

A Network Meta Analysis of Treatments for Advanced Pancreatic Cancer Using Parametric and Non-Parametric Survival Models

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Abstract

Five treatments for advanced pancreatic cancer were compared against the standard of care treatment in two network meta analyses. The first network meta analysis used parametric survival models, and the second used fractional polynomials. The parametric model results showed only one treatment gave improvements on the standard of care, but little to no improvements were found in overall survival.

Acknowledgements

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For my late grandfather, Norman Fredrick Taylor (July 1943 - April 2015).

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INTRODUCTION

1.1 Pancreatic Cancer

Pancreatic cancer is the 10th most common cancer in the UK, accounting for 3% of all new cases [Cancer Research UK, 2024]. Pancreatic cancer has a particularly poor prognosis. In 2016-2018, there were 9,558 deaths from 10,452 cases. Pancreatic cancer is hard to detect at early stages, meaning most people who present with symptoms already have advanced-stage pancreatic cancer. Often, patients only notice symptoms when the tumour has spread to surrounding tissues, or metastasises to other organs [Kelsen et al., 1997]. The liver is the most common site of pancreatic cancer metastases [Deeb et al., 2015]. Common symptoms of pancreatic cancer include indigestion, stomach or back pain, loss of appetite and jaundice [Pancreatic Cancer UK, 2022].

Risk factors of pancreatic cancer include smoking, diabetes, obesity, and high-fat diets. Smoking is the dominant cause, with around 20% of cases being caused by cigarette smoking. In addition, cancers from smokers contain more genetic mutations when compared to cancers from non-smokers [Blackford et al., 2009].

1.2 Treatment Landscape

Gemcitabine (GEM) ($C_9H_{11}F_2N_3O_4$) is a standard first-line treatment for pancreatic cancer administered intravenously [for Health and Excellence, 2018]. GEM is also used to treat other types of cancer, including breast cancer, bladder cancer and non-small-cell lung cancer [Wong et al., 2009]. GEM can be administered alone or in combination with another medication.

This dissertation considered five treatments that were given in combination with GEM: Cisplatin (CIS) ($PtCl_2(NH_3)_2$), Capecitabine (CAP) ($C_{15}H_{22}FN_3O_6$), Axitinib (AXI) ($C_{22}H_{18}N_4OS$), Pemetrexed (PEM) ($C_{20}H_{21}N_5O_6$), and Irinotecan (IRI) ($C_{33}H_{38}N_4O_6$).

SURVIVAL ANALYSIS BAKGROUND

2.1 Background and Survival Functions

Given a homogeneous population of individuals, the time of death for each individual is drawn from a continuous random variable $T > 0$ with probability density function $f(t)$ and distribution function $F(t) = \int_0^t f(\tau)d\tau$. Survival analysis is concerned with estimating the distribution T from Time-To-Event (TTE) data. There are two functions central to survival analysis, the *survival function* and *hazard function*.

Definition 2.1.1: Survival Function

The **Survival Function** $S(t)$, gives the probability of an individual surviving longer than time t .

$$S(t) = P(T \geq t) = 1 - F(t) = \int_t^\infty f(\tau)d\tau$$

Definition 2.1.2: Hazard Function

The **Hazard Function** gives the risk of death at time t , given that the individual has survived up to time t .

$$h(t) = -\frac{d}{dt} \log S(t)$$

2.2 Regression Models for Survival

The survival time of patients may be dependent on several explanatory variables such as age, sex, the presence of a genetic mutation, etc. We wish to incorporate these variables into our survival functions.

2.2.1 Accelerated Failure Time (AFT) Models

Let x be a vector of explanatory variables for each individual in a trial. The survival function can be extended to include this,

$$S(t, x) = S_0(t(x)).$$

Here, $S_0(t) = S(t, x = \mathbf{0})$, i.e the survival function at baseline. We define the density and hazard functions accordingly,

$$\begin{aligned} f(t, \mathbf{x}) &= f_0(t\Psi(\mathbf{x})) (\mathbf{x}) \\ h(t, \mathbf{x}) &= h_0(t\Psi(\mathbf{x})) (\mathbf{x}). \end{aligned}$$

This is equivalent to defining a random variable T such that

$$T = T_0/\Psi(\mathbf{x}).$$

Here, T_0 has survivor function S_0 . It is required that $\Psi(\mathbf{x}) \geq \mathbf{0}$ and $\Psi(\mathbf{0}) = \mathbf{1}$ [[NOTE TO MATT: WHY?]], leading to the natural choice

$$\Psi(\mathbf{x}) = \exp(-\beta' \mathbf{x}).$$

We can then write

$$\begin{aligned} T &= T_0/\Psi(\mathbf{x}) \\ \implies E(T) &= E(T_0)/E(e^{-\beta' x}) \\ &= E(T_0)/e^{-\beta' x} \\ &= E(T_0)e^{\beta' x} \end{aligned}$$

In practice, we assume a distribution for T , and estimate parameters using maximum likelihood estimation.

2.2.2 Proportional Hazards (PH) Models

Let h_0 represent the hazard function for an individual at baseline. In addition, let \mathbf{x} be a vector of explanatory variables. The proportional hazards model, also known as the Cox model [Cox, 1972] is then given by

$$h(t, \mathbf{x}) = \exp(\beta' \mathbf{x}) \mathbf{h}_0(\mathbf{t}) \quad (2.1)$$

Consider the following definition.

Definition 2.2.1: Semi Parametric Model

A statistical model is a parameterised family of distributions $\{P_\theta : \theta \in \Theta\}$. For a parametric model, $\Theta \subseteq \mathbb{R}^k$ for $k \in \mathbb{N}$. Similarly, for a non-parametric model, $\Theta \subseteq V$, where V is some (possibly infinite) dimensional space V . A **Semi-parametric** model is a statistical model with both parametric and non-parametric components. For a semi-parametric model we have $\Theta \subseteq \mathbb{R}^k \times V$.

The Cox model is semi-parametric then β is of finite dimension and $h_0(t)$ is infinite-dimensional and does not need to be specified.

2.3 Key Survival Metrics

2.3.1 The Hazard Ratio

The Hazard Ratio (HR) follows from Equation 2.1. Consider two treatments, $i = 1, 2$, then $h_1(t, \mathbf{x}) = \exp(\beta' \mathbf{x}) \mathbf{h}_0(\mathbf{t})$ and $h_2(t, \mathbf{x}) = \exp(\beta' \mathbf{x}) \mathbf{h}_0(\mathbf{t})$. The HR is obtained as in Equation 2.2.

$$HR = \frac{h_1}{h_2} = \exp(\beta' \mathbf{x}) \quad (2.2)$$

In practice, the HR is a useful endpoint in performing network meta-analyses on survival outcomes. However, in order to conduct a HR-based NMA, the proportional hazards assumption (PHA), must be satisfied. The PHA is the assumption that the HR remains constant throughout the observation period of a trial. It can be tested by visual-inspection of a log-cumulative hazards plot.

Definition 2.3.1: Cumulative Hazard Function

The **Cumulative Hazard Function**, $H(t)$ is given by

$$H(t) = \int_0^t h(t)dt = -\log(S(t))$$

By extension, the log-cumulative hazard function is given by $\log(-\log(S(t)))$. When plotting this for both arms of a clinical trial, if the curves remain roughly parallel, the PHA is likely satisfied, but if they curves cross, it indicates violation of the PHA.

2.3.2 Restricted Mean Survival Time

The Restricted Mean Survival Time (RMST) is alternative measure to the (log) HR in NMAs. RMST is the mean survival time up to a pre-specified time. This measure can be thought of visually as the area under the survival curve. We therefore define it formally as

Definition 2.3.2: RMST

For a survival function $S(t)$, the **RMST** for some pre-specified time $x > 0$,

$$RMST = \int_0^x S(t)dt$$

2.4 Parametric Models for Survival Analysis

This section discusses the parametric models commonly used in Survival Analysis. In particular, the seven parametric models recommended by the National Institute for Health and Care Excellence (NICE) in Technical Support Document (TSD) 14 [Latimer, 2011]. All parametric model fitting for this project was performed in R using the **flexsurv** package [Jackson, 2016]. The first section outlines how the **flexsurv** package works.

2.4.1 Model Setup

The general model of a **flexsurv** survival model takes the form

$$f(t|\mu(\mathbf{z}), \alpha(\mathbf{z})). \quad (2.3)$$

Equation 2.3 gives the probability density for death at time $t \geq 0$. The *mean* or *location* of the distribution is given by $\mu = \alpha_0$. The remaining parameters, $\alpha^1 = (\alpha_1, \dots, \alpha_R)$ are called *ancillary* parameters.

Chapter 2 discussed AFT and PH models. Under the **flexsurv** framework, if the hazard function, $h(t) = \frac{f(t)}{S(t)}$, can be factorised as

$$h(t|\alpha, \mu(\mathbf{z})) = \mu(\mathbf{z})\mathbf{h}_0(t|\alpha).$$

Then we have a PH model. On the other hand, an AFT model would be written as

$$S(t|\mu(\mathbf{z}), \alpha) = \mathbf{S}_0(\mu(\mathbf{z})\mathbf{t}/\alpha).$$

All parameters may depend on \mathbf{z} , a vector of covariates. This is done through the link-transformed linear models

$$\begin{aligned} g_0(\mu(\mathbf{z})) &= \gamma_0 + \beta_0^T \mathbf{z} \\ g_r(\alpha_r(\mathbf{z})) &= \gamma_r + \beta_\gamma^T \mathbf{z} \end{aligned} \quad (2.4)$$

g is usually chosen to be $\log()$ if the parameter is positive, or the identity function if the parameter is unrestricted.

Flexsurv contains several built-in models. Appendix B.1 presents these models.

2.4.2 Fitting Models

Let $t_i, i \in \{1, \dots, n\}$, be a sample of times from n individuals. Define c_i such that

$$c_i = \begin{cases} 1 & \text{if } t_i \text{ is an observed death time} \\ 0 & \text{if } t_i \text{ is censored} \end{cases}.$$

Introduce s_i , which are delayed-entry times. This means for an individual i who is delayed-entry, the survival time is only observed conditionally on individual i having survived up to time s_i . $s_i = 0$ when there is no delayed-entry.

2.4.2.1 Right Censoring

In the case of right-censoring and nothing else, the likelihood for the parameters $\theta = \{\gamma, \beta\}$ required in Equation 2.4 is given by

$$l(\theta | \mathbf{t}, \mathbf{c}, \mathbf{s}) = \frac{\prod_{i:c_i=1} f_i(t_i) \prod_{i:c_i=0} S_i(t_i)}{\prod_i S_i(s_i)} \quad (2.5)$$

2.4.2.2 Interval Censoring

In the case of interval-censoring, where the survival time is censored on (t_i^{\min}, t_i^{\max}) , the likelihood for $\theta = \{\gamma, \beta\}$ is

$$l(\theta | \mathbf{t}^{\min}, \mathbf{t}^{\max}, \mathbf{c}, \mathbf{s}) = \frac{\prod_{i:c_i=1} f_i(t_i) \prod_{i:c_i=0} (S_i(t_i^{\min}) - S_i(t_i^{\max}))}{\prod_i S_i(s_i)} \quad (2.6)$$

Maximum Likelihood Estimation is performed in **R** using the analytic derivatives of Equation 2.5 and/or Equation 2.6.

NETWORK META ANALYSIS

3.1 Building a Network of Evidence

Consider a set of N two-arm randomised-controlled trials (RCTs). In each trial $i \in 1, \dots, N$, the patients are randomised to receive a treatment A_i , or a placebo P_i . This can be represented as N graphs with two nodes, A_i and P_i , connected by an edge representing the trial comparing A_i and P_i . It is useful at this stage to recall the formal definition of an (undirected) graph.

Definition 3.1.1: Graph

A **Graph** is an ordered triple $G = (V, E, \varphi)$. Where V is a set of nodes, E is a set of edges, and $\varphi : E \rightarrow \{\{x, y\} | x, y \in V \text{ such that } x \neq y\}$ is an **incidence function** mapping every edge to a pair of vertices.

We can construct N graphs under the formal definition. Namely, for trial T_i , we have $G_i = (V_i, E_i, \varphi_i)$ where $V_i = \{A_i, P_i\}$, $E_i = \{T_i\}$ and $\varphi_i : E_i \rightarrow \{\{x, y\} | x, y \in V_i \text{ such that } x \neq y\}$. For construction of the graphs, we can drop the subscript on P_i , and take the placebo as a reference treatment. This is done under the assumption that the effect of placebo is constant across all trials. This is a strong assumption, and implications of this are discussed later. Under this assumption however, each V_i now contains a common element, P .

Let

$$V_{trts} = \bigcup_{i=1}^N V_i$$

$$E_{trials} = \bigcup_{i=1}^N E_i.$$

The incidence function becomes

$$\varphi : E_{trials} \rightarrow \{\{x, y\} | x, y \in V_{trts} \text{ such that } x = P\}.$$

Then the ordered triple $G = (V_{trts}, E_{trials}, \varphi)$ is the network of evidence given by these two arm trials that forms the basis of a network meta analysis. This process expands to trials that compare more than two treatments by weighting the edges by the number of trials making that particular comparison.

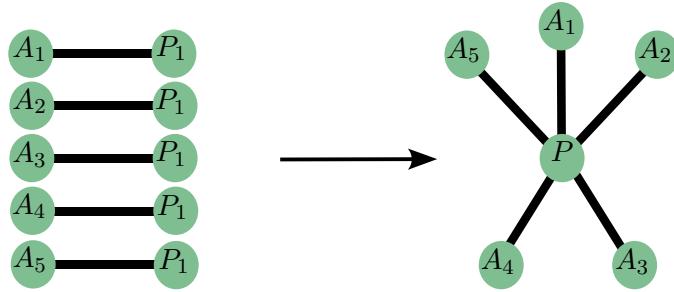


Figure 3.1: Visualisation of combining trials into a network of evidence

3.2 Deriving the NMA Model

The derivation in this chapter is based on the work of ??, but modified for this project. Under an NMA framework, we have J RCTs investigating a subset K_j ($j = 1, \dots, J$) of K treatments. In this project, $|K_j| = 2 \forall j$. Depending on data availability, we may have IPD for some studies, and only aggregate data for the remaining.

Definition 3.2.1: General IPD Meta-Regression Model

Let y_{ijk} be the IPD outcome for individual $i = 1, \dots, N_{kj}$ in study j receiving treatment $k \in K_j$ given the likelihood distribution $\pi_{Ind}(\theta_{ijk})$.

$$\begin{aligned} y_{ijk} &\sim \pi_{Ind}(\theta_{ijk}) \\ g(\theta_{ijk}) &= \mu_j + \mathbf{x}_{ijk}^T (\beta_1 + \beta_{2,k}) + \gamma_k \\ &= \eta_{jk}(\mathbf{x}_{ijk}) \end{aligned}$$

Here, g links the likelihood parameter θ_{ijk} to $\eta_{jk}(\mathbf{x}_{ijk})$. The μ_j are study-specific intercepts, and $\beta_1, \beta_{2,k}$ are regression coefficients for prognostic and effect-modifying covariates respectively. Additionally, the γ_k are individual-level treatment effects. For the reference treatment, $\beta_{2,1} = \gamma_1 = \mathbf{0}$.

3.3 Survival ML-NMR

Each study reports a pair $y_{ijk} = \{t_{ijk}, c_{ijk}\}$ consisting of outcome times t_{ijk} and censoring indicators c_{ijk} , either from IPD or reconstructed IPD. For IPD studies, the covariates \mathbf{x}_{ijk} will naturally be available, but for aggregate studies (those for which pseudo-IPD has been re-created), only the joint covariate distribution of covariates at baseline, denoted f_{jk} .

Let $S_{jk}(t|\mathbf{x})$ and $h_{jk}(t|\mathbf{x})$ be the survival and hazard functions conditional on the covariates \mathbf{x} . Then the individual conditional likelihood contributions for each time t_{ijk} in the IPD studies are given by

$$L_{ijk|x}^{Con}(\zeta; t_{ijk}, c_{ijk}, \mathbf{x}_{ijk}) = S_{jk}(t_{ijk}|\mathbf{x}_{ijk}) h_{jk}(t_{ijk}|\mathbf{x}_{ijk})^{c_{ijk}} \quad (3.1)$$

The forms of S and h depend on the specific models chosen.

SURVIVAL ANALYSIS OF PANCREATIC CANCER TRIALS

4.1 Median OS

Figure 4.1 and Figure 4.2 present the OS KM curves for GEM and the comparators, respectively. In addition, Table 4.1 presents the median OS estimates by study for GEM and the comparator treatment. In all studies except Oettle, GEM had a higher median OS. Note that more information about each included trial is given in Section A.

The PHA was deemed to be violated, based on the log-cumulative hazard plots, presented in Appendix A. The log-cumulative hazard curves crossed either once or several times in each of the five studies.

	Treatment = GEM			Treatment = Comparator		
	Median Survival	L95% CI	U95%CI	Median Survival	L95% CI	U95%CI
Colucci	8.5157	7.412	10.2119	7.2514	6.3844	8.7499
Cunningham	6.0892	5.4991	7.34	7.1984	6.3016	7.9773
Kindler	9.9477	7.2714	11.1849	9.0388	7.0821	10.3769
Oettle	6.1769	5.5159	7.2945	6.4053	5.4246	6.9519
Rocha Lima	6.7424	5.6812	7.9758	6.3989	4.8554	7.6321

Table 4.1: Median OS data (in months) from each of the studies, along with lower and upper 95% confidence intervals

4.2 Parametric Models

For each study, the standard seven parametric models were fit to each treatment arm, up to a maximum time of five years. Figure 4.3 to Figure 4.7 present the fitted models for each study. The median estimates given for each treatment arm of the studies are presenteed in Table C.5 Table C.5.

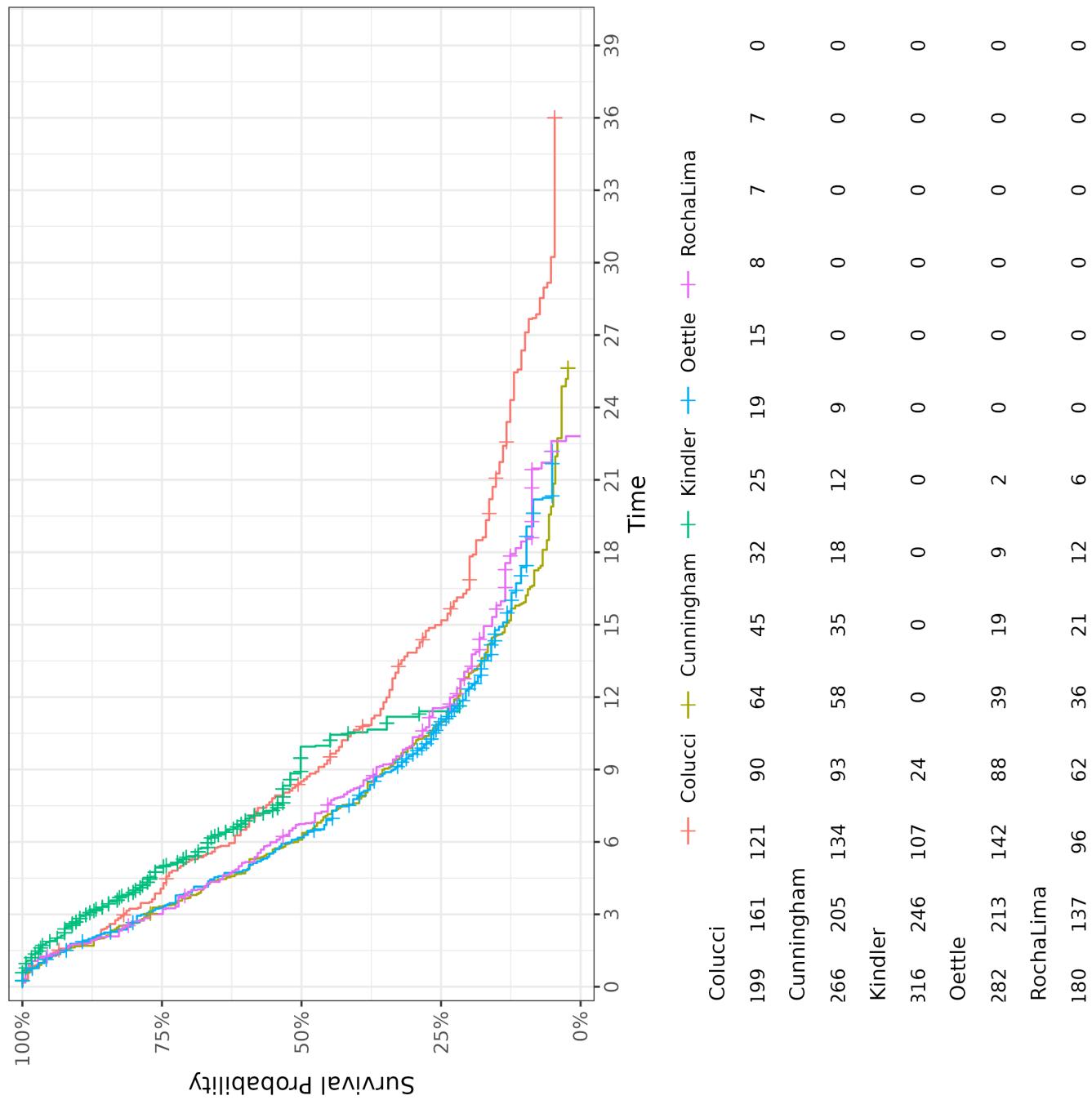


Figure 4.1: OS Kaplan-Meier data for Gemcitabine

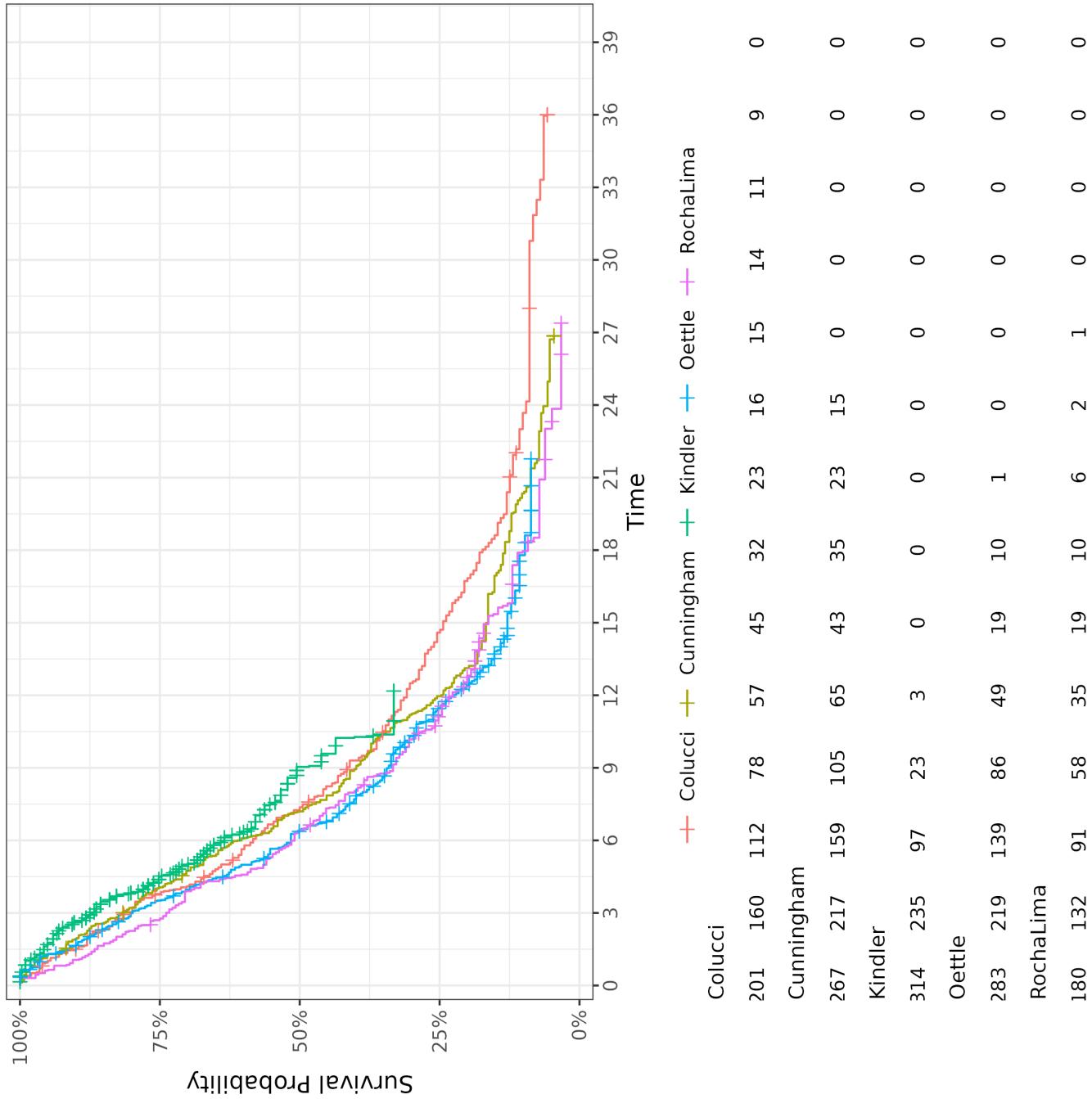


Figure 4.2: OS Kaplan-Meier data for comparators

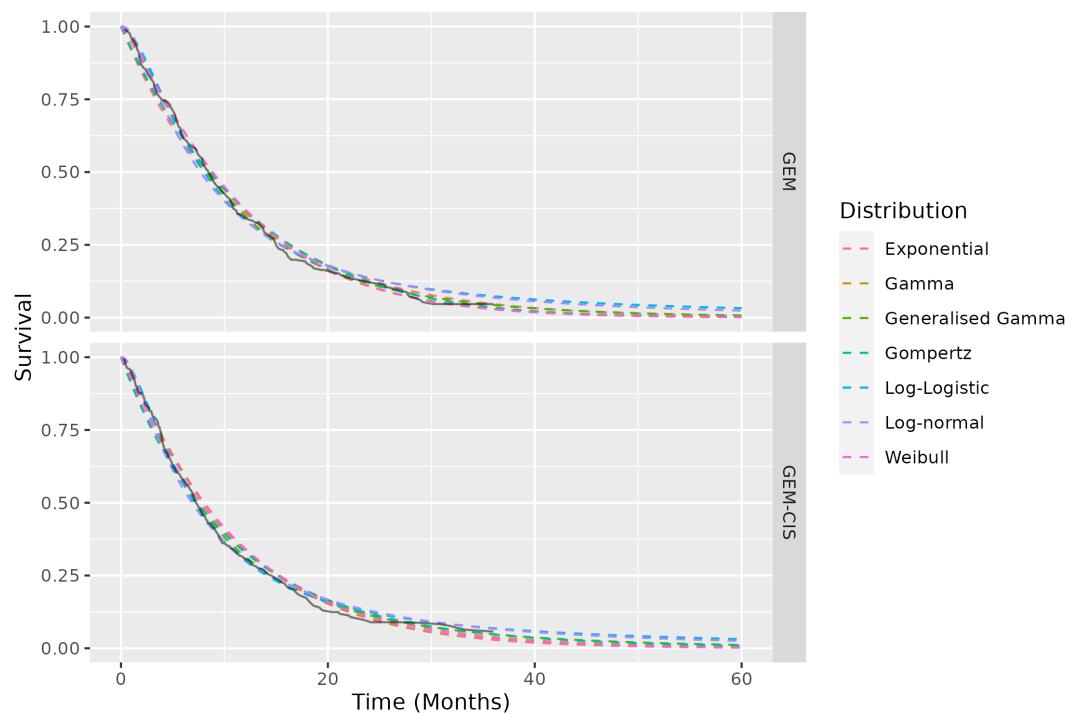


Figure 4.3: Colucci 2010 Models

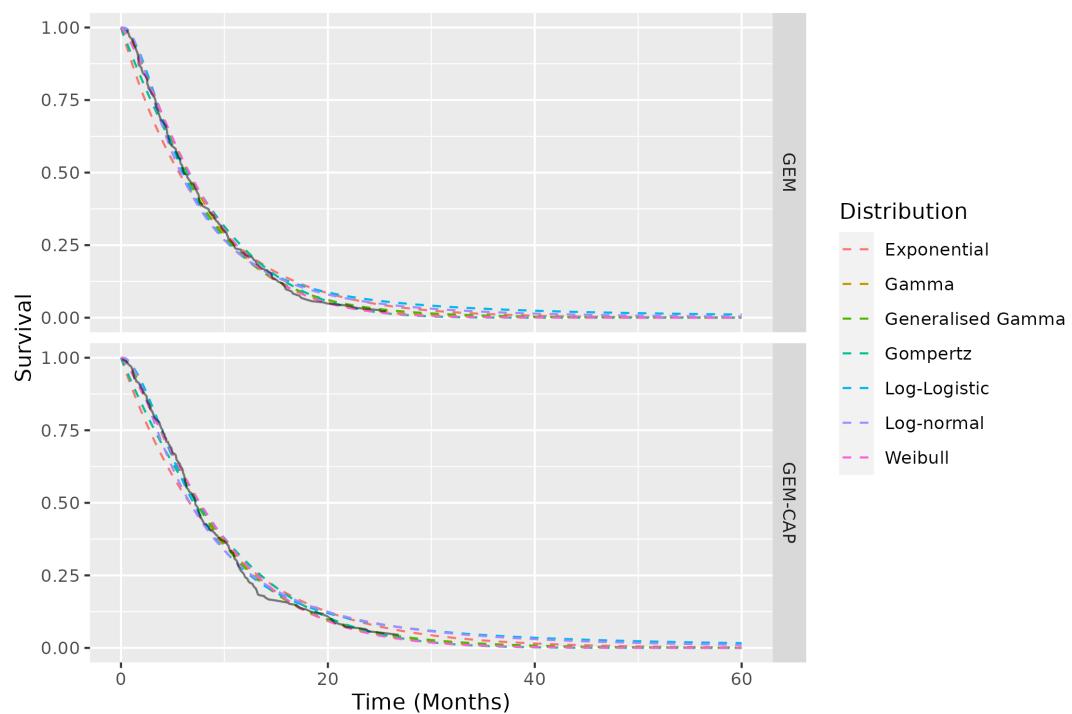


Figure 4.4: Cunningham 2009 Models

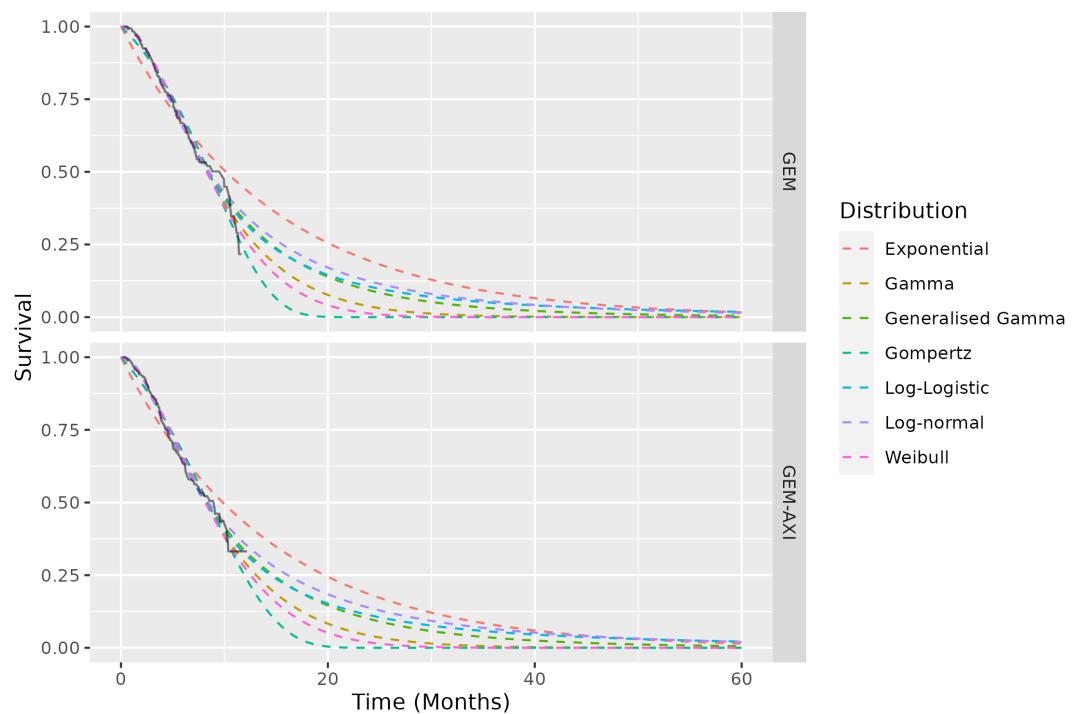


Figure 4.5: Kindler 2011 Models

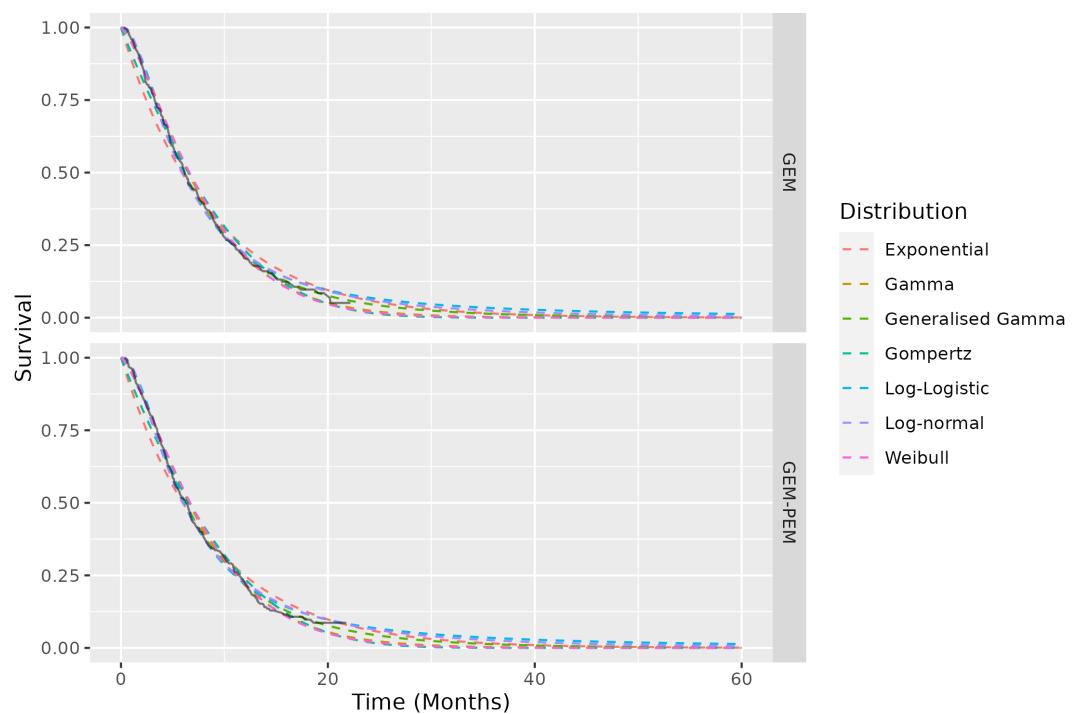


Figure 4.6: Oettle 2006 Models

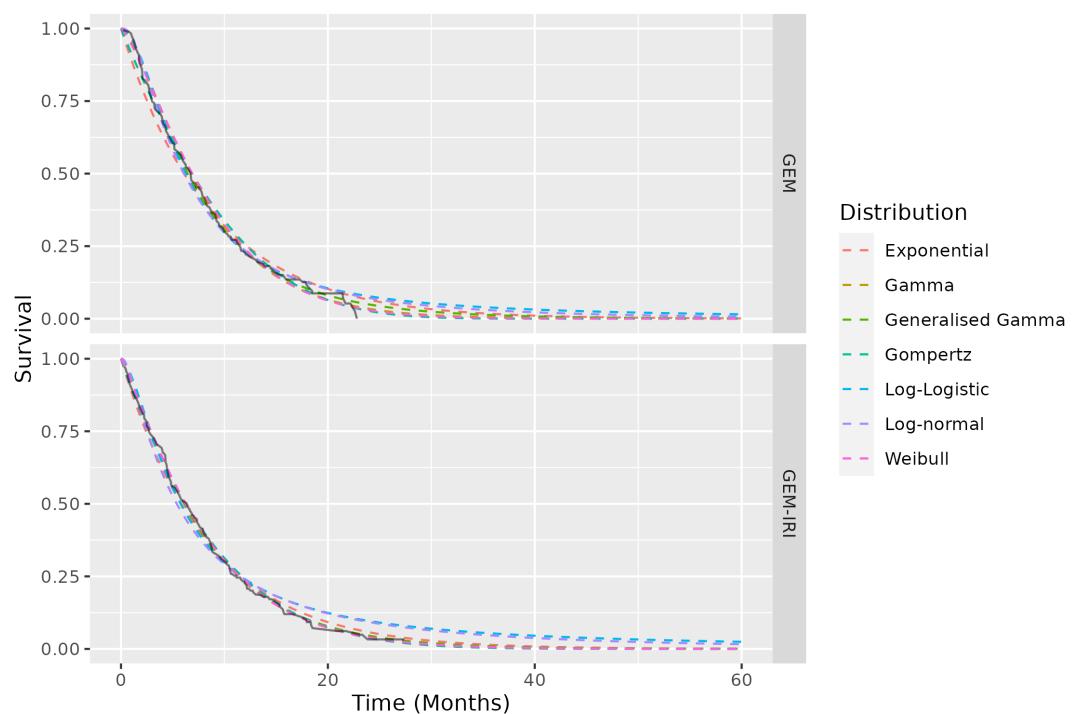


Figure 4.7: Rocha Lima 2004 Models

CHAPTER
FIVE

NMA OF PANCREATIC CANCER TRIALS

5.1 Data

CHAPTER
SIX

CONCLUSIONS AND RECOMMENDATIONS

The conclusions of the five studies included in the NMA are given below (with drug names abbreviated).

- Colucci: “GEM-CIS failed to demonstrate any improvements as a first-line treatment of advanced pancreatic cancer”
- Cunningham: “GEM-CAP should be considered as one of the standard first-line options in locally advanced and metastatic pancreatic cancer”
- Kindler: “GEM-AXI does not improve overall survival in advanced pancreatic cancer”
- Oettle: “GEM-PEM therapy did not improve OS”
- Rocha Lima: “IRI-GEM safely improved the tumour response rate compared with GEM but did not alter overall survival”

6.1 Parametric NMA

Based on guidance from NICE TSD 2 [Dias et al., 2011], the fixed effects model was selected as the best fitting model due to having a lower DIC score. However it should be noted that the differences between the models were very small, with only 0.2 separating the DIC scores. The model showed no significant change in overall survival for any of the 5 comparators to GEM in the treatment of pancreatic cancer. GEM-AXI, GEM-CAP, and GEM-PEM had positive treatment effects, although GEM-AXI and GEM-PEM were close to 0. GEM-CIS and GEM-IRI had slightly negative treatment effects, but were both close to 0.

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Appendices

APPENDIXA

INCLUDED TRIALS

This appendix presents the trial data for each trial included in this study. It should be noted that due to having to digitise the survival data, as opposed to having IPD, there may be some slight discrepancies between the numbers presented here, and in the original publications. Table A.1 presents the hazard ratios

Study	Comparator	HR	L95	U95	Time (Months)
Colucci	GEM+CIS	1.0746	0.8729	1.3227	36
Cunningham	GEM+CAP	0.8249	0.6928	0.9820	27
Kindler	GEM+AXI	1.0606	0.8132	1.3835	13
Oettle	GEM+PEM	0.9826	0.8186	1.1796	24
RochaLima	GEM+IRI	1.0365	0.8305	1.2936	30

Table A.1: Hazard ratios for each study

A.1 Colucci, 2010

The Colucci et. al study [Colucci et al., 2010] compared Gemcitabine plus Cisplatin (GEM+CIS) with Gemcitabine (GEM) in a total of 400 patients.

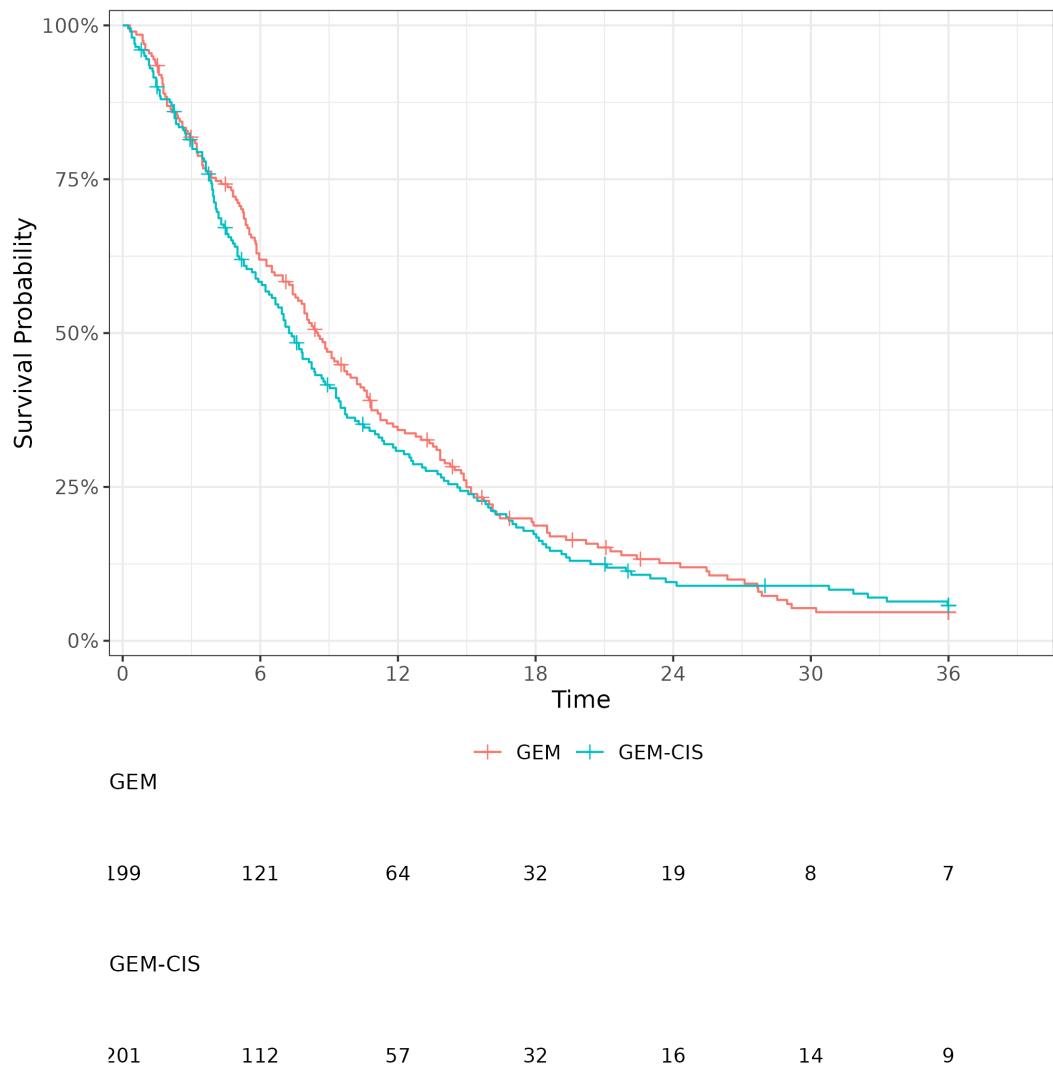


Figure A.1: Colucci 2010 KM Curve

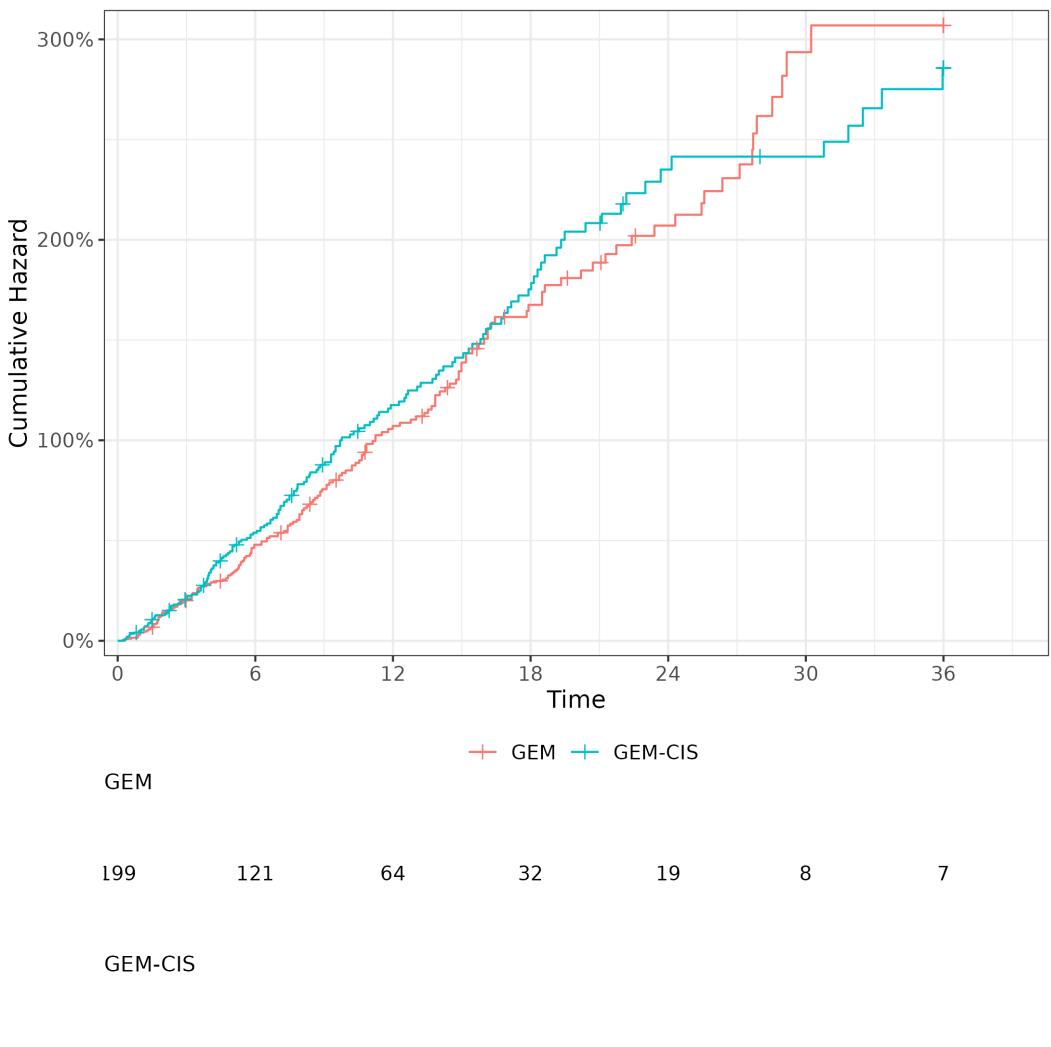


Figure A.2: Colucci 2010 Cumulative Hazard

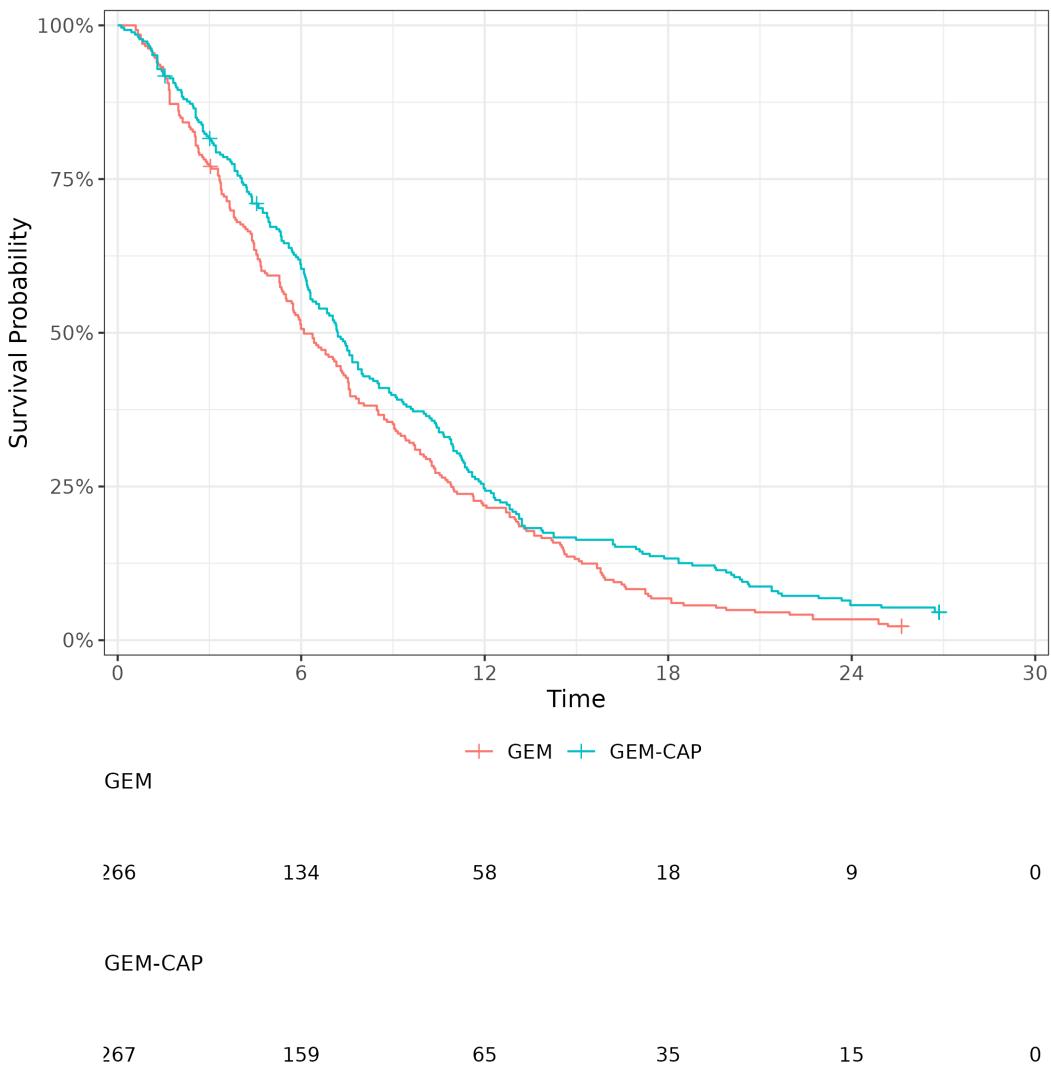


Figure A.3: Cunningham 2009 KM Curve

A.2 Cunningham, 2009

The Cunningham et. al study [Cunningham et al., 2009] compared Gemcitabine plus Capecitabine (GEM+CAP) with Gemcitabine (GEM) in a total of 533 patients.

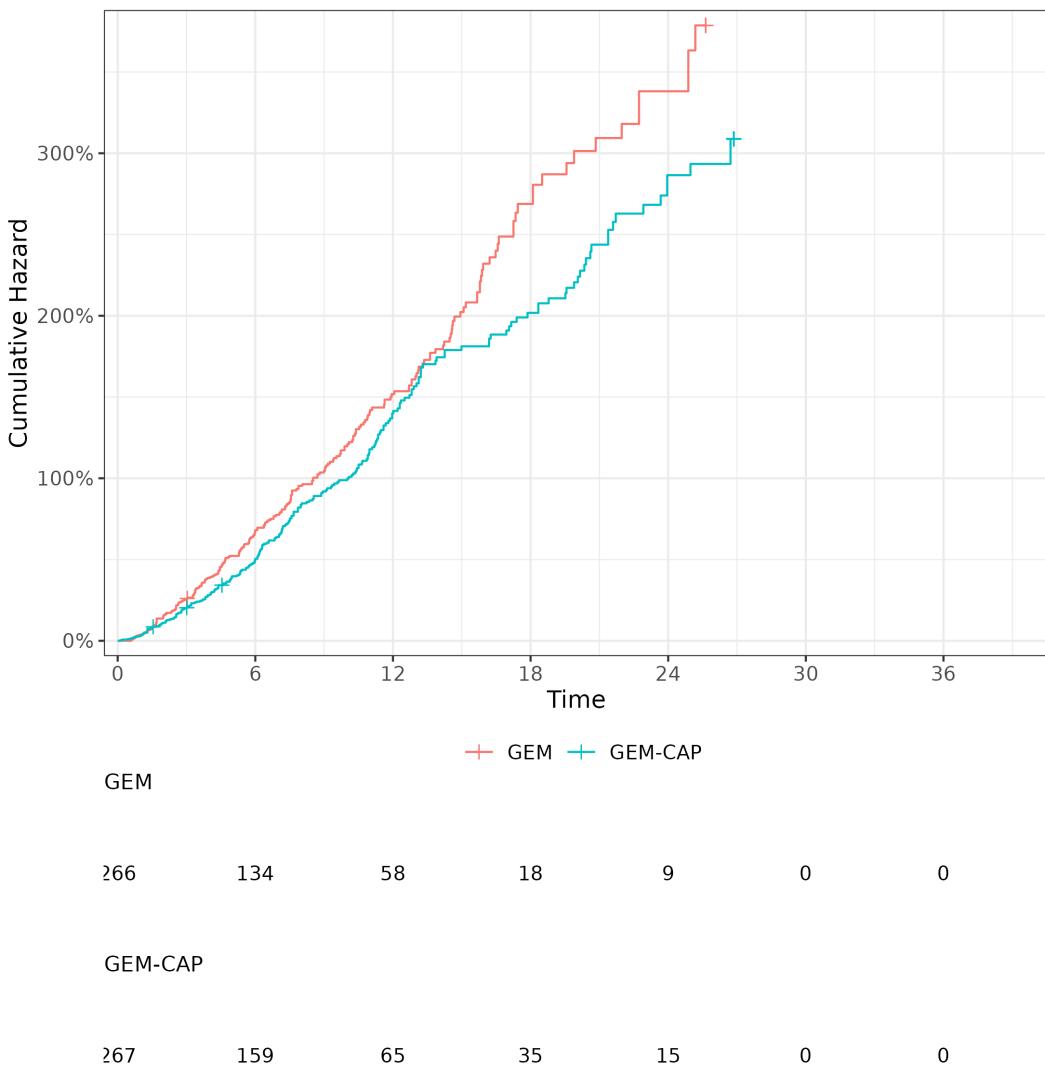


Figure A.4: Cunningham 2009 Cumulative Hazard

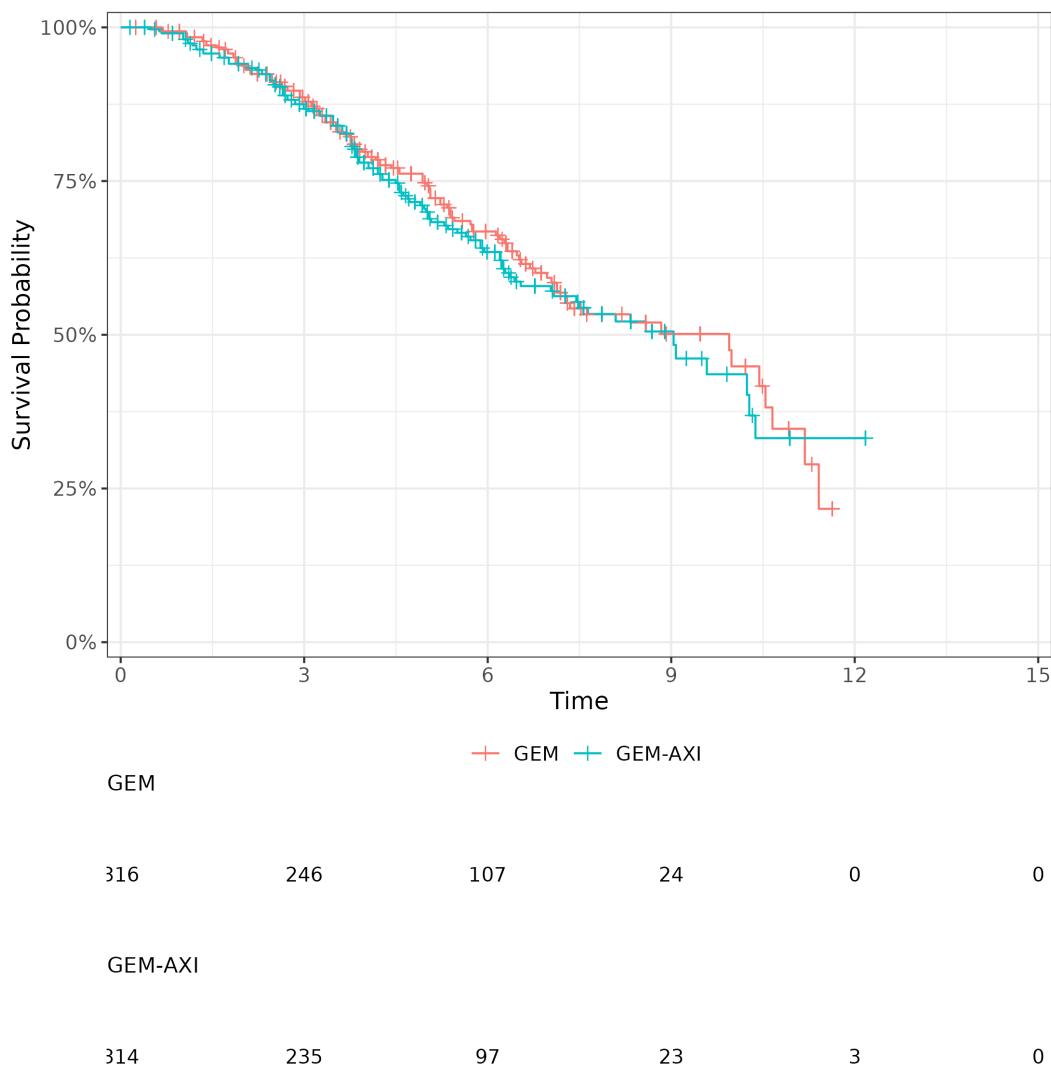


Figure A.5: Kinder 2011 KM Curve

A.3 Kindler, 2011

The Cunningham et. al study [Kindler et al., 2011] compared Gemcitabine plus Axitinib (GEM+AXI) with Gemcitabine (GEM) in a total of 632 patients.

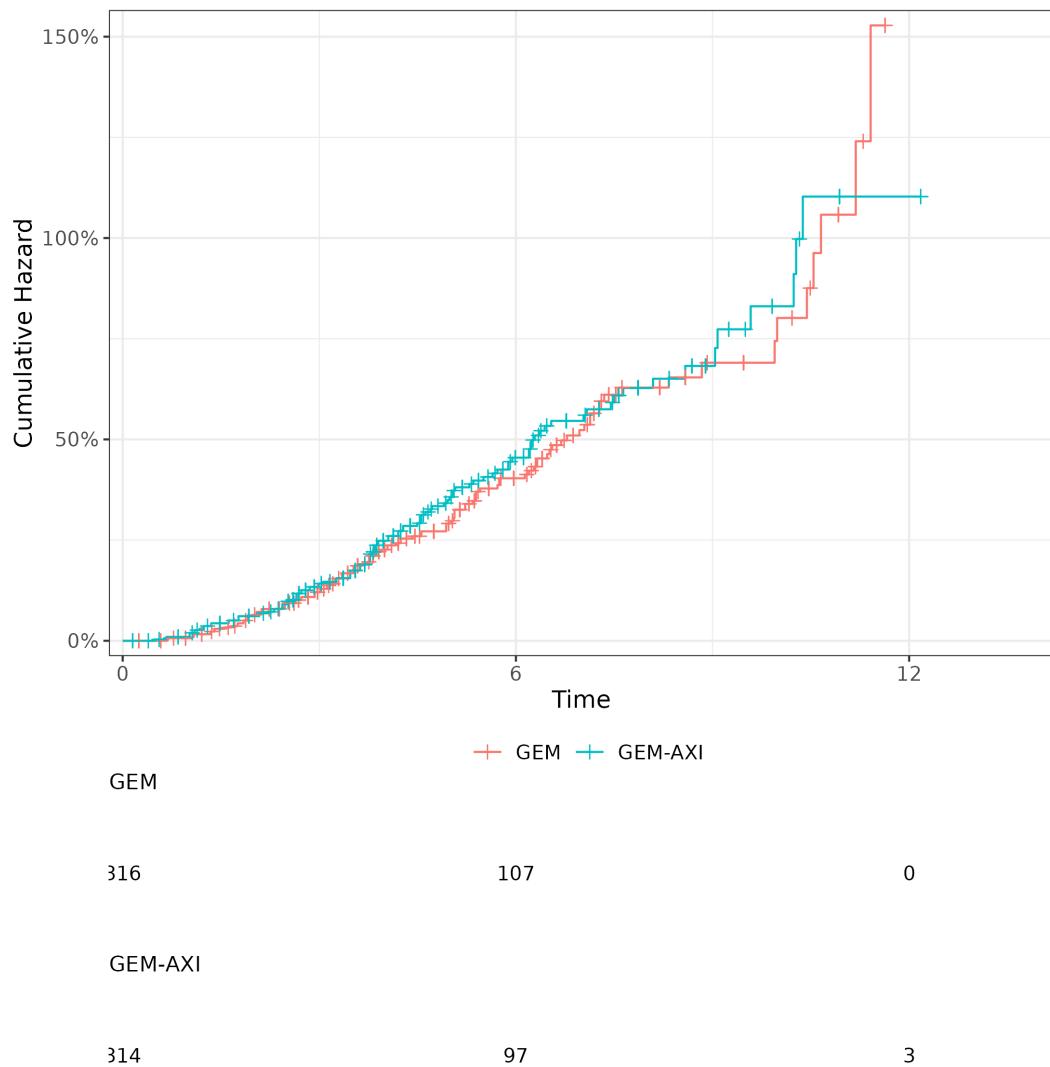


Figure A.6: Kinder 2011 Cumulative Hazard

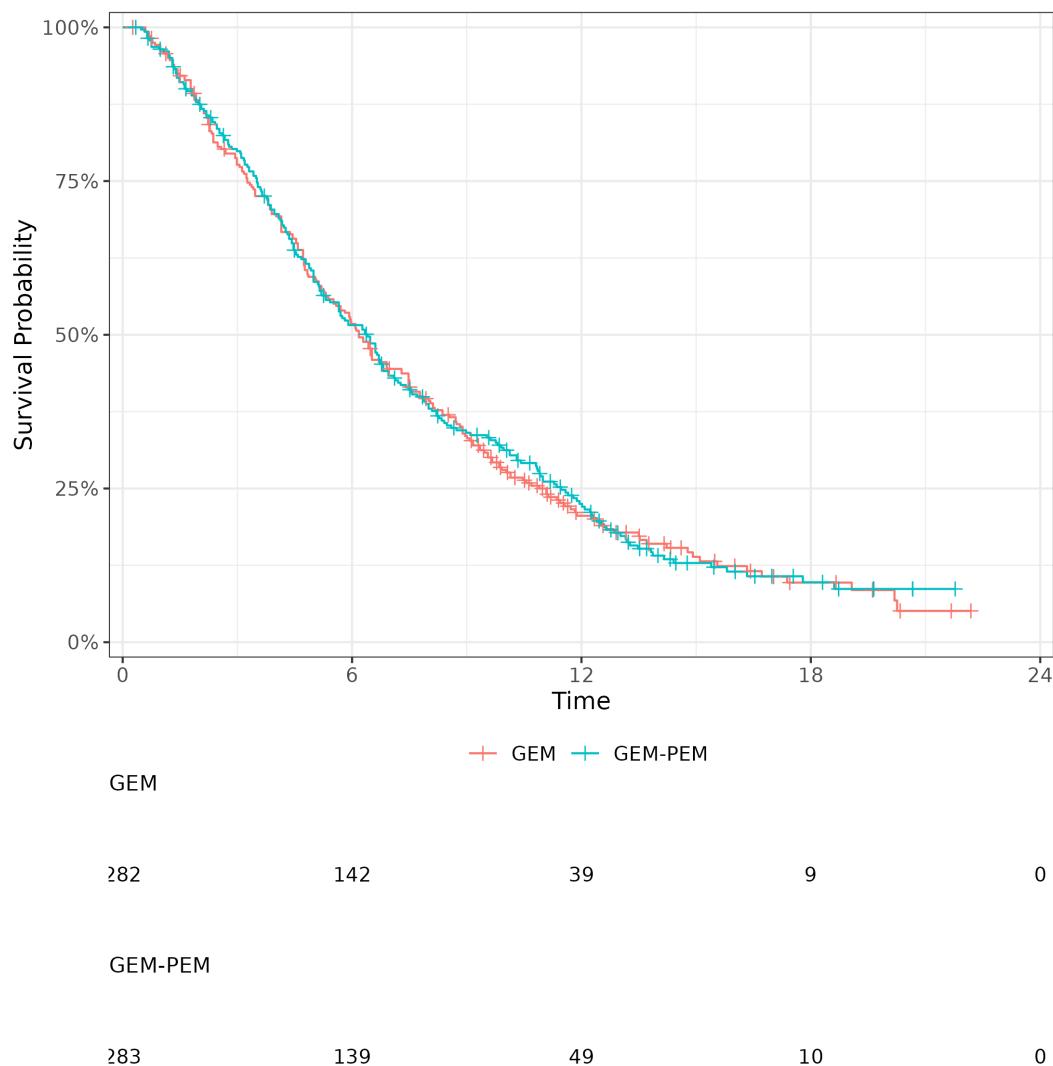


Figure A.7: Oettle 2005 KM Curve

A.4 Oettle, 2005

The Cunningham et. al study [Oettle et al., 2005] compared Gemcitabine plus Pemetrexed (GEM+PEM) with Gemcitabine (GEM) in a total of 565 patients.

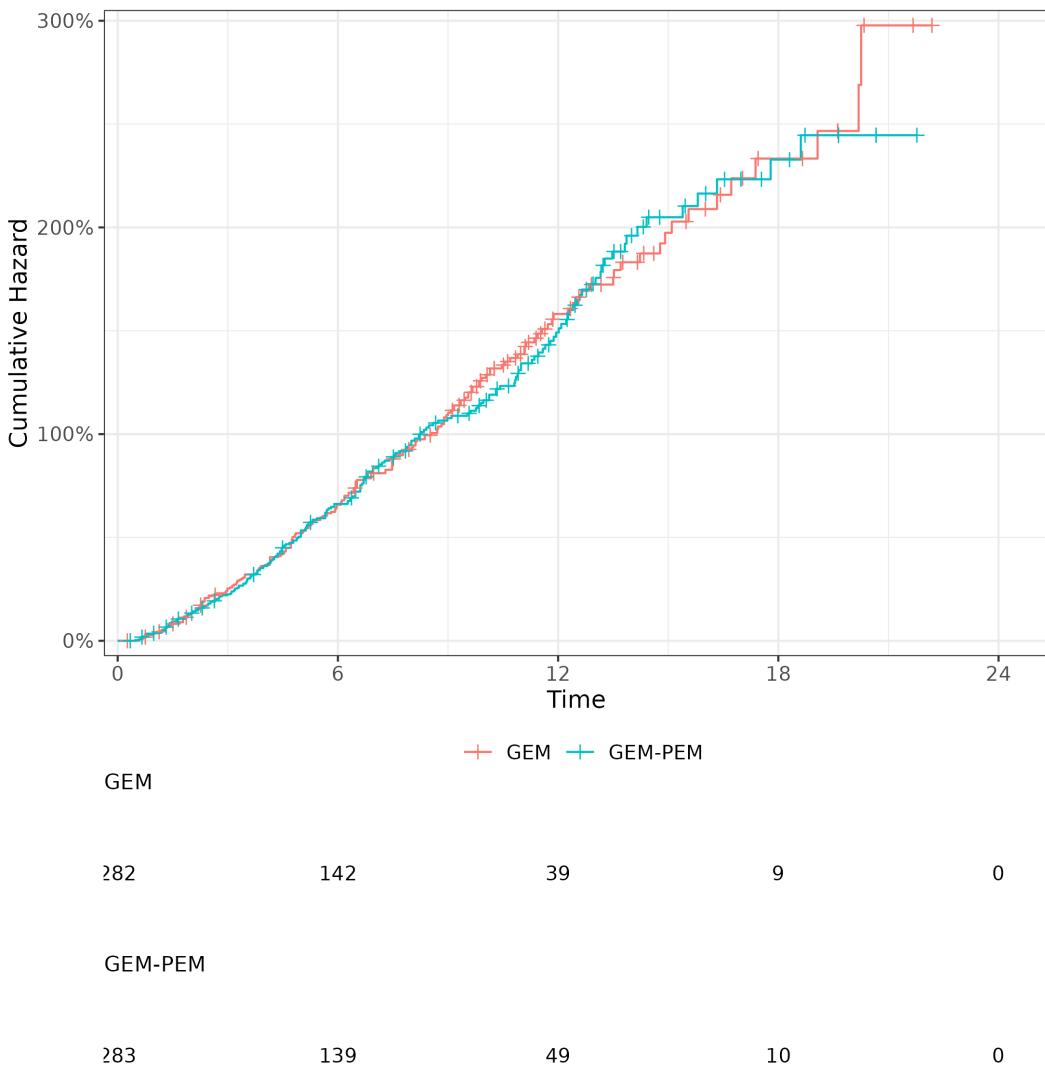


Figure A.8: Oettle 2005 Cumulative Hazard

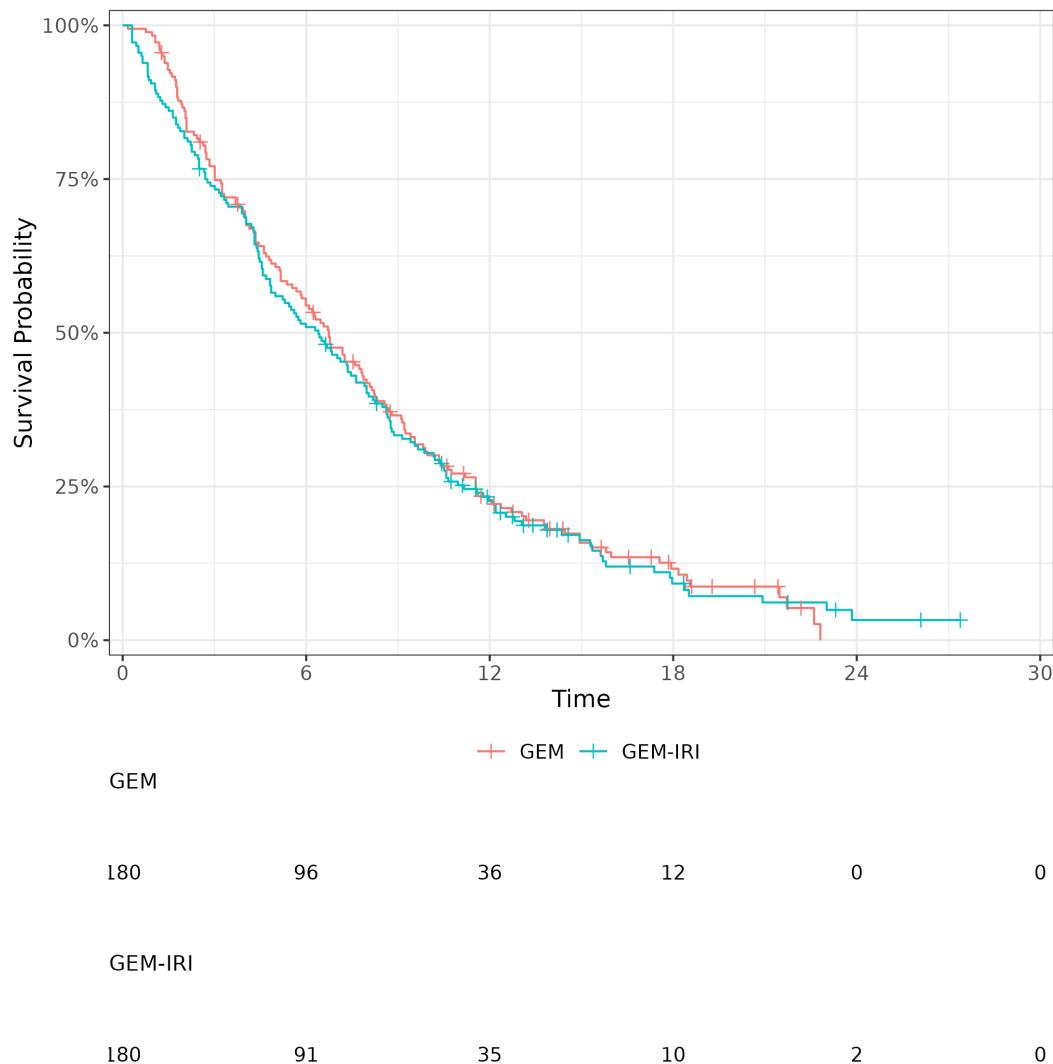


Figure A.9: Rocha Lima 2004 KM Curve

A.5 Rocha Lima, 2004

The Cunningham et. al study [Rocha Lima et al., 2004] compared Gemcitabine plus Irinotecan (GEM+IRI) with Gemcitabine (GEM) in a total of 360 patients.

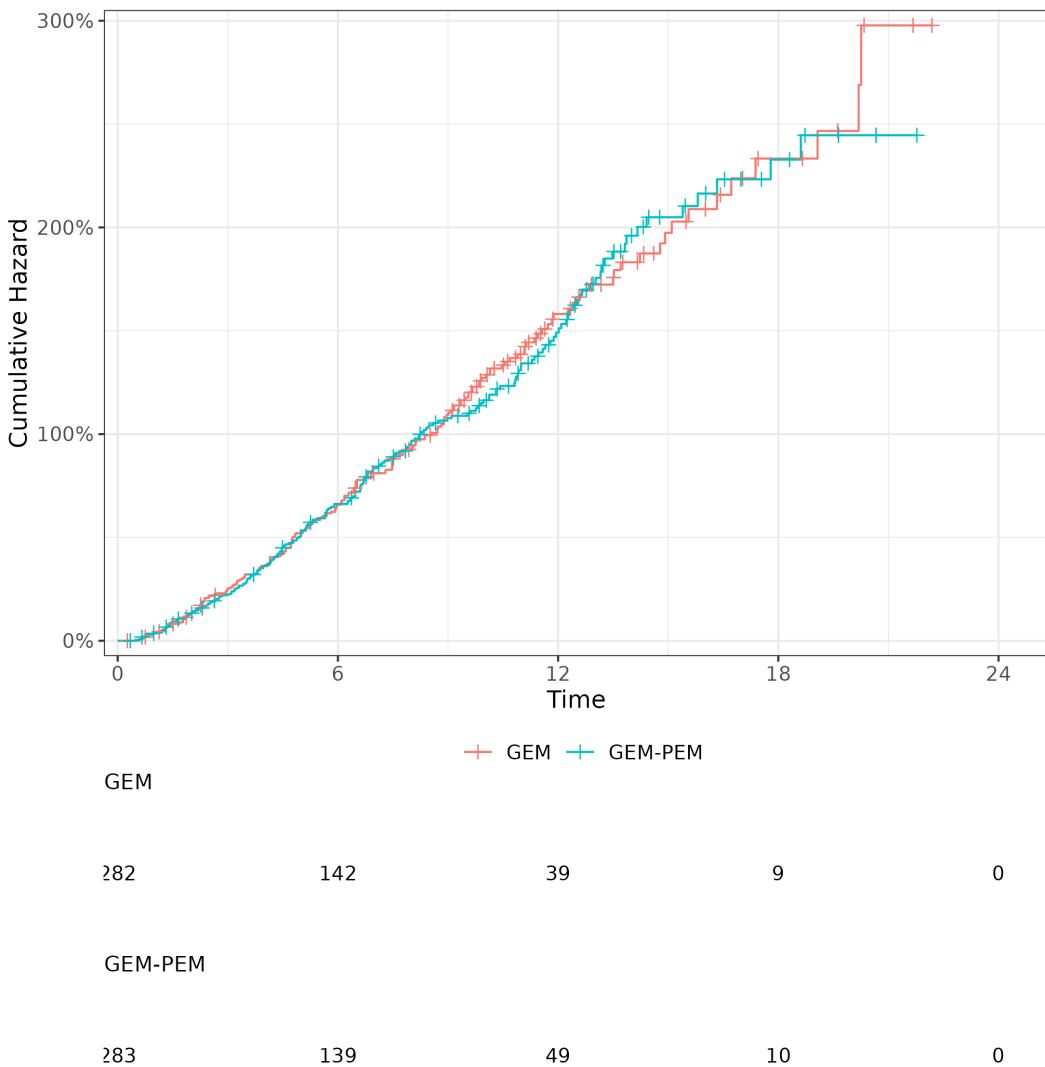


Figure A.10: Rocha Lima 2004 Cumulative Hazard

APPENDIX
B

SURVIVAL DISTRIBUTIONS REFERENCE

This appendix outlines the mathematical definitions of the parametric and non-parametric survival models used in this project. In addition, some information on model selection is given.

B.1 Parametric Survival Models

B.1.1 Exponential Model

The survival function for the exponential model is given by

$$S(t|\lambda) = \exp(-\lambda t)$$

for $\lambda > 0$.

B.1.2 Gamma

The survival function for the gamma model is give by

$$S(t|a, \mu) = 1 - \int_0^t \frac{x^{a-1} \exp(-x/\mu)}{\mu^a \Gamma(a)} dx$$

for $\mu > 0, a > 0$.

B.1.3 Generalised Gamma

The survival function for the generalised gamma model, by default, uses the Prentice parameterisation [REFERENCE]. The survival function is given by

$$S(t|\mu, \sigma, Q) = \begin{cases} S_G\left(\frac{\exp(Qw)}{Q^2} \mid \frac{1}{Q^2}, 1\right) & \text{if } Q > 0 \\ S_L(t|\mu, \sigma) & \text{if } Q = 0 \\ 1 - S_G\left(\frac{\exp(Qw)}{Q^2} \mid \frac{1}{Q^2}, 1\right) & \text{if } Q < 0 \end{cases}$$

Where S_G, S_L are the survival functions gor the gamma and log-normal distributions respectively. In addition, $w = \frac{\log(t)-\mu}{\sigma}$. Where $\sigma > 0$.

B.1.4 Gompertz

The survival function for the Gompertz model is given by

$$S(t|a, b) = \exp(-(b/a) \exp(at) - 1)$$

for $b > 0$.

Remark B.1.1: Gompertz special case

Strictly speaking, $a < 0$ is permitted, however, this causes the survival function to take the form $S(t|a, b) = \exp(b/a \exp(at) - 1)$. We therefore have, using the fact that $\lim_{t \rightarrow \infty} \exp(at) = 0$,

$$\begin{aligned} S(t) &= \exp(b/a \exp(at) - 1) \\ \lim_{t \rightarrow \infty} S(t) &= \lim_{t \rightarrow \infty} \exp(b/a \exp(at) - 1) \\ \lim_{t \rightarrow \infty} S(t) &= \exp(-1). \end{aligned}$$

Therefore, $S(t)$ tending to a non-zero probability as $t \rightarrow \infty$ is clinically implausible.

B.1.5 Log-Logistic

The survival function for the log-logistic model is given by

$$S(t|a, b) = \frac{1}{1 + (t/b)^a}$$

for $a > 0, b > 0$.

B.1.6 Log-Normal

The survival function for the log-normal model is given by

$$S(t|\mu, \sigma) = 1 - \int_0^t \frac{1}{x\sigma\sqrt{2\pi}} \exp\left(-\frac{(\log x - \mu)^2}{2\sigma^2}\right) dx$$

for $\sigma > 0$.

B.1.7 Weibull

The AFT Weibull parameterisation is used in this project. The survival function for the AFT Weibull is given by

$$S(t|\mu, a) = \exp(-(t/\mu)^a)$$

B.2 Selection of Survival Models

Selecting the survival model for a given study is done for the GEM arm only, as this is the reference treatment. Akaikie's Information Criterion (AIC) [REFERENCE] is used.

Definition B.2.1: Akaikie's Information Criterion

For a given set of models, the Akaikie's Information Criterion (AIC) score is given by

$$AIC = 2k - 2 \log(\hat{L}).$$

Where k is the number of parameters in the model, and \hat{L} be the maximised value of the likelihood function for the model.

When selecting models based on AIC score, the lowest scoring model is considered the best fitting model. The intrinsic value of the scores is irrelevant, only their values relative to one another. Models with an AIC score of ≤ 2 of the best fitting model are also considered well-fitting models.

ADDITIONAL SURVIVAL RESULTS

C.1 Parametric Models

C.1.1 OS Models Medians

Distribution	Treatment	Median	L95	U95
Observed	GEM	8.5157	7.412	10.2119
	GEM-CIS	7.2514	6.3844	8.7499
Exponential	GEM	8.1234	6.9493	9.4466
	GEM-CIS	7.6616	6.6008	8.9021
Gamma	GEM	8.7724	7.6247	10.003
	GEM-CIS	8.0314	6.9656	9.1877
Generalised Gamma	GEM	8.2727	7.1396	9.6683
	GEM-CIS	7.3009	6.2946	8.5681
Gompertz	GEM	8.5075	7.2161	9.8798
	GEM-CIS	7.3675	6.1209	8.7140
Log-logistic	GEM	8.0213	6.9556	9.2219
	GEM-CIS	7.1097	6.1058	8.2559
Log-normal	GEM	7.6805	6.6084	8.8155
	GEM-CIS	6.8680	5.9323	8.0454
Weibull	GEM	8.8475	7.7009	10.2251
	GEM-CIS	7.9688	6.7904	9.3044

Table C.1: Median OS given by parametric models in the Colucci study

Distribution	Treatment	Median	L95	U95
Observed	GEM	6.0892	5.4991	7.3400
	GEM-CAP	7.1984	6.3016	7.9773
Exponential	GEM	5.6085	4.9624	6.3901
	GEM-CAP	6.6375	5.8911	7.5465
Gamma	GEM	6.4666	5.8425	7.1250
	GEM-CAP	7.4944	6.7405	8.3269
Generalised Gamma	GEM	6.1874	5.5036	7.0080
	GEM-CAP	7.2947	6.4937	8.1853
Gompertz	GEM	6.4492	5.6250	7.2386
	GEM-CAP	7.3936	6.4646	8.3530
Log-logistic	GEM	5.9954	5.3559	6.6976
	GEM-CAP	7.0087	6.2950	7.7824
Log-normal	GEM	5.7668	5.1624	6.4003
	GEM-CAP	6.6665	5.9897	7.5201
Weibull	GEM	6.6091	5.9635	7.3700
	GEM-CAP	7.6326	6.8715	8.5703

Table C.2: Median OS given by parametric models in the Cunningham study

Distribution	Treatment	Median	L95	U95
Observed	GEM	9.9477	7.2714	11.185
	GEM-AXI	9.0388	7.0821	10.377
Exponential	GEM	10.1538	8.3617	12.2346
	GEM-AXI	9.8440	8.0866	11.9079
Gamma	GEM	8.2747	7.3351	9.3104
	GEM-AXI	8.1444	7.0687	9.2525
Generalised Gamma	GEM	8.4180	7.3651	10.0551
	GEM-AXI	8.3027	7.2284	9.8471
Gompertz	GEM	8.4702	7.6250	9.3354
	GEM-AXI	8.3951	7.5094	9.4282
Log-Logistic	GEM	8.3027	7.2623	9.5072
	GEM-AXI	8.1373	7.1005	9.3542
Log-normal	GEM	8.5320	7.3888	9.8280
	GEM-AXI	8.4620	7.2940	9.8507
Weibull	GEM	8.2853	7.3825	9.3263
	GEM-AXI	8.1662	7.2363	9.2119

Table C.3: Median OS given by parametric models in the Kindler study

Distribution	Treatment	Median	L95	U95
Observed	GEM	6.1769	5.5159	7.2945
	GEM-PEM	6.4053	5.4246	6.9519
Exponential	GEM	5.8920	5.1904	6.6821
	GEM-PEM	5.9741	5.2446	6.7782
Gamma	GEM	6.4966	5.8781	7.1511
	GEM-PEM	6.5691	5.9370	7.2294
Generalised Gamma	GEM	6.1225	5.4698	6.8491
	GEM-PEM	6.2246	5.5628	7.0092
Gompertz	GEM	6.5459	5.7562	7.3281
	GEM-PEM	6.6121	5.7187	7.3890
Log-Logistic	GEM	6.0681	5.4335	6.7508
	GEM-PEM	6.1365	5.4998	6.9122
Log-normal	GEM	5.9424	5.3308	6.6071
	GEM-PEM	6.0029	5.3325	6.6544
Weibull	GEM	6.6223	5.9917	7.3652
	GEM-PEM	6.6945	6.0326	7.4350

Table C.4: Median OS given by parametric models in the Oettle study

Distribution	Treatment	Median	L95	U95
Observed	GEM	6.7424	5.6812	7.9758
	GEM-IRI	6.3989	4.8554	7.6321
Exponential	GEM	6.0863	5.2315	7.0918
	GEM-IRI	5.8213	5.0071	6.8319
Gamma	GEM	6.7650	5.9739	7.6337
	GEM-IRI	6.1703	5.3646	7.1195
Generalised Gamma	GEM	6.4347	5.5706	7.4502
	GEM-IRI	6.1123	5.1773	7.3023
Gompertz	GEM	6.8572	5.8092	7.9001
	GEM-IRI	6.2212	5.1709	7.3794
Log-Logistic	GEM	6.2578	5.4026	7.2107
	GEM-IRI	5.7680	4.9301	6.8834
Log-normal	GEM	6.0975	5.2549	7.0205
	GEM-IRI	5.3922	4.6066	6.4738
Weibull	GEM	6.8985	6.0681	7.9502
	GEM-IRI	6.2512	5.3474	7.2818

Table C.5: Median OS given by parametric models in the Rocha Lima study

NMA OF PANCREATIC CANCER TRIALS USING MEDIAN OS

This appendix presents NMA results using median OS as the outcome measure instead of

D.1 Parametric Models

Table D.1 presents the input data used for the parametric NMA.

Distribution	Treatment	Median	L95	U95	Study	n	SE
Gompertz	GEM	8.5075	7.0869	9.9992	Colucci	400	14.859
Generalised Gamma	GEM-CIS	7.3009	6.2111	8.5350	Colucci	400	11.857
Log-Logistic	GEM	5.9954	5.4301	6.6452	Cunningham	533	7.1564
Generalised Gamma	GEM-CAP	7.2947	6.5520	8.1846	Cunningham	533	9.6151
Exponential	GEM	10.154	8.5389	12.230	Kindler	632	23.675
Exponential	GEM-AXI	9.8440	8.0901	11.928	Kindler	632	24.613
Generalised Gamma	GEM	6.1225	5.4602	6.9002	Oettle	565	8.7319
Gamma	GEM-PEM	6.5691	5.9814	7.2575	Oettle	565	7.7381
Gamma	GEM	6.7650	5.9708	7.6333	Rocha Lima	360	8.0471
Weibull	GEM-IRI	6.2512	5.3539	7.3042	Rocha Lima	360	9.4399

Table D.1: Input data for the parametric NMA

Figure D.1 presntes the forest plots of the NMA conducted on median survival estimates. Both fixed and random effects models were fit. There was little difference between the two models, as shown by the selection statistics in Table ???. Note that the forest plots in Figure D.1 have been zoomed in to show the differences more clearly, the full figures are presented in Section E, along with further model diagnostic plots. The models were fit with uninformative priors of $N(0, 100^2)$, $N(0, 10^2)$, and $hN(0, 5^2)$ for the intercept, treatment and heterogeneity respectively. Here hN is the half-normal distribution. The trace plots, as presented in Section E suggested good convergence for both models.

Model	pD	DIC
Fixed Effects	6.5	13.1
Random Effects	6.6	13.3

Table D.2: Model selection statistics for the parametric NMA (Medain OS) models

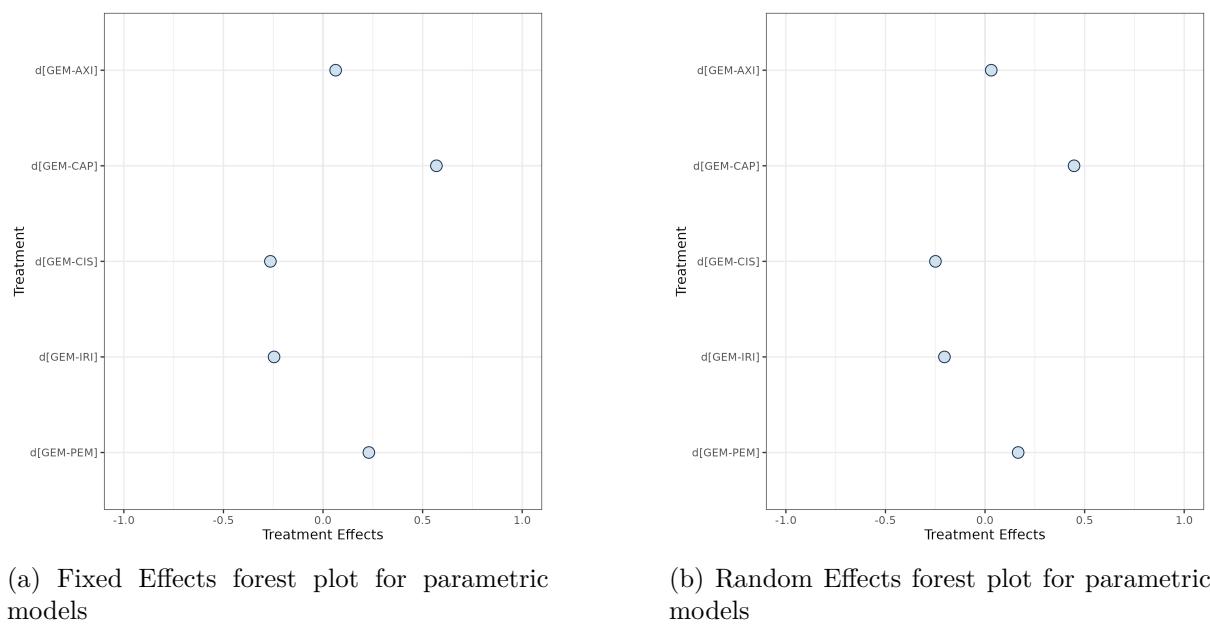


Figure D.1: Forest plots for the fixed and random effects models of survival

ADDITIONAL NMA RESULTS

E.1 Parametric Models - RMST NMA

E.1.1 Fixed Effect Model

E.1.1.1 12 Month Timepoint

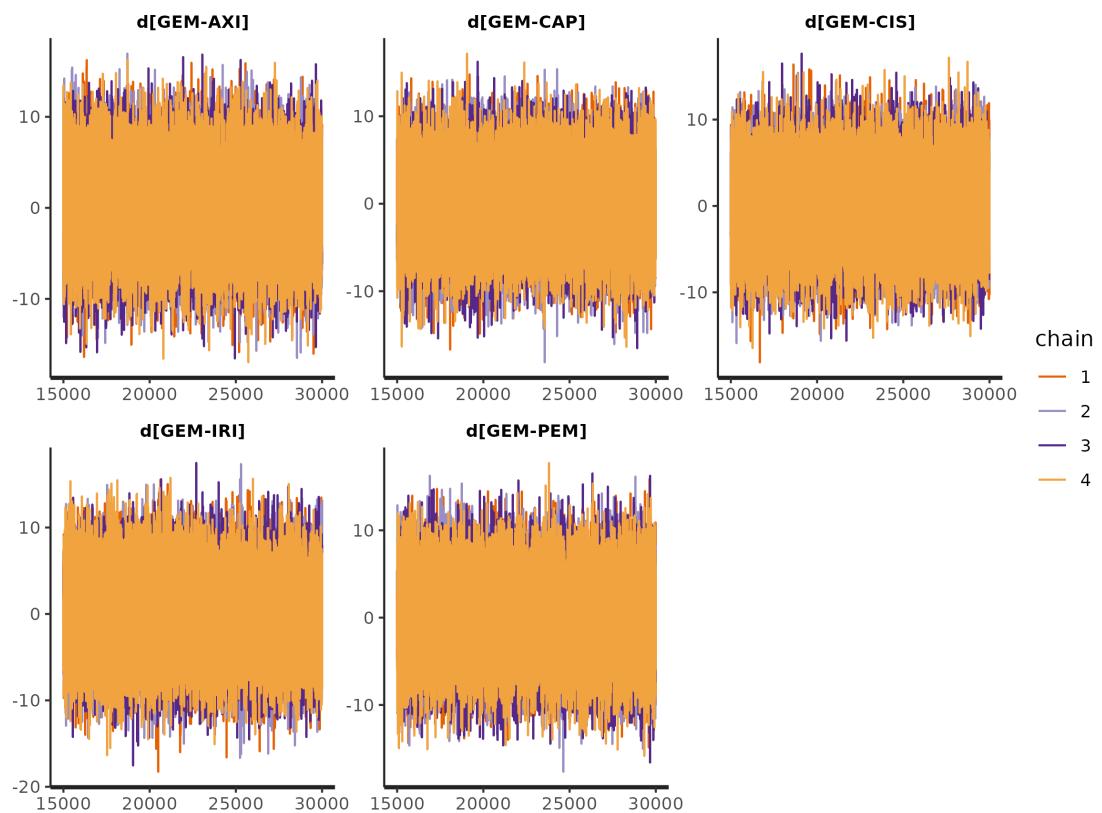


Figure E.1: Trace plot of the fixed effect parametric NMA - 12 month timepoint

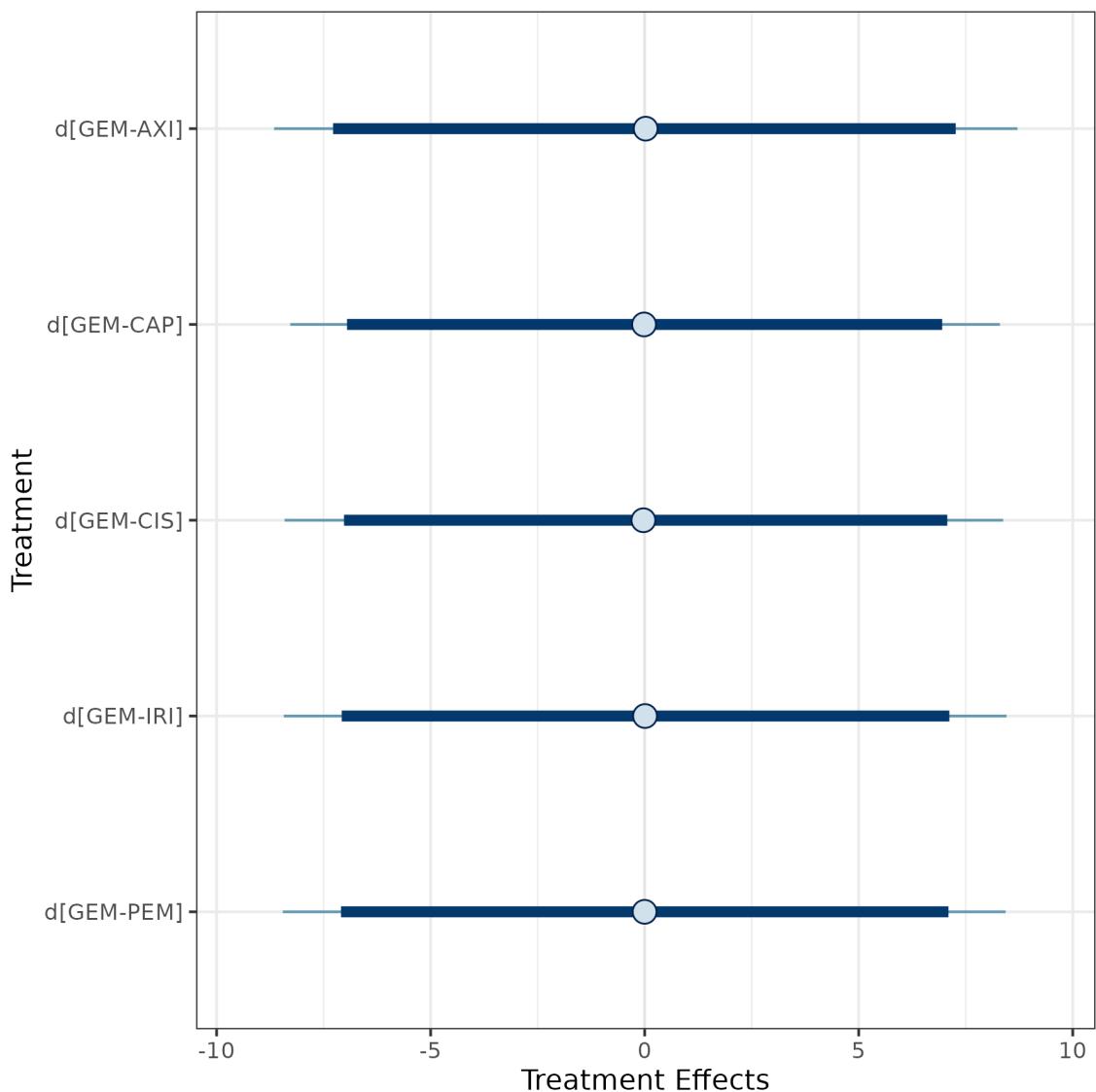


Figure E.2: Full forest plot of the fixed effect parametric NMA - 12 month timepoint

E.1.1.2 18 Month Timepoint

E.1.1.3 24 Month Timepoint

E.2 Random Effects Model

E.2.0.1 12 Month Timepoint

E.2.0.2 18 Month Timepoint

E.2.0.3 24 Month Timepoint

E.3 Parametric Models - Median OS NMA

E.3.1 Fixed Effect Model

E.4 Random Effects Model

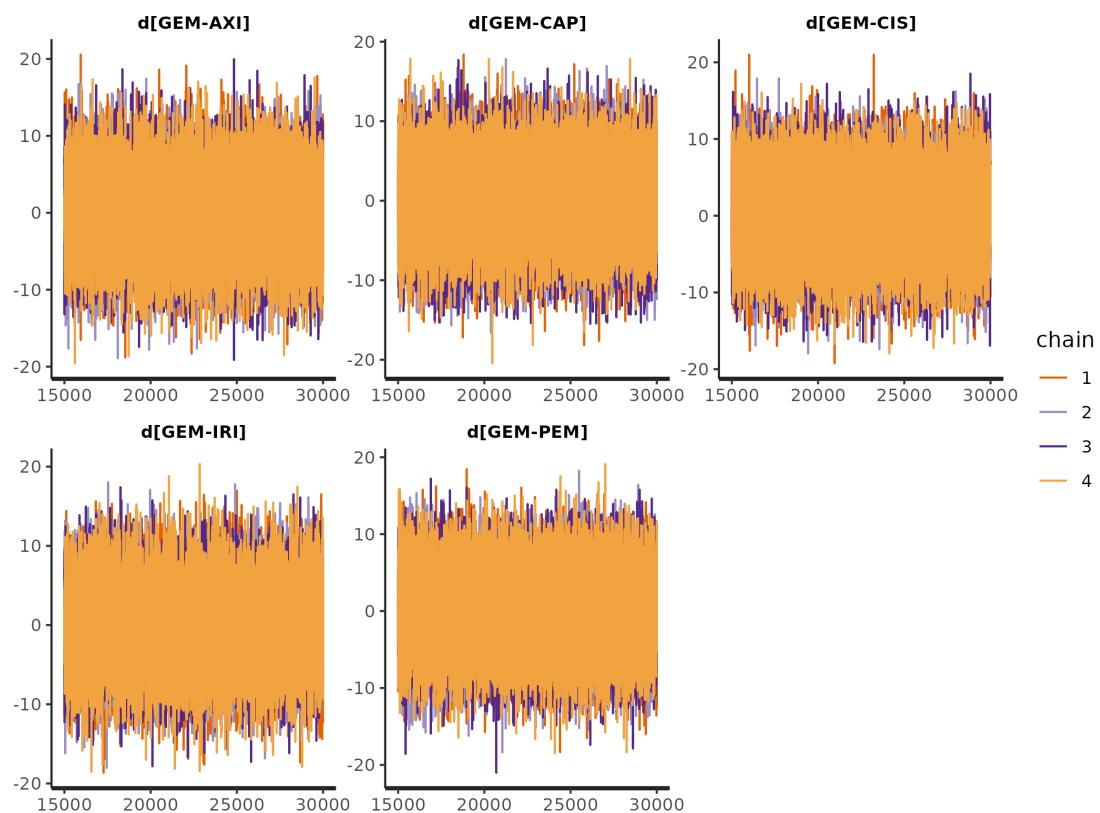


Figure E.3: Trace plot of the fixed effect parametric NMA - 18 month timepoint

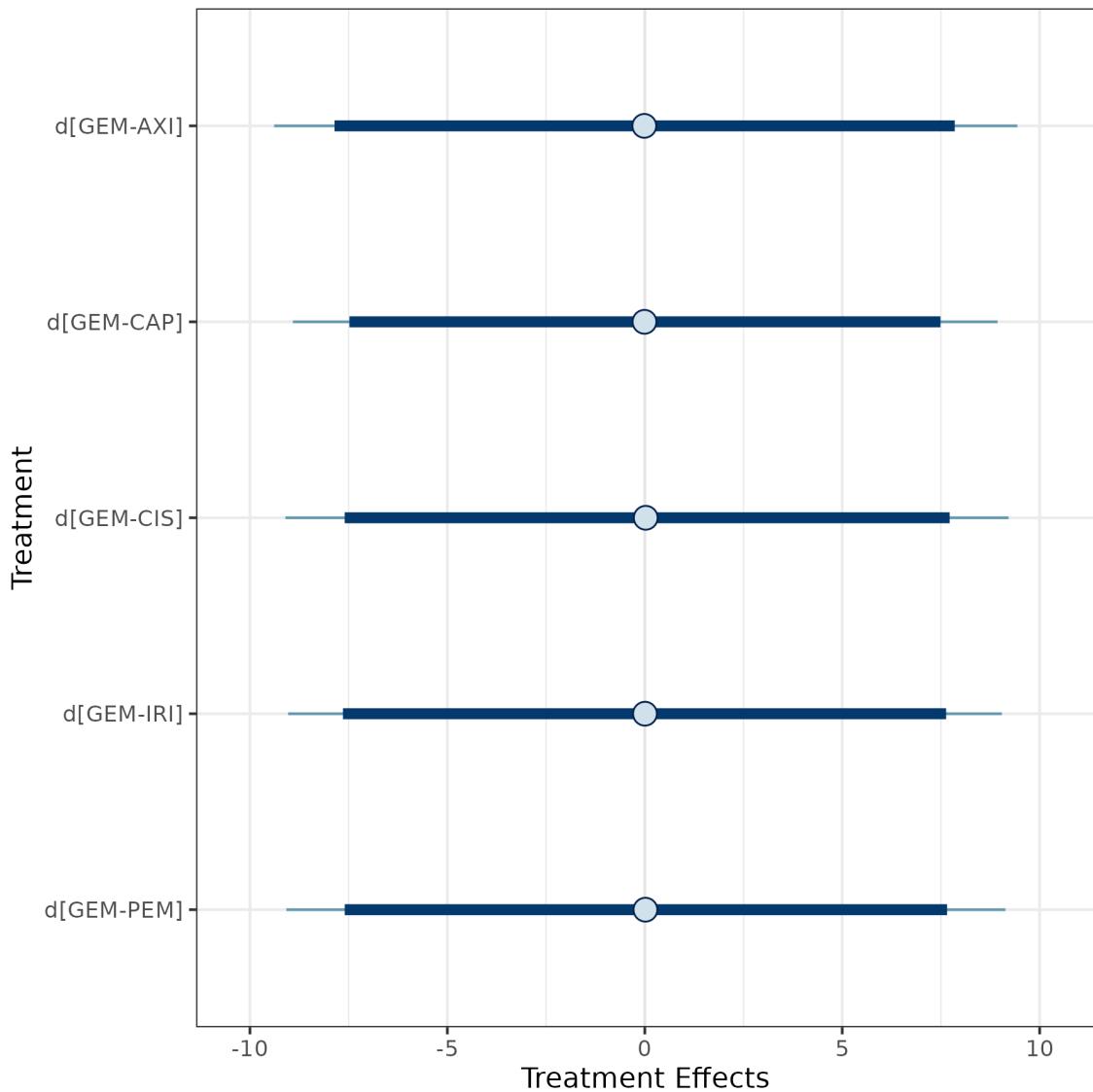


Figure E.4: Full forest plot of the fixed effect parametric NMA - 18 month timepoint

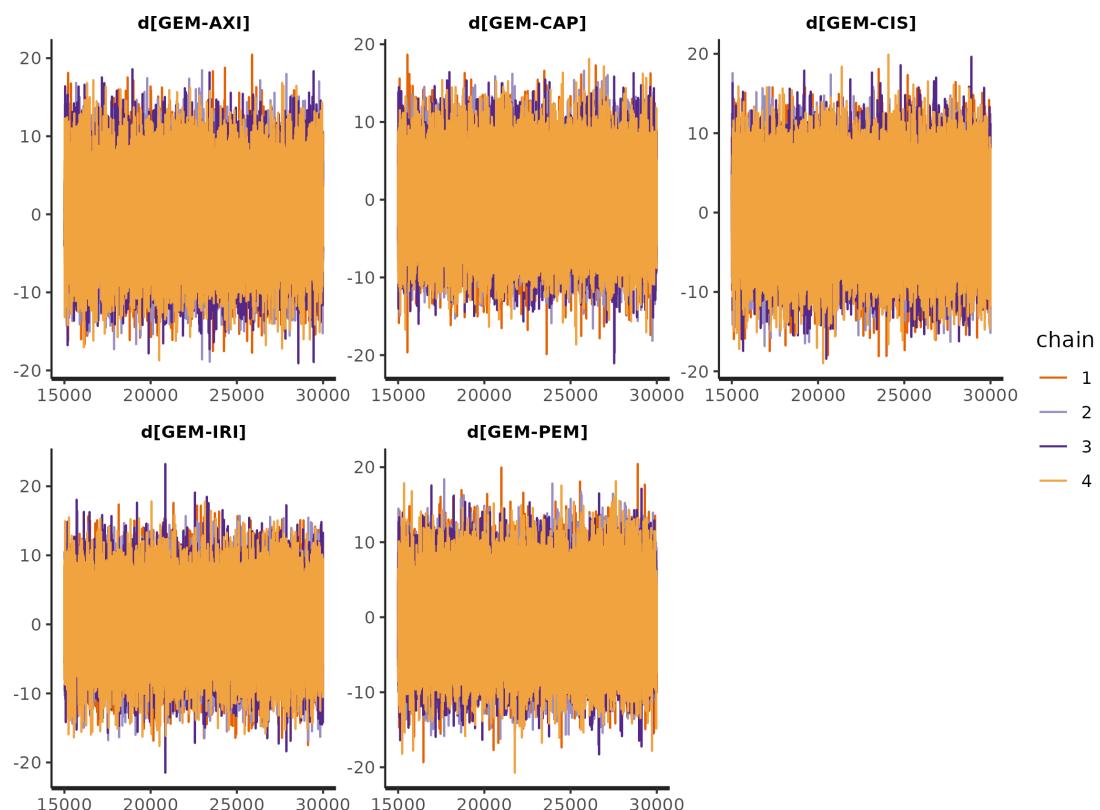


Figure E.5: Trace plot of the fixed effect parametric NMA - 24 month timepoint

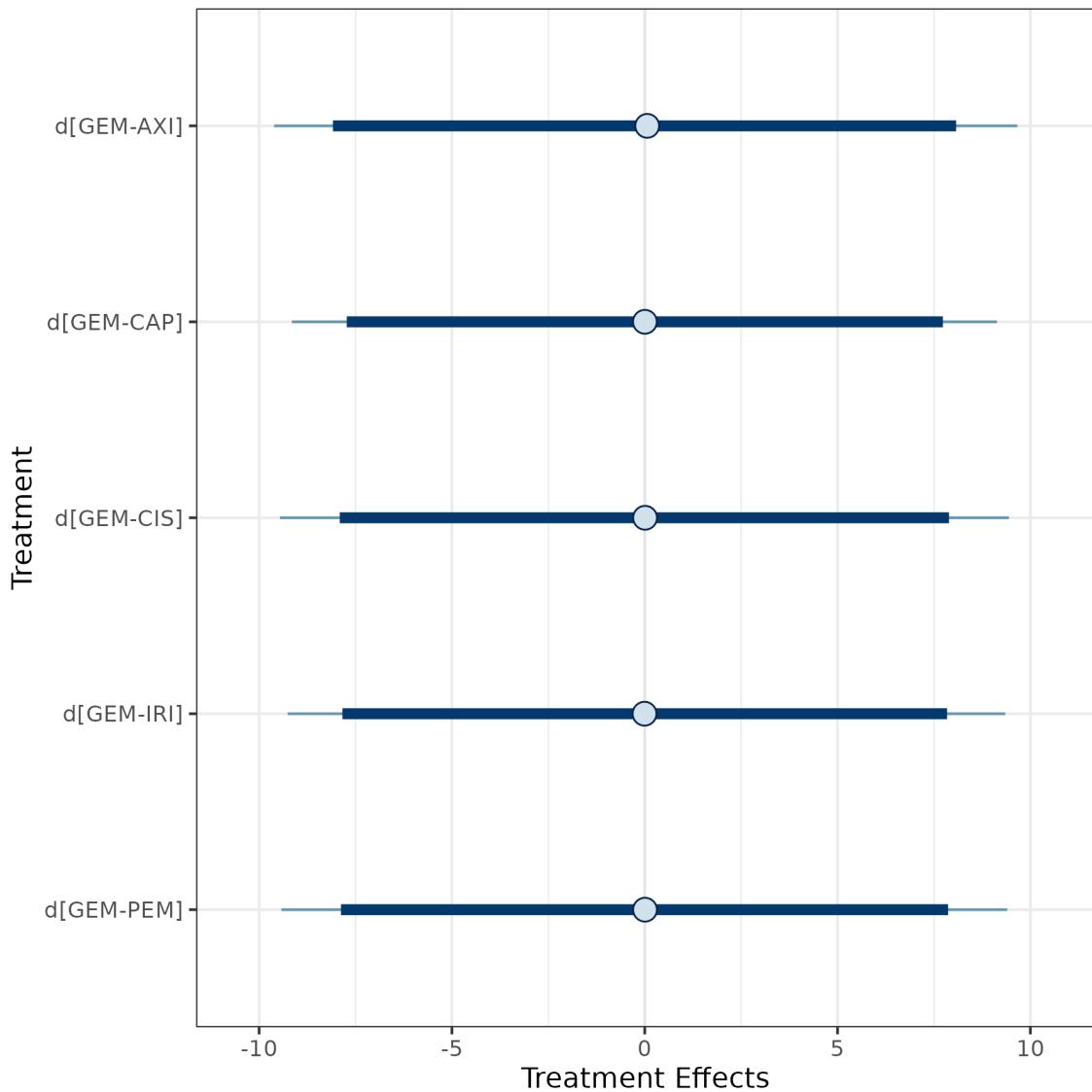


Figure E.6: Full forest plot of the fixed effect parametric NMA - 24 month timepoint

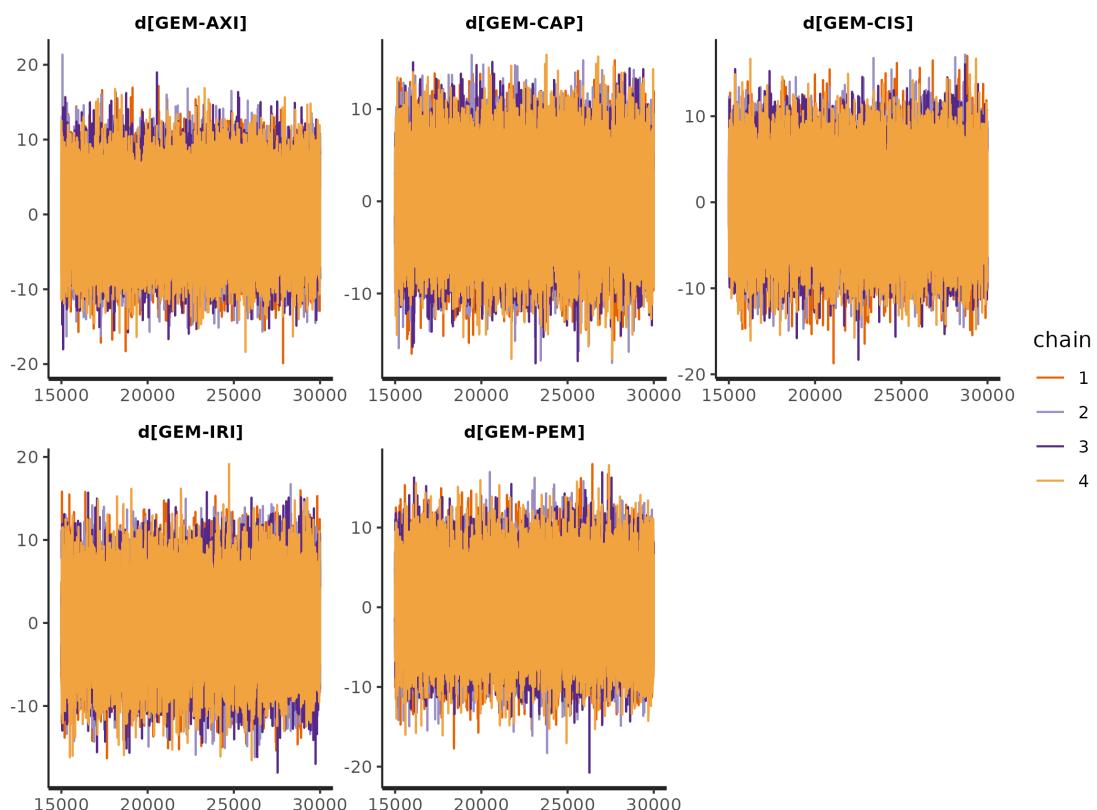


Figure E.7: Trace plot of the fixed effect parametric NMA - 12 month timepoint

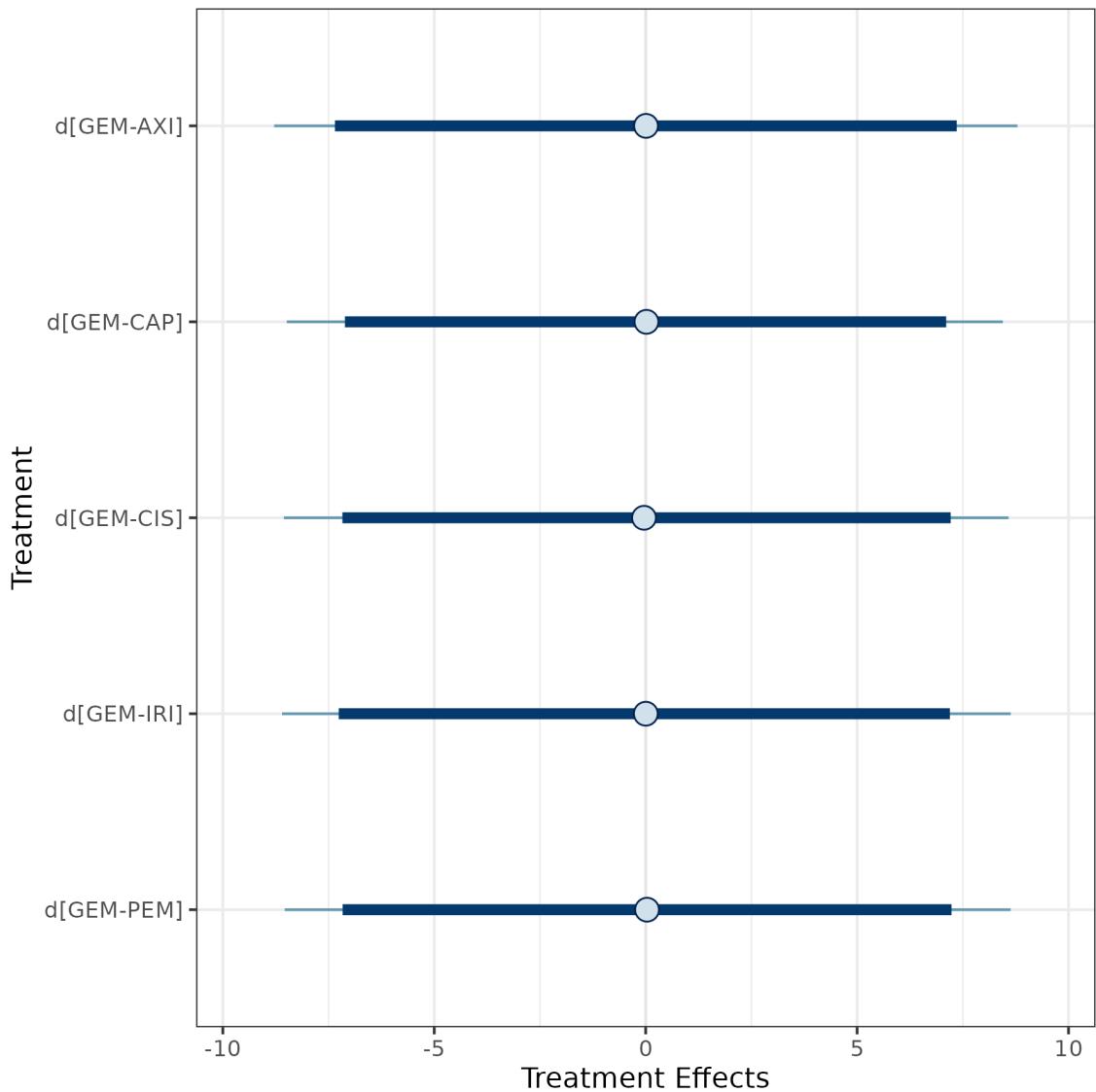


Figure E.8: Full forest plot of the random effects parametric NMA - 12 month timepoint

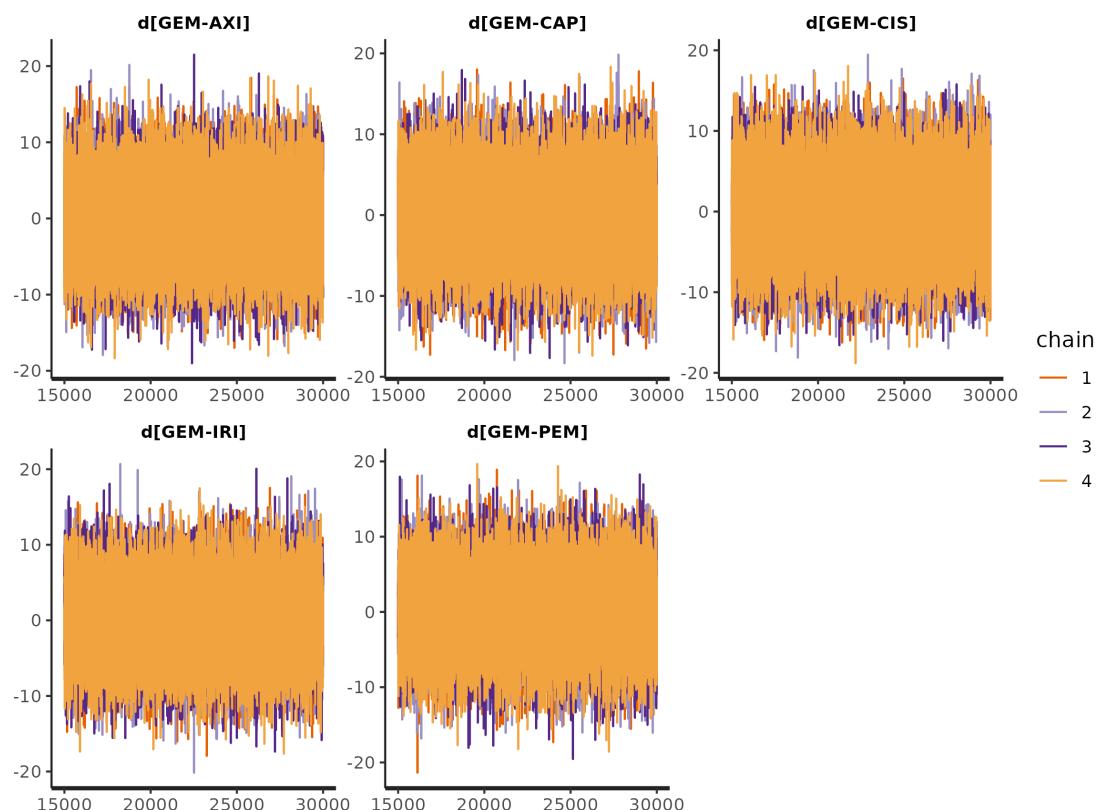


Figure E.9: Trace plot of the fixed effect parametric NMA - 18 month timepoint

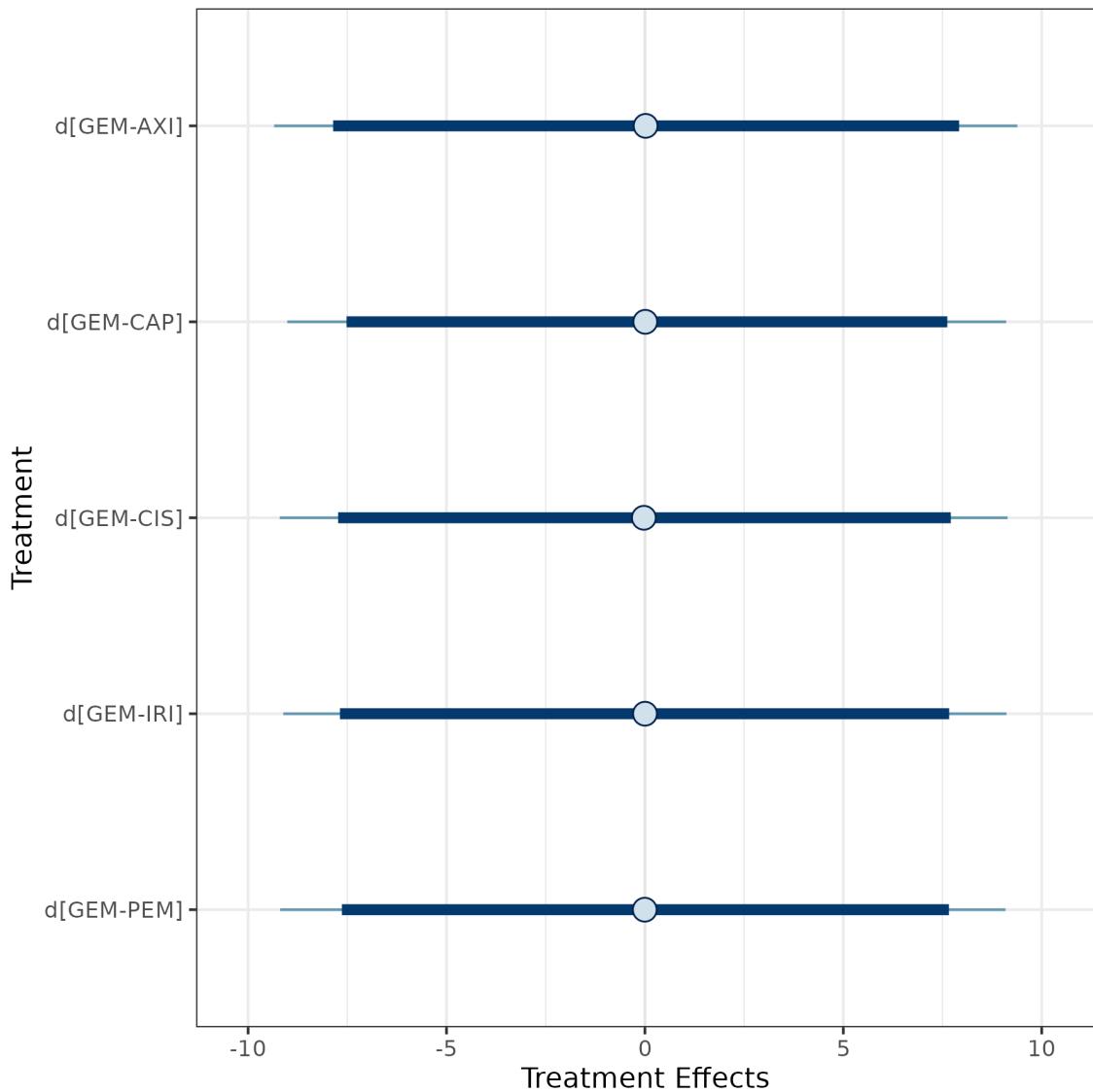


Figure E.10: Full forest plot of the random effects parametric NMA - 18 month timepoint

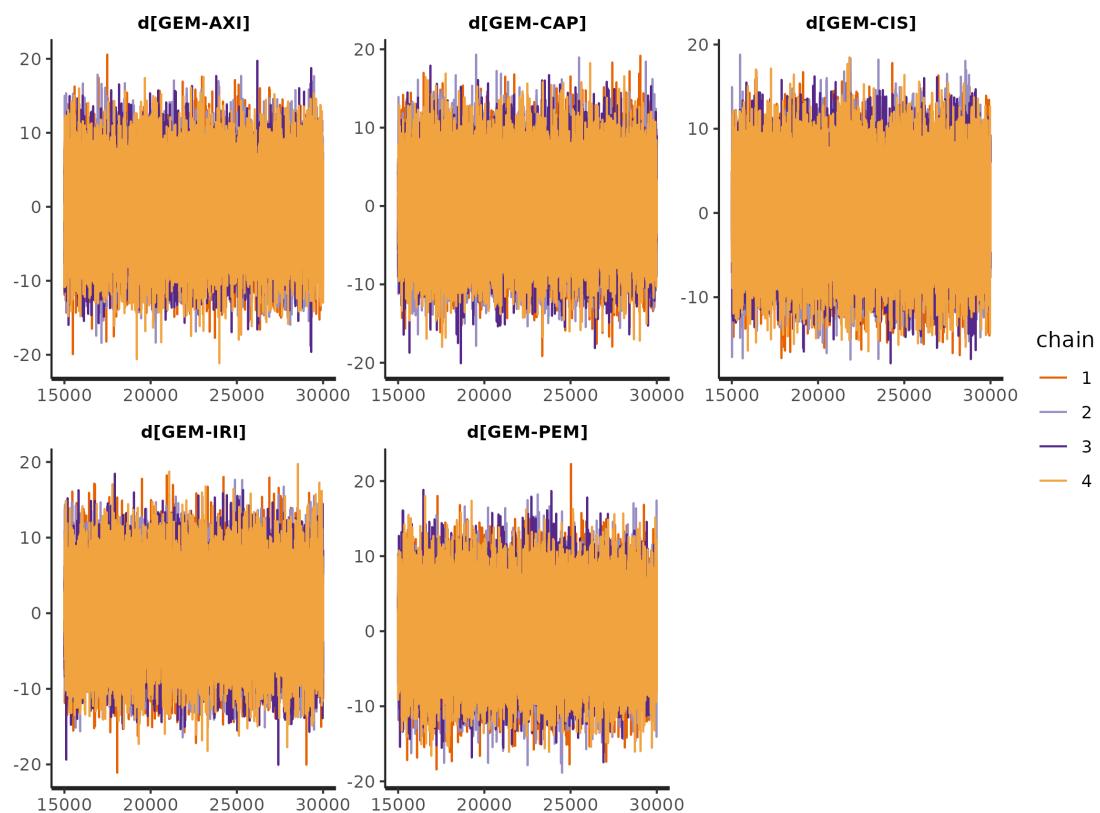


Figure E.11: Trace plot of the fixed effect parametric NMA - 24 month timepoint

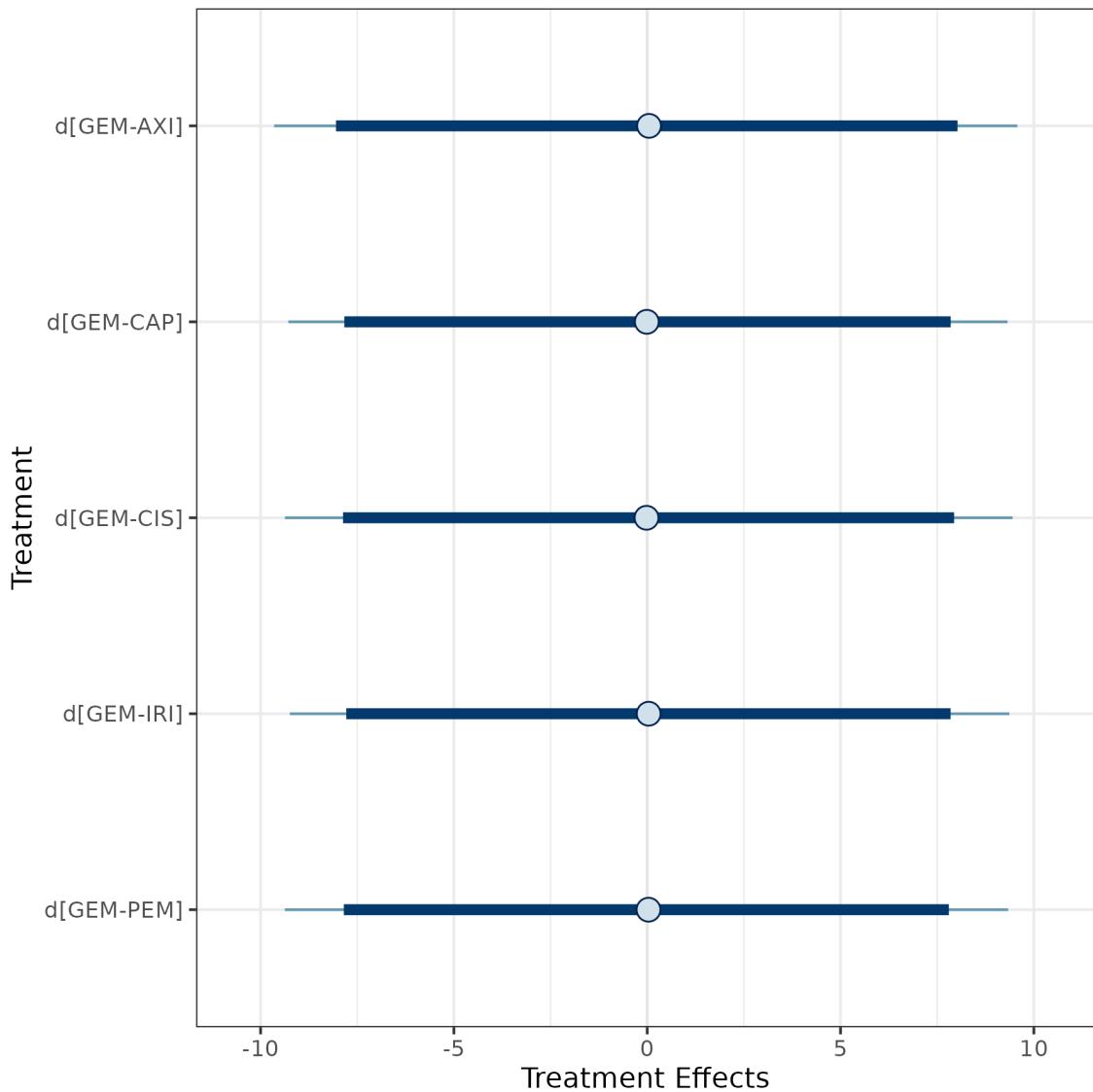


Figure E.12: Full forest plot of the random effects parametric NMA - 24 month timepoint

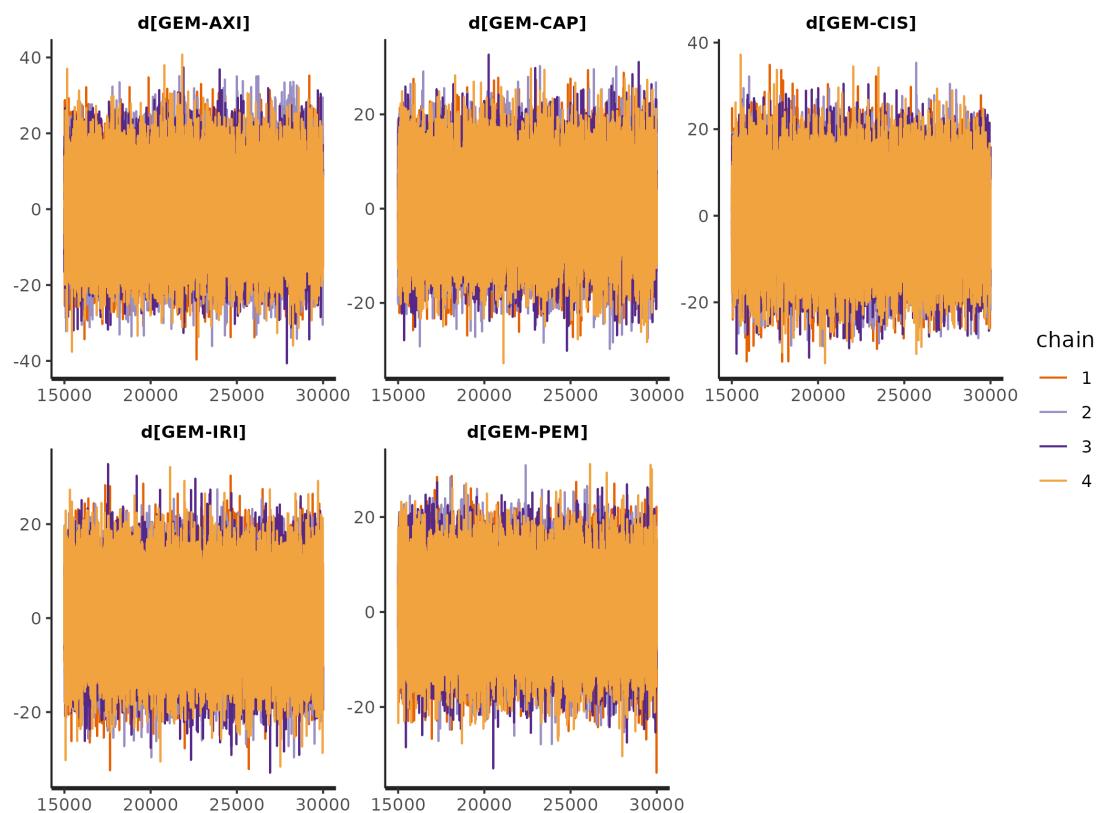


Figure E.13: Trace plot of the fixed effect parametric NMA

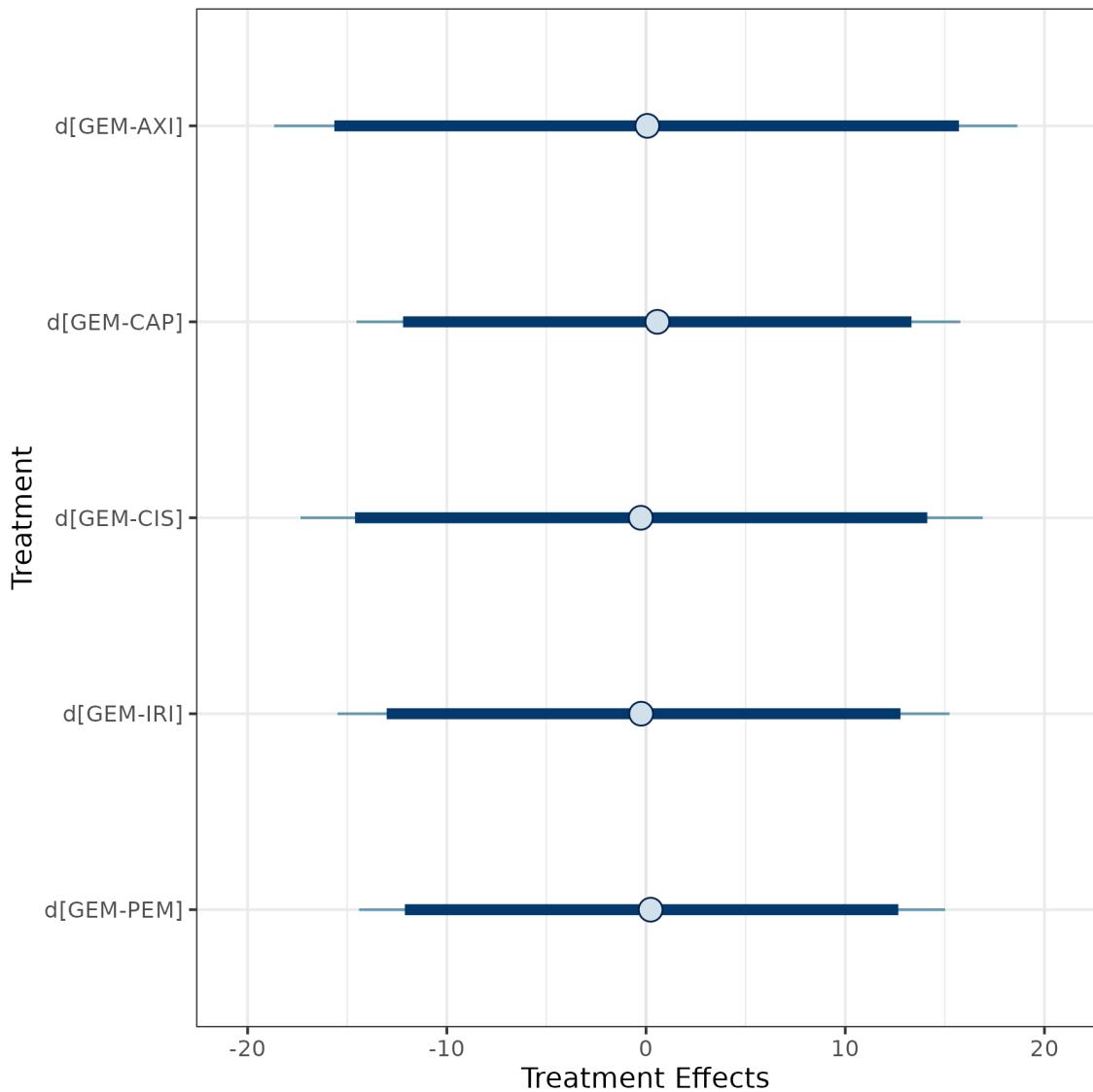


Figure E.14: Full forest plot of the fixed effect parametric NMA

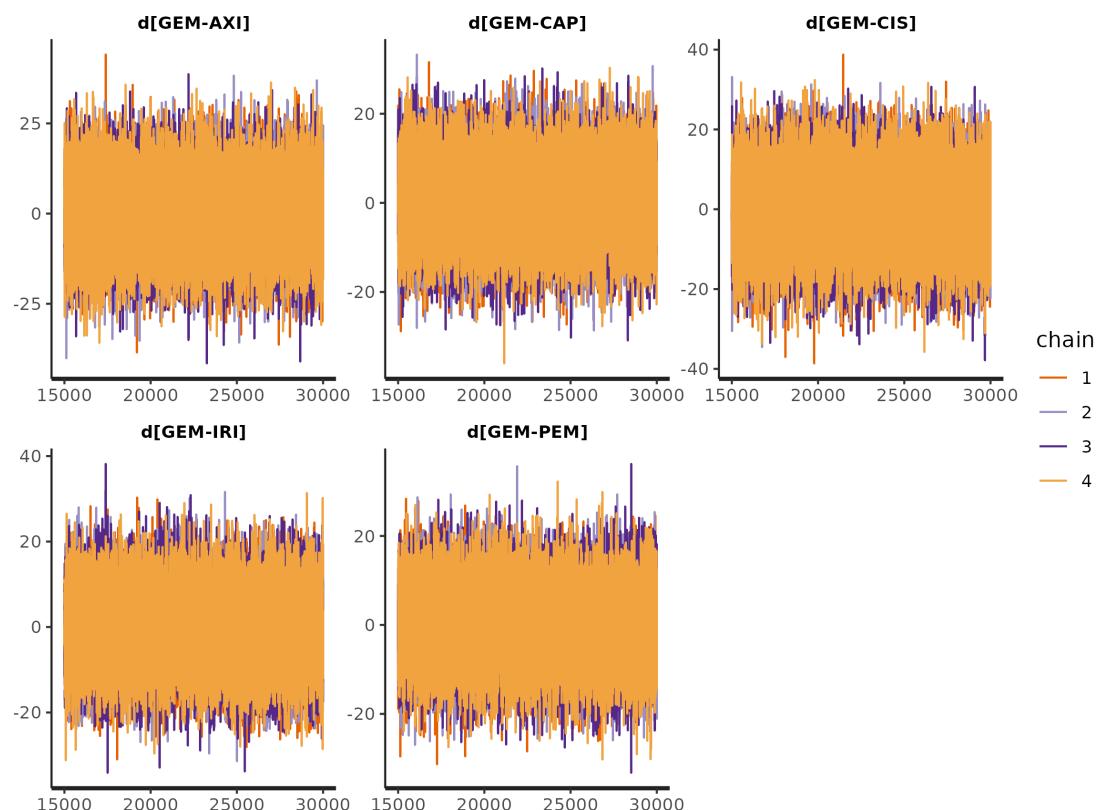


Figure E.15: Trace plot of the fixed effect parametric NMA

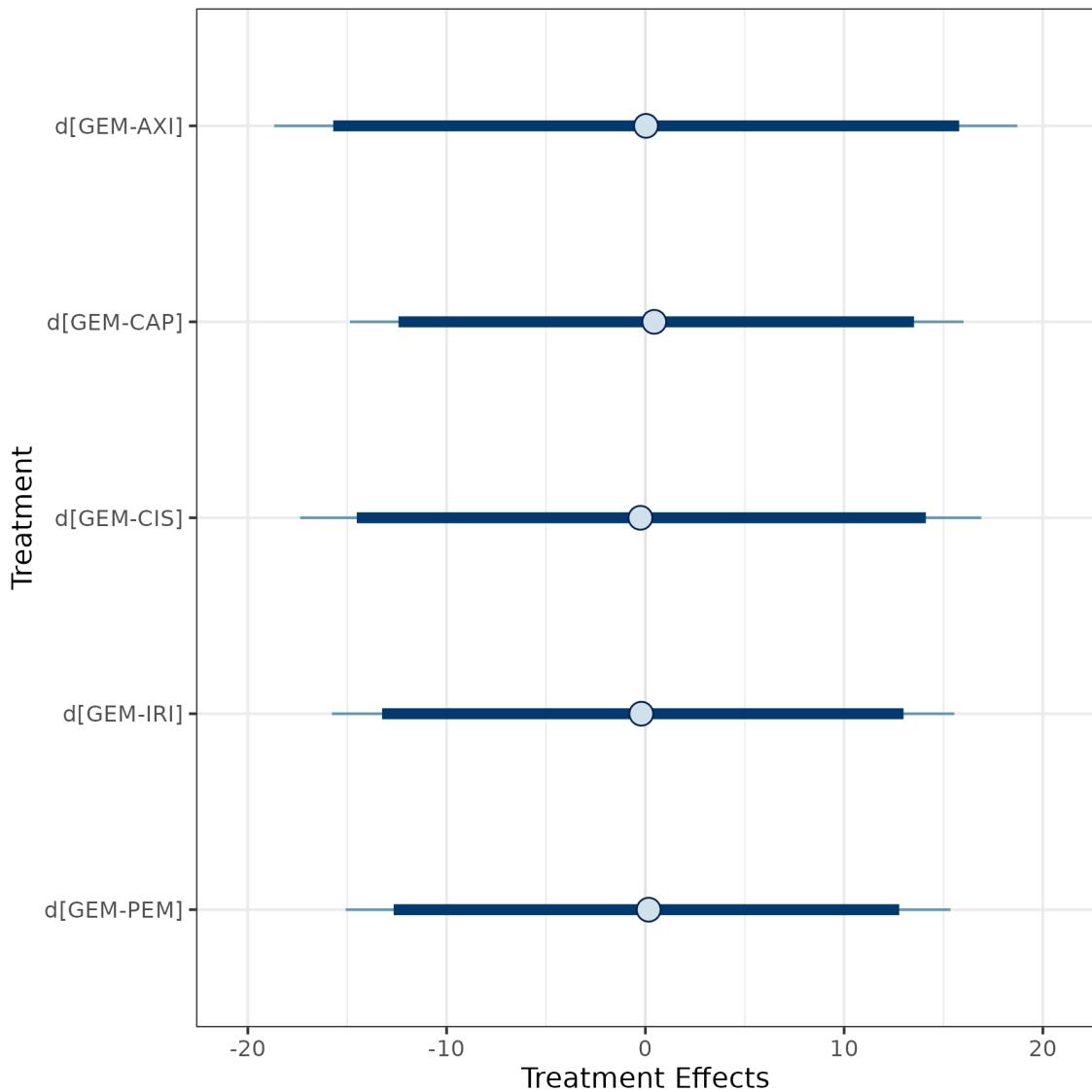


Figure E.16: Full forest plot of the random effects parametric NMA

THE PCNMA PACKAGE

To facilitate the analysis conducted in this project, an R package was constructed. Performing the analysis in this way ensures easy reproducibility for further analysis in the future. The package is roughly split into two parts: survival code, and NMA code.

F.1 Survival Functions

The central function in the package for survival analysis is the *fit_distribution* function. This function is a wrapper around the *flexsurvreg* function from *flexsurv*. It is designed to take a list object containing the names of distributions and the associated argument to pass that distribution to *flexsurv*. For example,

```
1 distributions <- list("Weibull" = "weibull")
```

The reason for defining the distributions in this way is because the default *Flexsurv* arguments are somewhat untidy. For example, the exponential distribution is passed as just “exp”. The beauty of the *fit_distribution* function is that several distributions can be passed with a tidier name, which *flexsurvreg* never sees. This purely aesthetic change can be seen by comparing Figure F.1, and Figure F.2.

Any default *flexsurv* distribution will work with *fit_distribution*, it just needs a suitable name in the list object . The *fit_distribution* function itself doesn’t actually fit any distributions. There is a sub-function, *.fit_distribution* which takes a single distribution as an argument, and some data on which to fit that distribution. This function takes the “weibull” element of the above list and passes it to *flexsurv*. The *fit_distribution* function maps *.fit_distribution* across the list of distributions, using the *purrr::map* function [Wickham and Henry, 2023]. After some data cleaning, the object that is returned by *fit_distribution* is given the class “*fitted_distribution*”.

Several S3 methods exist for objects of class “*fitted_distribution*”, these are *plot.fitted_distribution*, *summary.fitted_distribution*, and *coef.fitted_distribution*. These functions allow for plotting fitted models, accessing information such as AIC scores, and accessing the model coefficients respectively.

Package ‘PancSurv’

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Type Package

Title Parametric and Non-Parametric Survival Models in Pancreatic Cancer Trials

Version 0.1

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Description This package contains the functions and data for my MSc Thesis, concerning the use of parametric and non-parametric models for survival in pancreatic cancer

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Encoding UTF-8

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.fit_distribution *Fit a single survival distribution*

Description

This function is a wrapper on ‘flexsurv::flexsurvreg‘, and fits a single distribution to the specified data.

Usage

```
.fit_distribution(distribution, data, strata = "Treatment")
```

Arguments

distribution	A single distribution
data	An IPD dataset
strata	Strata for the RHS of the ‘survival::Surv‘ function

Value

A [flexsurv::flexsurvreg] object

boxTid *Box-Tidwell Transformation*

Description

Box-Tidwell Transformation

Usage

```
boxTid(x, p)
```

Arguments

x	A real value
p	The p-value to raise x to

```
coef.fitted_distribution  
Coefficients of fitted models
```

Description

Coefficients of fitted models

Usage

```
## S3 method for class 'fitted_distribution'  
coef(fit, studies, ...)
```

Arguments

fit	A [PCNMA::fitted_distribution] object
...	for S3 consistency

```
fit_distribution      Fit survival distributions to a dataset.
```

Description

This function extends the ‘PCNMA:::fit_distribution’ function, by fitting a given set of distributions to a TTE dataset.

Usage

```
fit_distribution(distributions, data, strata = "Treatment", maxT = 60)
```

Arguments

distributions	A list of distributions
data	An IPD dataset
strata	Stratification variables
maxT	maximum time to calculate fitted values at

Value

A dataframe with fitted values

fit_model*Run an NMA***Description**

Run an NMA

Usage

```
fit_model(network, effects, iter, seed = 1, chains = 4)
```

Arguments

<code>network</code>	A [multinma::nma_data] object
<code>L</code>	Character string specifying a likelihood function
<code>link</code>	Character string specifying a link function (defaults to "log")
<code>...</code>	Other parameters to pass to [multinma::nma]

gen_network*Generate a network of evidence***Description**

Generate a network of evidence

Usage

```
gen_network(net_data, ref)
```

Arguments

<code>net_data</code>	A dataset created by [PCNMA::gen_network_data]
<code>ref</code>	A character reference treatment

Value

A [mutlinma::nma_data] object

gen_network_data	<i>Generate network data</i>
------------------	------------------------------

Description

Generate network data

Usage

```
gen_network_data(data, ref)
```

Arguments

data	A date extraction dataset
ref	A character reference treatment

Value

A dataframe

H	<i>H-function for FPs</i>
---	---------------------------

Description

H-function for FPs

Usage

```
H(x, P, zeta, j)
```

Arguments

x	A real value
P	A vector of powers
zeta	A vector of zeta values
j	The index

<code>hr</code>	<i>Hazard Ratio</i>
-----------------	---------------------

Description

Hazard Ratio

Usage

```
hr(TTE, strata = "1")
```

Arguments

<code>TTE</code>	A TTE dataframe
<code>strata</code>	A strata variable

<code>km_estimates</code>	<i>Generate KM estimates</i>
---------------------------	------------------------------

Description

Generate Kaplan-Meier estimates from a TTE object. Uses ‘ggsurvfit::survfit2‘ to generate KM estimates. Only requires strata to be specified.

Usage

```
km_estimates(TTE, strata = "1")
```

Arguments

<code>TTE</code>	A TTE dataframe
------------------	-----------------

Value

A [PCNMA::km_obj] object

phi	<i>Fractional Polynomial Function</i>
-----	---------------------------------------

Description

Fractional Polynomial Function

Usage

```
phi(x, m, P, zeta)
```

Arguments

x	A real value
m	The degree of the polynomial
P	A vector of powers
zeta	A vector of zeta values

plot.fitted_distribution	<i>Plot a fitted distributions object</i>
--------------------------	---

Description

Creates a plot for a result of ‘PCNMA::fit_distribution’.

Usage

```
## S3 method for class 'fitted_distribution'
plot(
  fit,
  CI = FALSE,
  km = FALSE,
  km_alpha = 0.5,
  linewidth = 1,
  facet_by = "Treatment",
  ...
)
```

Arguments

fit	A ‘PCNMA::fitted_distribution’ object
CI	Include a confidence interval?
km	Add the original KM curve?
...	For S3 consistency

plot.fitted_model *Plots for an NMA model*

Description

Plots for an NMA model

Usage

```
## S3 method for class 'fitted_model'
plot(model, type = "trace", pars = parsForStan)
```

Arguments

model	A ‘PancSurv::fitted_model‘ obj
type	Type of plot to produce

plot.km_obj *Plot a KM curve*

Description

Plot a KM curve

Usage

```
## S3 method for class 'km_obj'
plot(
  fit,
  type = "survival",
  risk.table = TRUE,
  break.x.by = 5,
  xMax = 40,
  risktable.height = 0.3,
  ...
)
```

Arguments

fit	A ‘PCNMA::km_obj‘ object
type	See ‘ggsurvfit::ggsurvfit‘ for details.
risk.table	Add numbers at risk?
break.x.by	A numeric value for splitting x axis
xMax	The maximum time value to plot
risktable.height	The proportion of the figure to be taken up by the risk table
...	For S3 consistency

Value

A plotted km curve

plot_aic

Plot AIC Bar plot

Description

Plot AIC Bar plot

Usage

`plot_aic(model)`

Arguments

`model` A [PCNMA::fitted_distribution] object

plot_network

Plot a network of evidence

Description

Plot a network of evidence

Usage

`plot_network(network, ...)`

Arguments

`network` A network dataset

save_nma_summary *Write model summary to xlsx*

Description

Write model summary to xlsx

Usage

```
save_nma_summary(nma, PARAMCD, effects, model_type)
```

Arguments

nma	A [mutinma::stan_data] object
PARAMCD	one of OS or PFS
model_type	one of parametric or fp
effect	type

summary.fitted_distribution *Summary of a set of fitted models*

Description

Summary of a set of fitted models

Usage

```
## S3 method for class 'fitted_distribution'
summary(fit, AIC = FALSE, median = FALSE)
```

Arguments

fit	A 'PCNMA::fitted_distributions' object.
AIC	Returns the AIC scores for a set of models
median	Returns a table of median estimates for a set of models

summary.hr_obj	<i>Summarise a Hazard Ratio</i>
----------------	---------------------------------

Description

Summarise a Hazard Ratio

Usage

```
## S3 method for class 'hr_obj'  
summary(hr)
```

summary.km_obj	<i>Summarise KM data</i>
----------------	--------------------------

Description

Summarise KM data

Usage

```
## S3 method for class 'km_obj'  
summary(fit, ...)
```

Arguments

fit A ‘PCNMA::km_obj‘ object

Value

A summary table of the KM data

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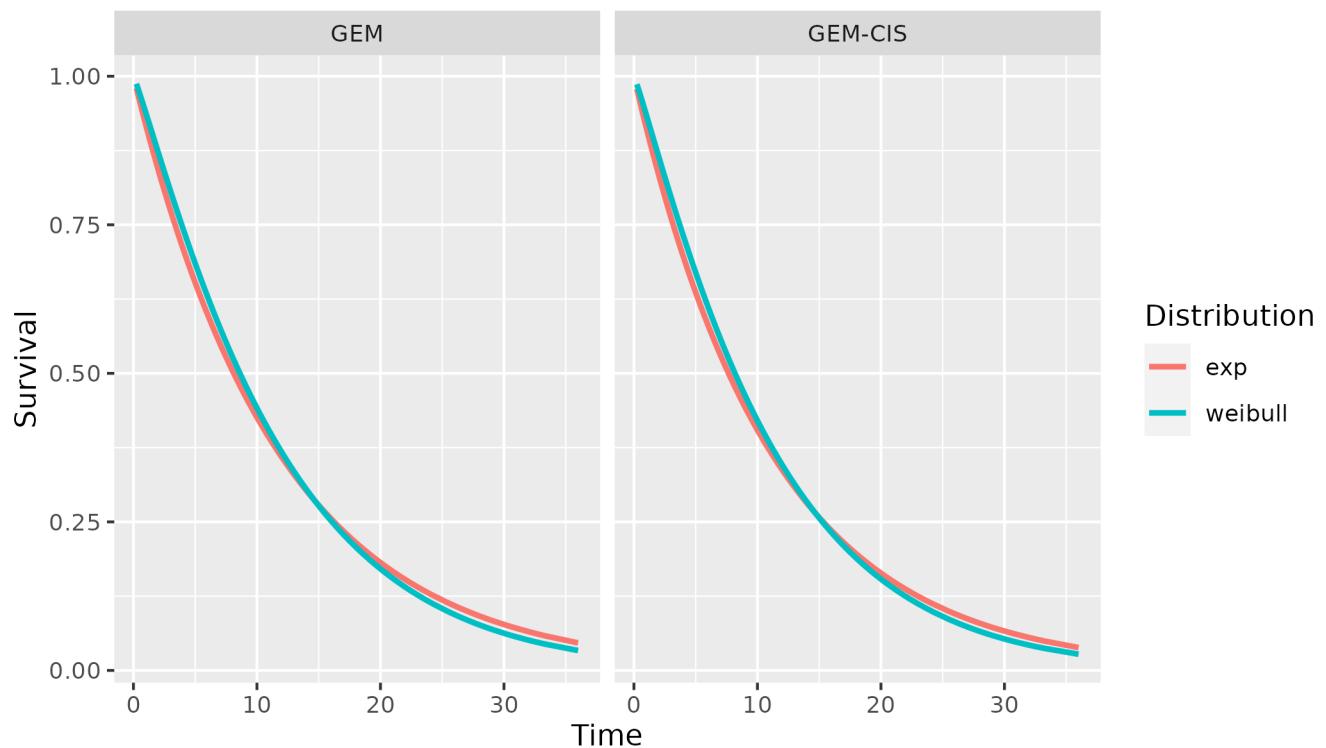
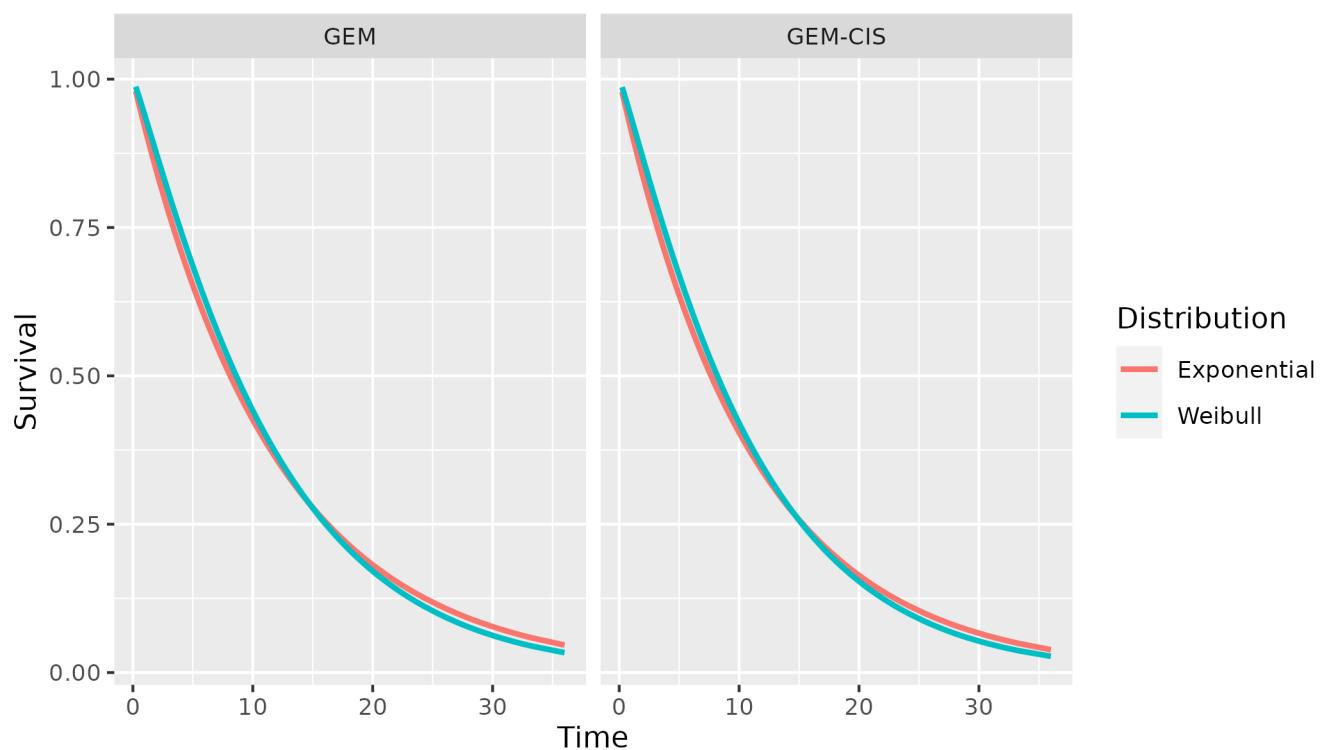


Figure F.1: Fitted Models as in Flexsurv

Figure F.2: Fitted Models with *fit_distribution*