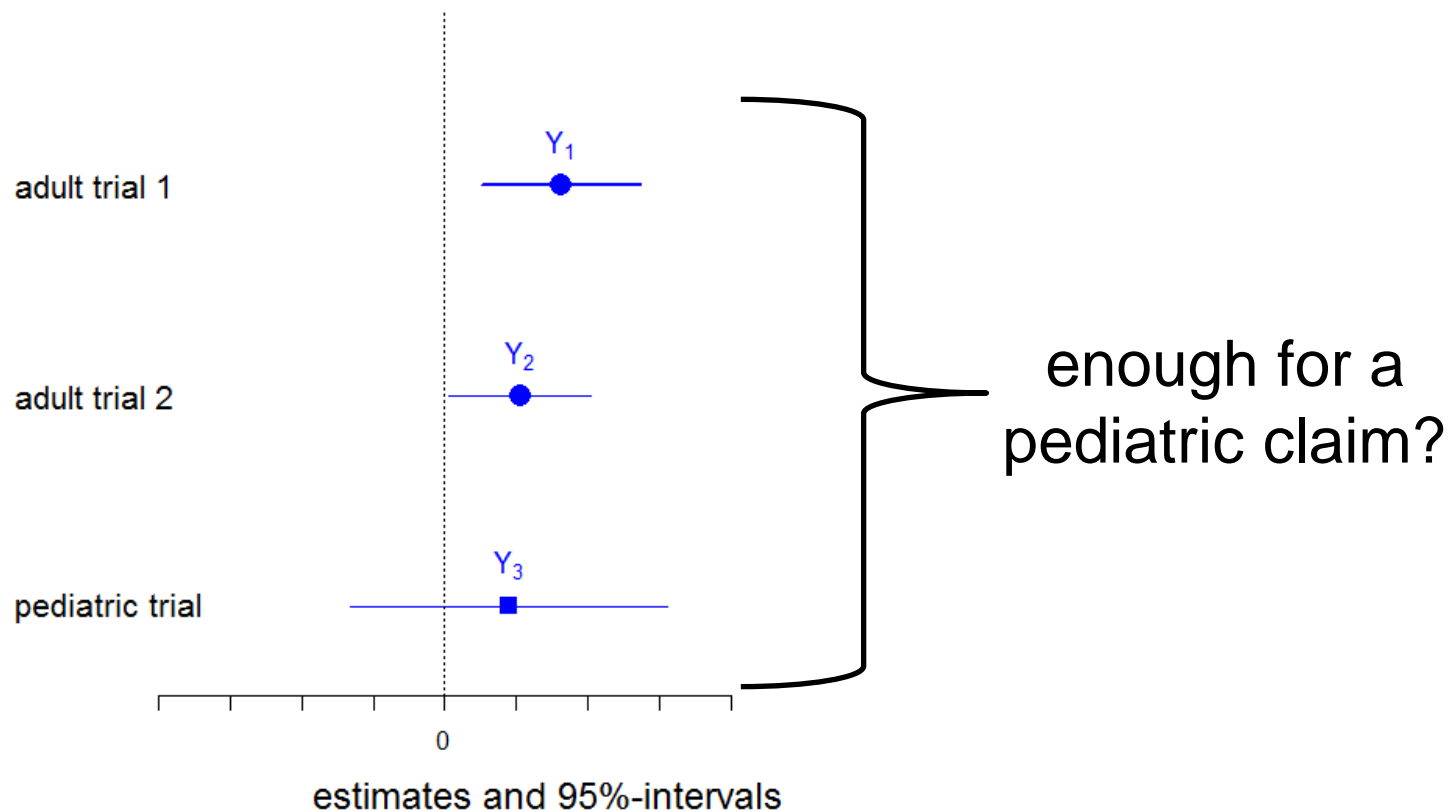
* normal approximation: est (se) of log-median PFS

- phase I expansion (PROFILE 1001) and phase II single-arm trial (PROFILE 1005)
- typical (control) median-PFS is 3 to 4 months
- FDA granted breakthrough designation
- How do these data compare to a confirmatory standard?

Scope & Objective

Example 2: extrapolation from adults to pediatrics

Assume we have promising adult evidence for a treatment effect. How much pediatric data is needed?



Scope & Objective

Quantifying Real World Evidence

- Setting: actual **RWE** Y_E for a clinical endpoint
- Objective: to propose a quantitative approach that
 - allows comparing the actual evidence Y_E to a confirmatory standard
 - complements and improves qualitative decisions
- Disclaimer: what follows
 - is not meant to replace the standard confirmatory approach
 - is meant to complement it

Predictive Evidence Threshold Scaling

Idea

Predictive Evidence Threshold Scaling (PETS)

Three requirements

Three requirements

1. a *confirmatory standard*: (hypothetical) data $Y_{(c)}$
2. a *metric* to compare Y_E to $Y_{(c)}$
3. a *rule* to decide whether the non-confirmatory data is sufficiently strong

PETS

Hierarchical structure

- Actual, non-confirmatory data Y_E from J sources
 - estimates Y_1, Y_2, \dots, Y_J
 - standard errors s_1, s_2, \dots, s_J
 - **parameters** $\theta_1, \theta_2, \dots, \theta_J$
- Hypothetical (minimal) confirmatory data $Y_{(c)}$
 - e.g., two significant trials; or one in Oncology
 - **estimates** $Y_{(1)}, Y_{(2)}$
 - **standard errors** $s_{(1)}, s_{(2)}$
 - **parameters** $\theta_{(1)}, \theta_{(2)}$
- The effect parameters differ (heterogeneity!)

PETS

Metric

- Metric to compare actual and hypothetical confirmatory evidence
 - metric should be trial-independent—not the effect parameter of one of the trials in the database!
 - choice: probability of a «positive» effect θ_P in a new trial
$$\text{pr}(\theta_P > 0 \mid \text{data})$$
 - note: inequality cutoff may be non-zero (e.g. NI trials)

PETS

Three heterogeneities

- Heterogeneities: deviations from mean value μ
 - for effect parameters in **actual trials** τ_E
 - for effect parameters in **confirmatory trials** τ_C
 - for effect parameter in **new trial** τ_P

$$\theta_1, \theta_2, \dots, \theta_J \approx \theta_P \approx \theta_{(1)}, \theta_{(2)}$$



If parameters are similar, the actual evidence Y_E will have higher confirmatory relevance

If parameters differ considerably, the evidence will be discounted due to larger heterogeneity

PETS

Predictive Evidence Probability (PEP) and Threshold (PET)

- Scaling of Y_E vs. $Y_{(C)}$

- For the actual evidence Y_E

PEP (predictive evidence probability) $\text{pr}(\theta_P > 0 \mid Y_E)$

- predictive probability of a «positive effect» (in a new trial)

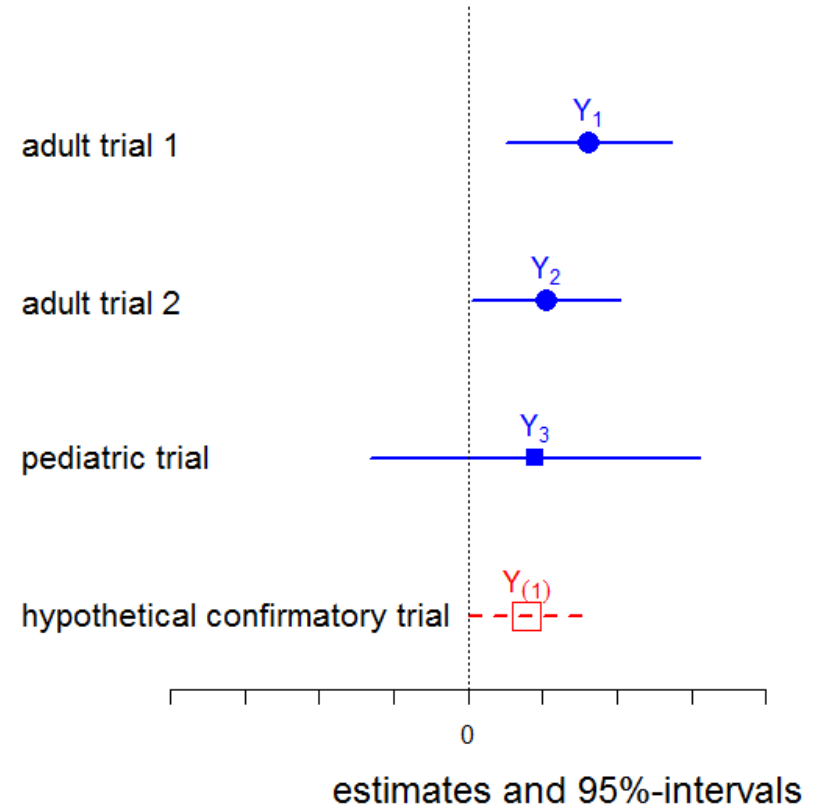
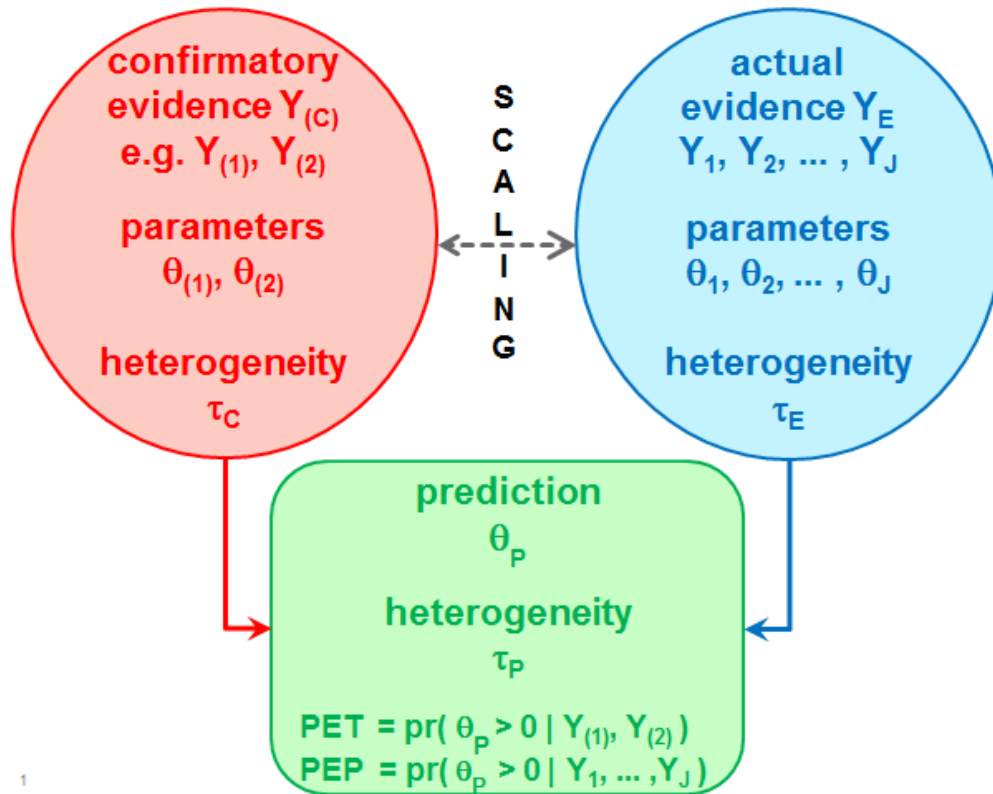
- For the (hypothetical) confirmatory evidence $Y_{(C)}$

PET (predictive evidence threshold) $\text{pr}(\theta_P > 0 \mid Y_{(C)})$

- How large are PEP and PET? Is $\text{PEP} \geq \text{PET}$

PETS

PETS framework: summary



Predictive Evidence Threshold Scaling

Methodology

PETS

Methodology: hierarchical model

- The normal-normal hierarchical model (NNHM)
 - (approximately) normally distributed estimates Y
 - normally distributed parameters θ
- Heterogeneity parameters τ_C, τ_P, τ_E
 - similar (or equal) small *confirmatory and predictive heterogeneity*, $\tau_C \approx \tau_P$, since confirmatory setting is more relevant
 - two approaches
 - assumed parameters \rightarrow sensitivity analyses for plausible scenarios
 - or uncertain parameters, with prior distributions on parameters
 - choices must be sensible (context-specific)

PETS

Normal-normal hierarchical model and predicted effect θ_p

■ NNHM with differential heterogeneity

- data model $Y_k | \theta_k, s_k^2 \sim N(\theta_k, s_k^2)$
- parameter model $\theta_k | \mu, \tau_k^2 \sim N(\mu, \tau_k^2)$
- $\tau_k = \tau_E$ for actual, $\tau_k = \tau_C$ for confirmatory evidence
- prediction $\theta_p | \mu, \tau_p^2 \sim N(\mu, \tau_p^2)$
- note: standard meta-analysis uses a common τ

■ Two calculations with NNHM: **PET** and **PEP**

- **PET**: $\text{pr}(\theta_p > 0 \mid \text{confirmatory data } Y_{(c)})$
- **PEP**: $\text{pr}(\theta_p > 0 \mid \text{actual data } Y_E)$

PETS

NNHM PET and PEP calculations for fixed heterogeneities

- **PET** and **PEP** calculation for fixed τ parameters
 - Bayesian with flat prior for μ

$$\theta_P | Y_1, \dots \sim N(\hat{\mu}, \frac{1}{w_+} + \tau_p^2)$$

$$\hat{\mu} = \sum_k w_k Y_k / w_+$$

$$w_k = \frac{1}{s_k^2 + \tau_k^2} \quad (\text{precisions})$$

$$w_+ = \sum_k w_k \quad (\text{total precision})$$

- «equivalent» classical result: $\hat{\theta}_P = \hat{\mu}, \quad \widehat{se}^2 = \frac{1}{w_+} + \tau_p^2$

PETS

Extensions

- Other sampling models
- Analyses with uncertainty for τ
- Inclusion of covariates
- Individual patient data
- ...
- *Systematic biases*

PETS

Extensions: systematic biases

- So far: no systematic biases assumed.
All distributions centered at μ
- (Sensitivity) analyses with systematic biases
 - allow for trial-specific biases δ_k
 - require judgement about plausible bias scenarios
 - simple model extension

$$\theta_k | \mu, \tau_k^2, \delta_k \sim N(\mu + \delta_k, \tau_k^2)$$

- biases
 - can be fixed (scenarios) or uncertain (priors)
 - but must be plausible

Example 1:

Breakthrough Designation

Crizotinib for NSCLC

Crizotinib

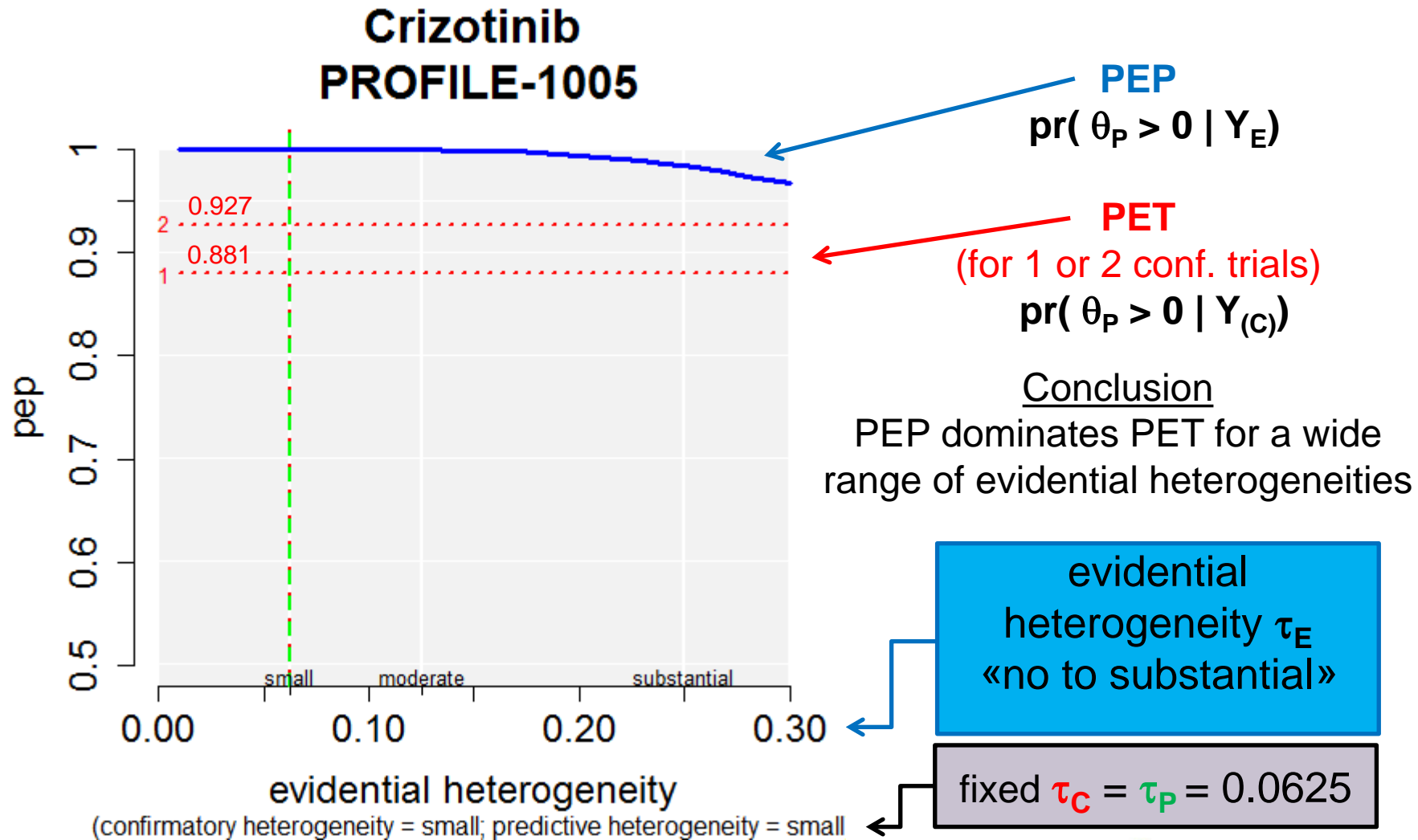
Data

Trial	median (95%-int)	y (s)
actual data		
PROFILE 1001	9.7 (7.7, 12.8)	2.272 (0.130)
PROFILE 1005	8.1 (6.8, 9.7)	2.092 (0.091)
hypothetical confirmatory data (one trial)		
CONF*	5.12 (4.5, 5.83)	1.635 (0.066)

* one confirmatory trial with 225 events;
 $H_0: \theta = \log(4.5 \text{ months}); \sigma=1$; one-sided p-value = 0.025.

Crizotinib

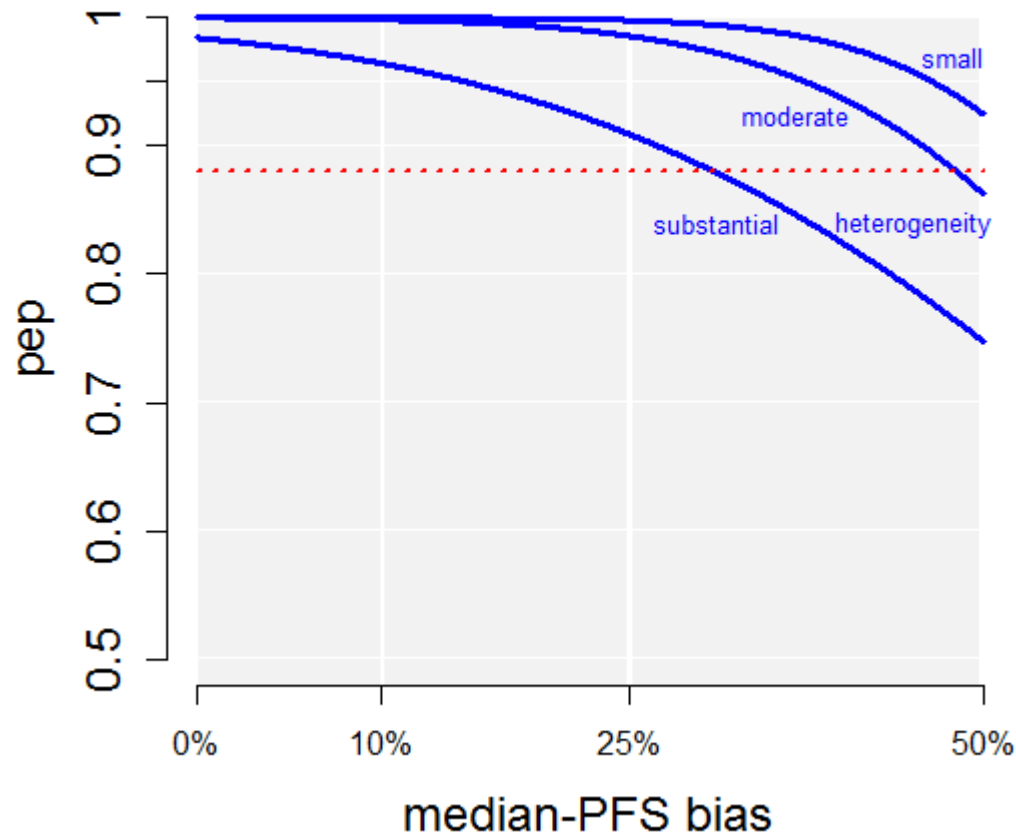
PETS graph: PEP vs. PET (single-arm analyses)



Crizotinib

Phase II trial: systematic bias sensitivity analyses

Crizotinib PROFILE-1005



(confirmatory heterogeneity = small; predictive heterogeneity = small)

Heterogeneities

Three blue lines are for **small**, **moderate**, and **substantial** evidential heterogeneity (τ_E)

Conclusions

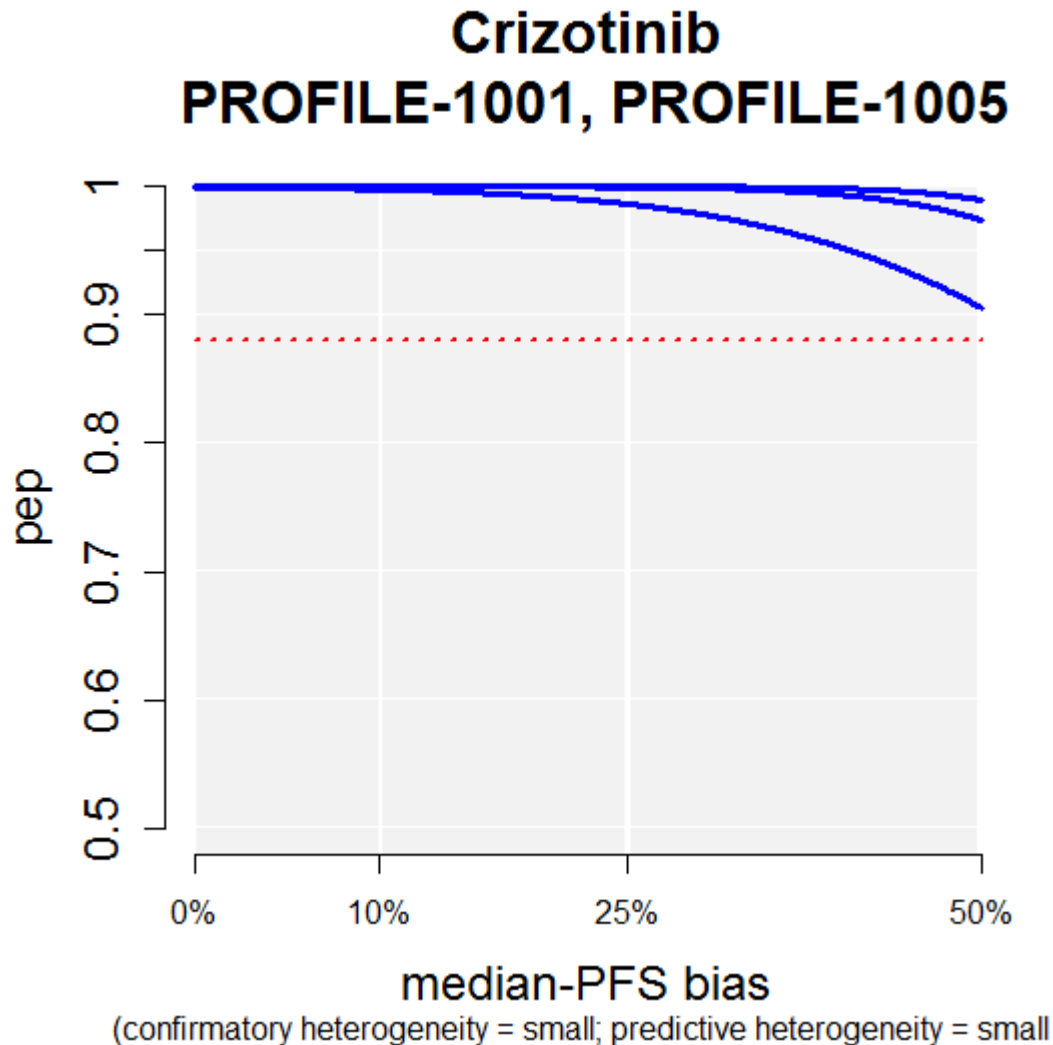
PEP dominates PET

- for small to substantial heterogeneity if bias is <25%
- for small to moderate heterogeneity if bias <50%

PEP is not sufficient if bias is > 25% and heterogeneity is substantial (plausible?)

Crizotinib

Bias sensitivity analyses using both trials



Heterogeneities

Three blue lines are for **small**, **moderate**, and **substantial** evidential heterogeneity (τ_E)

Crizotinib

Later confirmatory data were consistent with earlier data

Median-PFS results		
Trial	median (95%-int)	y (s)
actual non-confirmatory data		
PROFILE 1001	9.7 (7.7, 12.8)	2.272 (0.130)
PROFILE 1005	8.1 (6.8, 9.7)	2.092 (0.091)
hypothetical confirmatory data		
CONF	5.12 (4.5, 5.83)	1.633 (0.066)
later confirmatory data		
PROFILE 1007*	7.7 (6.0, 8.8)	



* Randomized phase 3 trial PROFILE-1007 with standard 2nd line chemotherapy (pemetrexed or taxotere) confirmed the effect of Crizotinib. **Median PFS for chemotherapy: 3 (2.6, 4.3)**

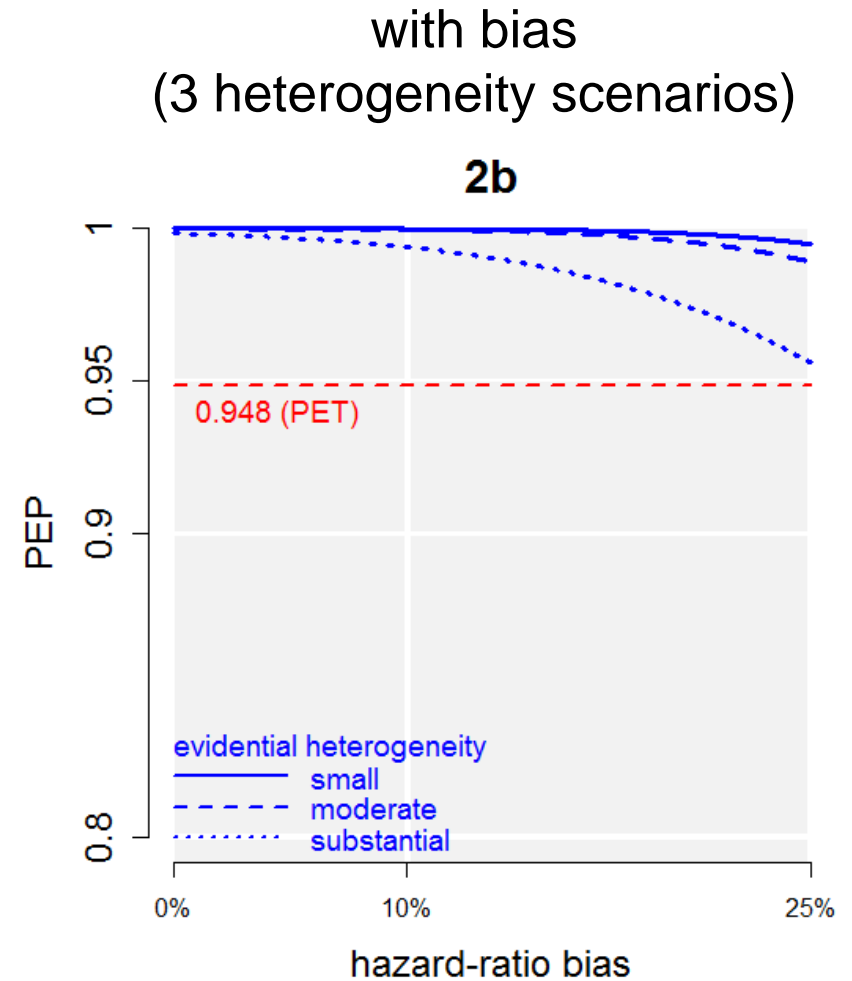
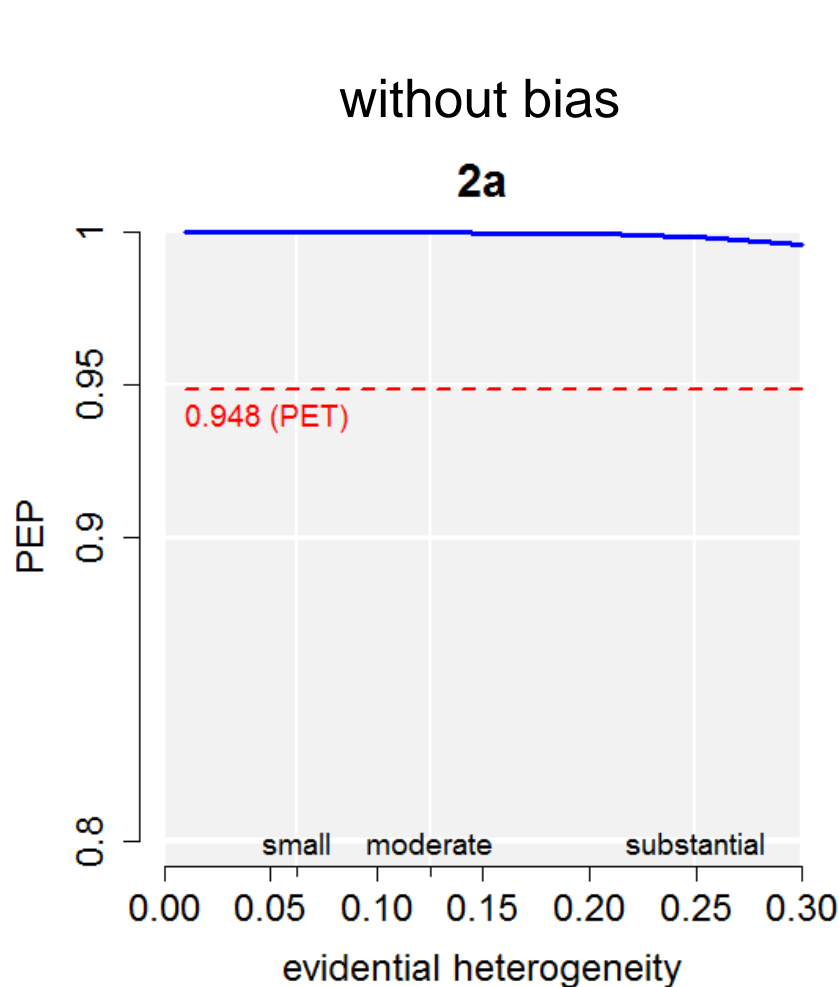
Crizotinib

Complication: single-arm vs. randomized

- Phase I and II trials were single-arm
- PETS analyses compared Crizotinib to a fixed control median of 4.5 months
- What about the randomized setting?
 - hazard-ratio Crizotinib vs. SoC. Two scenarios
 1. assuming a fixed control effect: median = 4.5 months
 2. **assuming uncertain control effect:
median = 4.5 months (worth ~ 50 events)**
 - results qualitatively similar to single-arm PETS analyses

Crizotinib

PETS for hazard-ratio scale (uncertain control median)



Example 2:

Extrapolation from Adults to Pediatrics

Plasmapheresis for Guillain-Barré
Syndrome (GBS)

Source: Goodman & Sladky (2004)

Plasmapheresis for childhood GBS

Introduction

- Guillain-Barré syndrome
 - a rare neurologic disease
 - affects all age groups, but is more common in children
 - main treatments:
 - ***plasmapheresis (plasma exchange, PE)***
 - *intravenous immune globulin (IVIg)*
 - Both treatments were shown to be effective in adults and then used in children off-label
- Here, we apply PETS to ***PE***
 - to predict efficacy in children, using adult data (and sparse children data)

Plasmapheresis for childhood GBS

Data

- A1-2: 2 trials in adults in the 1980s
- C1-C4: 4 small trials in children in the 1990s
- Endpoint: time to independent walking
- Does the evidence from these trials meet a confirmatory standard? For example, for trials A1, A2, and C1

	HR	95%-CI	y	s
A1. McKhann 1985	0.62	(0.46-0.84)	-0.472	0.153
A2. Raphael 1987	0.63	(0.47-0.84)	-0.461	0.149
C1. Epstein 1990	0.4	(0.17-0.94)	-0.916	0.434
C2. Lamont 1991	0.4	(0.16-1.03)	-0.916	0.481
C3. Jansen 1993	0.55	(0.23-1.34)	-0.598	0.455
C4. Graf 1999	1.52	(0.54-4.29)	0.419	0.529


Plasmapheresis for childhood GBS

PETS scenario analyses: assumptions

- Scenario assumptions for heterogeneities/biases
 - Y_E : actual trials
 - **3 heterogeneity scenarios** for adult/children trials:
 - moderate/small, substantial/moderate, large/substantial
 - **3 bias scenarios** for children trials
 - 0% (no bias), 10% bias, 25% bias
 - Y_C : one confirmatory children trial (1-sided p-value=0.025)
 - 200 events
 - confirmatory heterogeneity = small
- ⇒ **PET = 0.95**
- predictive heterogeneity = small

Plasmapheresis for childhood GBS

PETS scenario analyses: results

bias (trials C1-C4)	heterogeneity: adult/children		
	moderate/small	substantial/moderate	large/substantial
	adult trials		
	0.999	0.985	 0.894
	adult trials + children trial 1		
no	1	0.997	0.98
10%	1	0.996	0.974
25%	1	0.994	0.958

- Extrapolation based on adult data only is insufficient if heterogeneity is large/substantial: **PEP = 0.894**
- With 1st children trial (C1), PEP > PET for all scenarios
- Conclusion: strong adult data combined with sparse pediatric data provides sufficient evidence

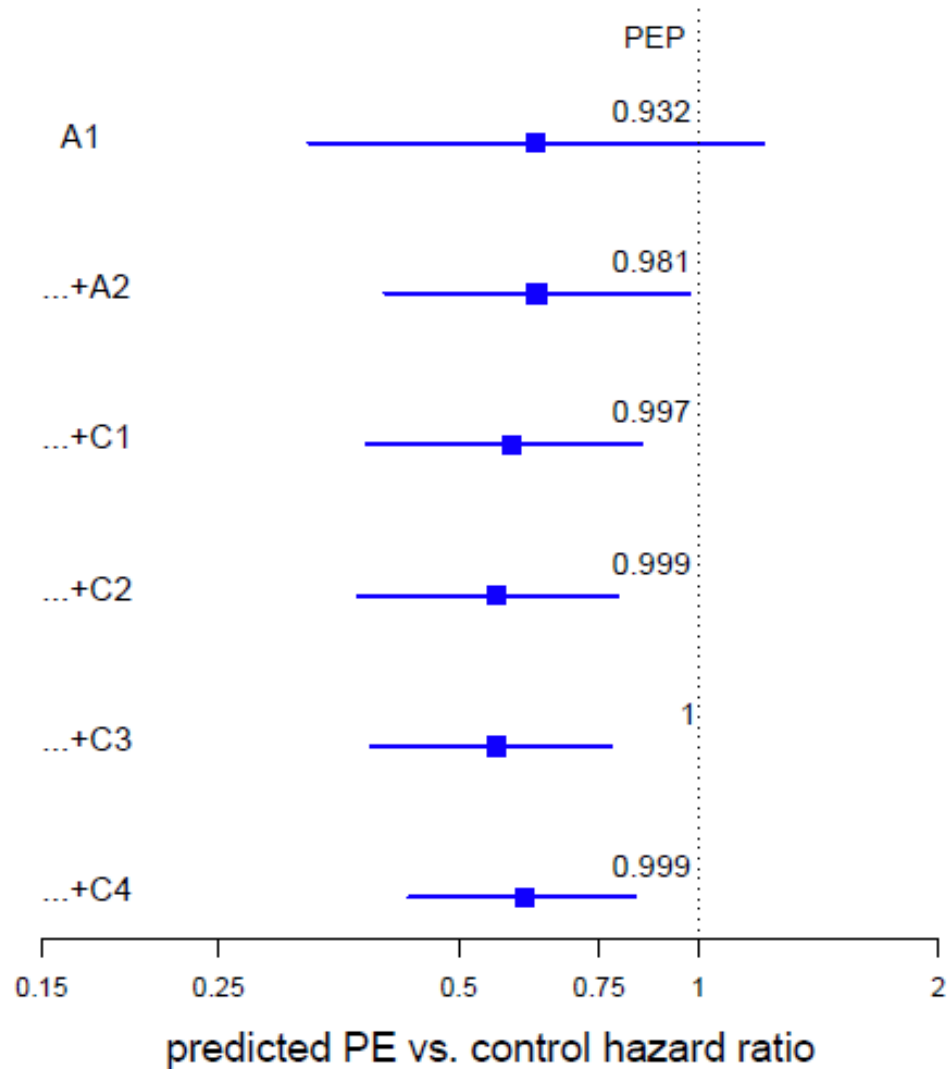
Plasmapheresis for childhood GBS

Bayesian PETS analyses

- Alternative to fixed scenarios: prior distributions on
 - heterogeneities: log-normal priors on τ parameters
 - biases: normal priors on δ parameters
- PETS results
 - are similar if priors cover the range of the fixed scenarios used previously
 - are shown cumulatively on next slide:
trial A1, trials A1+A2, trials A1+A2+C1, etc.

Plasmapheresis for childhood GBS

Bayesian PETS analyses: cumulative results



Note:
PET = 0.95

Conclusions

- Increasing pressure on the pharmaceutical industry
 - scope for innovation is broad (for policy and science)
 - one aspect is to better use the evidence, which includes real-world evidence (21st Century Cures Act)
 - this is challenging and requires that
 - 1) data are accessible
 - 2) data quality is understood
 - 3) data are properly analyzed (hierarchical modeling)
 - 4) results of the analysis are properly interpreted
 - PETS contributes to the inferential 3) and 4)
 - NNHM: the basic model (extensions possible)

Conclusions

- PETS has limitations
 - although quantitative, PETS requires contextual judgement about plausible *heterogeneities* and *biases*
 - for these, robustness of PEP>PET is needed
- Examples
 1. robust PETS results for Crizotinib, which clearly support FDA's breakthrough designation
 2. PETS supports intuition that strong adult data combined with sparse children data suffices for a pediatric claim
- NNHM can be easily implemented in *R* (for fixed scenarios) and *WinBUGS/JAGS/Stan* (for priors)

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