

Jiaqi's Thesis Progress Report

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1. To Do List

1. Simulation Study

2. Notations

List of Notations

i	Individual index
j	Family (Cluster) index
p	Proband index
d_j	Number of events in family j
t	Some time
a	Some Time for the proband
T	Event Time
δ_{ij}	Event indicator for individual i in family j
w	The observed survival data (t, δ)
n	Number of individuals
J	Number of Families (Clusters)
m	Index of the sampled completed dataset in the MCEM
M	Number of the sampled completed dataset in the MCEM
z	Frailty term
q	q -th element of Gauss Hermite Quadrature
ω	q -th weight of Gauss Hermite Quadrature
y_q	q -th node of Gauss Hermite Quadrature
N_q	Total number of quadratures
$h(\cdot)$	Hazard fuction
$h_0(\cdot)$	Baseline hazard function
$H(\cdot)$	Cumulative hazard fuction
$S(\cdot)$	Survival fuction
$A_j(\cdot)$	Ascertainment of family j into the study

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$L(\cdot)$	Likelihood function
$\ell(\cdot)$	Log-likelihood function
$\mathcal{L}(\cdot)$	Laplace transform
\mathbf{x}	Covariates
$\boldsymbol{\beta}$	Model coefficients vector
$\boldsymbol{\theta}$	Parameter vector
Λ	The combination of $(\boldsymbol{\beta}, \lambda, \alpha)$
λ	Weibull shape parameter
α	Weibull scale parameter
v	General form of the parameter in an undefined frailty distribution
k	Gamma shape and rate parameters
σ^2	Log-Normal variance parameter
ψ	Missing data distribution parameters

3. Frailty Model with Weibull Baseline Hazard

For the model efficiency of the analyses in a genetic research, a parametric survival analysis is usually chosen over semi-parametric survival analysis [1, 2]. From the beginning of the discussion, I have obtained the model, i.e., the hazard function is

$$h_{ij}(t_{ij}|\mathbf{x}_{ij}, z_j) = h_0(t_{ij}) \exp(\beta_1 x_{1,ij} + \beta_2 x_{2,ij}) z_j \quad (1)$$

There are total n_j individuals in family j , where $i = 1, \dots, n_j$, and total J families that $j = 1, \dots, J$. $x_{1,ij}$ is the genotype, or say mutation gene status for individual i in family j . $x_{2,ij}$ is the PRS for individual i in family j . The frailty term z_j , has a pdf of $f(z)$, which can be Gamma, log-normal, or other frailty distributions. The support of $f(z)$ is always non-negative. The Weibull baseline hazard function is defined as

$$h_0(t_{ij}) = \alpha^\lambda \lambda t_{ij}^{\lambda-1} \quad (2)$$

where λ is the shape parameter and α is the rate parameter. Let $\xi_{ij} = \exp(\beta_1 x_{1,ij} + \beta_2 x_{2,ij})$, the hazard function is

$$h_{ij}(t_{ij}|\mathbf{x}_{ij}, z_j) = \alpha^\lambda \lambda t_{ij}^{\lambda-1} \xi_{ij} z_j \quad (3)$$

The survival function $S(t)$ can be obtained through cumulative hazard function $H(t)$

$$H(t_{ij}|\mathbf{x}_{ij}, z_j) = \int_0^t h_{ij}(u|\mathbf{x}_{ij}, z_j) du \quad (4)$$

$$= \alpha^\lambda \xi_{ij} z_j \lambda \int_0^t u^{\lambda-1} du \quad (5)$$

$$= \alpha^\lambda \xi_{ij} z_j \lambda \cdot \frac{1}{\lambda} t_{ij}^\lambda = \alpha^\lambda \xi_{ij} z_j t_{ij}^\lambda \quad (6)$$

and the survival function

$$S(t_{ij}|\mathbf{x}_{ij}, z_j) = \exp(-H(t_{ij}|\mathbf{x}_{ij}, z_j)) = \exp(-\alpha^\lambda \xi_{ij} z_j t_{ij}^\lambda) \quad (7)$$

Let $\boldsymbol{\theta} = \{\boldsymbol{\beta}, \alpha, \lambda, v\}$, where v is the parameter for the frailty distribution of the choice. In our example dataset, $\boldsymbol{\beta} = (\beta_1, \beta_2)$. Therefore, the likelihood assuming missing data and frailties are observed can be written as

$$L(\boldsymbol{\theta}|z_j) = \prod_{j=1}^J \prod_{i=1}^{n_j} (\alpha^\lambda \lambda t_{ij}^{\lambda-1} \xi_{ij} z_j)^{\delta_{ij}} \exp(-\alpha^\lambda \xi_{ij} z_j t_{ij}^\lambda) \quad (8)$$

$$= \prod_{j=1}^J \prod_{i=1}^{n_j} h(t_{ij}|\mathbf{x}_{ij}, z_j)^{\delta_{ij}} \exp(-H(t_{ij}|\mathbf{x}_{ij}, z_j)) \quad (9)$$

When there is no missing data but frailties are present, the frailty term can be integrated where the likelihood is taken to be the expectation with respect to the frailty z_j . The likelihood can be written as

$$L(\boldsymbol{\theta}) = \prod_{j=1}^J \prod_{i=1}^{n_j} \int_{z_j} (\alpha^\lambda \lambda t_{ij}^{\lambda-1} \xi_{ij} z_j)^{\delta_{ij}} \exp(-\alpha^\lambda \xi_{ij} z_j t_{ij}^\lambda) f(z_j) dz_j \quad (10)$$

$$= \prod_{j=1}^J \prod_{i=1}^{n_j} \int_{z_j} h(t_{ij}|\mathbf{x}_{ij}, z_j)^{\delta_{ij}} \exp(-H(t_{ij}|\mathbf{x}_{ij}, z_j)) f(z_j) dz_j \quad (11)$$

But when the missing data and the frailty both exist in the model, we will need to account for their joint distribution within the likelihood according to Herring et al. [3].

$$L(\boldsymbol{\theta}) = \prod_{j=1}^J \prod_{i=1}^{n_j} \int_{z_j, \mathbf{x}_{mis,ij}} (\alpha^\lambda \lambda t_{ij}^{\lambda-1} \xi_{ij} z_j)^{\delta_{ij}} \exp(-\alpha^\lambda \xi_{ij} z_j t_{ij}^\lambda) f(z_j, \mathbf{x}_{mis,ij}) dz_j d\mathbf{x}_{mis,ij} \quad (12)$$

$$= \prod_{j=1}^J \prod_{i=1}^{n_j} \int_{z_j, \mathbf{x}_{mis,ij}} h(t_{ij}|\mathbf{x}_{ij}, z_j)^{\delta_{ij}} \exp(-H(t_{ij}|\mathbf{x}_{ij}, z_j)) f(z_j, \mathbf{x}_{mis,ij}) dz_j d\mathbf{x}_{mis,ij} \quad (13)$$

17 The following section 5 and section 6 discuss how to handle the frailty within the likeli-
 18 hood when there are no missing data, which are corresponding to the Equation 10 and 11.
 19 The section 7 will discuss how to handle the frailty and the missing data jointly, which is
 20 corresponding to the likelihood equation and 13.

21 4. Ascertainment Correction

22 Within a genetic study, those families are typically selected when there is an affected
 23 person called a proband. This will yield a selection bias because this is no long a case-
 24 control study, and can potentially defect the statistical power [4, 5]. It is crucial to address
 25 the ascertainment bias. Consider A as the event of being ascertained, D as the data, we
 26 then have $P(D, A|\boldsymbol{\theta}) = P(A|D, \boldsymbol{\theta})P(D|\boldsymbol{\theta})$. Also, we know A is included in D , from Baye's
 27 rule

$$P(D|\boldsymbol{\theta}) = \frac{P(D, A|\boldsymbol{\theta})}{P(A|D, \boldsymbol{\theta})} \propto \frac{L(\boldsymbol{\theta}|D)}{P(A|D, \boldsymbol{\theta})} \quad (14)$$

For each family j , the ascertainment A_j is defined to be the probability of the proband p being ascertained by the age a_{p_j} at examination, i.e., $A_j = P(T_{p_j} < a_{p_j})$ where a_{p_j} is proband's age at study entry. Applying the ascertainment correction for the log-likelihood in family j :

$$\tilde{\ell}_j(\boldsymbol{\theta}) = \ell_j(\boldsymbol{\theta}) - \log A_j(\boldsymbol{\theta}) \quad (15)$$

where $\tilde{\ell}$ is the log-likelihood with ascertainment correction, and ℓ is the crude log-likelihood. Define \mathbf{x}_{p_j} the covariates for proband in family j , so we can further write the formula for the ascertainment correction within different frailty models.

5. Gamma Frailty

We can obtain the likelihood for Gamma frailty model following the instruction by Balan and Putter [6]. The Laplace transform of the frailty $z \sim \text{Gamma}(k, k)$, for the simplicity of the mathematical expression, the following Laplace transform will ignore the subscript, denote $\mathcal{L}(f(z)) = \phi(s)$ where $s = \sum_{i=1}^{n_j} H(t_{ij}|\mathbf{x}_{ij})$:

$$\phi(s) = \int_0^\infty e^{-sz} f(z) dz \quad (16)$$

$$= \int_0^\infty e^{-sz} \frac{k^k}{\Gamma(k)} z^{k-1} e^{-kz} dz \quad (17)$$

Using the Gamma property: $\int_0^\infty z^{n-1} e^{-az} dz = \frac{\Gamma(n)}{a^n}$, $\phi(s)$ can be further written as

$$\phi(s) = \frac{k^k}{\Gamma(k)} \int_0^\infty e^{-(s+k)z} z^{k-1} dz = \frac{k^k}{\Gamma(k)} \cdot \frac{\Gamma(k)}{(s+k)^k} = \left(1 + \frac{s}{k}\right)^{-k} \quad (18)$$

The second derivative is $\frac{d^2\phi(s)}{ds^2} = \int_0^\infty (-z)^2 e^{-sz} f(z) dz$.

The third derivative is $\frac{d^3\phi(s)}{ds^3} = \int_0^\infty (-z)^3 e^{-sz} f(z) dz$, ... Therefore, its d -th derivative, denote $\phi(s)^{(d)}$:

$$\phi(s)^{(d)} = (-1)^d \int_0^\infty z^d e^{-sz} f(z) dz \quad (19)$$

$$= (-1)^d \frac{(k+d-1)!}{(k-1)!(s+k)^d} \left(1 + \frac{s}{k}\right)^{-k} \quad (20)$$

Let $\boldsymbol{\theta} = (\beta_1, \beta_2, \alpha, \lambda, k)$ for Gamma frailty model, the log-likelihood is then written as

$$\ell(\boldsymbol{\theta}) = \sum_{j=1}^k \log \left[\int_0^\infty \prod_{i=1}^{n_j} (h(t_{ij}|\mathbf{x}_{ij}, z_j))^{\delta_{ij}} \exp(-H(t_{ij}|\mathbf{x}_{ij}, z_j)) f(z_j) dz_j \right] \quad (21)$$

$$= \sum_{j=1}^J \log \left[\int_0^\infty \prod_{i=1}^{n_j} (z_j h(t_{ij}|\mathbf{x}_{ij}))^{\delta_{ij}} \exp(-z_j H(t_{ij}|\mathbf{x}_{ij})) f(z_j) dz_j \right] \quad (22)$$

$$= \sum_{j=1}^J \log \left[\prod_{i=1}^{n_j} (h(t_{ij}|\mathbf{x}_{ij}))^{\delta_{ij}} \int_0^\infty z_j^{d_j} \exp(-z_j \sum_{i=1}^{n_j} H(t_{ij}|\mathbf{x}_{ij})) f(z_j) dz_j \right] \quad (23)$$

$$= \sum_{j=1}^J \log \left[\prod_{i=1}^{n_j} (h(t_{ij}|\mathbf{x}_{ij}))^{\delta_{ij}} \frac{(k + d_j - 1)!}{(k - 1)! (\sum_{i=1}^{n_j} H(t_{ij}|\mathbf{x}_{ij}) + k)^{d_j}} \left(1 + \frac{\sum_{i=1}^{n_j} H(t_{ij}|\mathbf{x}_{ij})}{k} \right)^{-k} \right] \quad (24)$$

$$= \sum_{j=1}^J \log \left[\prod_{i=1}^{n_j} ((h(t_{ij}|\mathbf{x}_{ij}))^{\delta_{ij}}) \frac{(k + d_j - 1)!}{k! k^{d_j - 1}} \left(1 + \frac{\sum_{i=1}^{n_j} (H(t_{ij}|\mathbf{x}_{ij}))}{k} \right)^{-k - d_j} \right] \quad (25)$$

$$= \sum_{j=1}^J \log \left[h(t_{ij}|\mathbf{x}_{ij})^{\delta_{ij}} \frac{(k + d_j - 1)!}{k! k^{d_j - 1}} \left(1 + \frac{\sum_{i=1}^{n_j} (H(t_{ij}|\mathbf{x}_{ij}))}{k} \right)^{-k - d_j} \right] \quad (26)$$

$$= \sum_{j=1}^J \left[\sum_{i=1}^{n_j} (\delta_{ij} \log h(t_{ij}|\mathbf{x}_{ij})) + \log \left(\frac{(k + d_j - 1)!}{k! k^{d_j - 1}} \left(1 + \frac{\sum_{i=1}^{n_j} (H(t_{ij}|\mathbf{x}_{ij}))}{k} \right)^{-k - d_j} \right) \right] \quad (27)$$

Not all probands in their study entry ages are affected, so it is crucial to apply a ascertainment correction accordingly. Denote $I(T_{p_j} < a_{p_j})$ as an indicator of the proband was affected before their entry to the study. Note we can still apply Laplace transform for the ascertainment correction, such that

$$A_j(\boldsymbol{\theta}) = \left[1 - S_{p_j}(a_{p_j}|\mathbf{x}_{p_j}) \right]^{I(T_{p_j} < a_{p_j})} S_{p_j} \left[(a_{p_j}|\mathbf{x}_{p_j}) \right]^{1 - I(T_{p_j} < a_{p_j})} \quad (28)$$

$$= \left[1 - \int_0^\infty S_{p_j}(a_{p_j}|\mathbf{x}_{p_j}, z_j) f(z_j) dz_j \right]^{I(T_{p_j} < a_{p_j})} \left[\int_0^\infty S_{p_j}(a_{p_j}|\mathbf{x}_{p_j}, z_j) f(z_j) dz_j \right]^{1 - I(T_{p_j} < a_{p_j})} \quad (29)$$

$$= \left[1 - \int_0^\infty \exp(-z_j \cdot H_{p_j}(a_{p_j}|\mathbf{x}_{p_j})) f(z_j) dz_j \right]^{I(T_{p_j} < a_{p_j})} \quad (30)$$

$$\times \left[\int_0^\infty \exp(-z_j \cdot H_{p_j}(a_{p_j}|\mathbf{x}_{p_j})) f(z_j) dz_j \right]^{1 - I(T_{p_j} < a_{p_j})} \quad (31)$$

$$= \left[1 - \left(1 + \frac{H_{p_j}(a_{p_j}|\mathbf{x}_{p_j})}{k} \right)^{-k} \right]^{I(T_{p_j} < a_{p_j})} \left[\left(1 + \frac{H_{p_j}(a_{p_j}|\mathbf{x}_{p_j})}{k} \right)^{-k} \right]^{1 - I(T_{p_j} < a_{p_j})} \quad (32)$$

38 6. Log-Normal Frailty

The log-normal frailty is not the power-variance-function (PVF) family, so there is no closed form for Laplace transform or expressions for survivors. But we are able to estimate

the Laplace transform using Gauss Hermite Quadrature. We typically standardize the log-normal frailty Z as

$$E(\log Z) = 0 \quad (33)$$

$$\text{Var}(\log Z) = \sigma^2 \quad (34)$$

39 That is, $z \sim \text{log-Normal}(0, \sigma^2)$. The probability density function $f(z)$ is then

$$f(z) = \frac{1}{\sqrt{2\pi}\sigma} z^{-1} \exp\left(-\frac{\log(z)^2}{2\sigma^2}\right) \quad (35)$$

40 The Laplace transform is then

$$\phi(s) = \mathcal{L}(f_Z)(s) = \int_0^\infty \exp(-sz) \cdot f(z) dz \quad (36)$$

Using variable transformation, let $y = \frac{\log(z)}{\sqrt{2}\sigma}$, then $z = \exp(\sqrt{2}\sigma y)$, and $dz = \sqrt{2}\sigma \exp(\sqrt{2}\sigma y) dy$. Therefore, for d -th derivative:

$$\phi(s)^d = \int_{-\infty}^\infty z^d \exp(-sz) \cdot \frac{1}{\exp(\sqrt{2}\sigma y) \sigma \sqrt{2\pi}} \cdot \exp(-y^2) \cdot \sqrt{2}\sigma \exp(\sqrt{2}\sigma y) dy \quad (37)$$

$$= \int_{-\infty}^\infty \exp(\sqrt{2}\sigma y)^d \exp(-s \exp(\sqrt{2}\sigma y)) \cdot \frac{1}{\sqrt{\pi}} \exp(-y^2) dy \quad (38)$$

41 **Definition 1** (Gauss-Hermite Quadrature). *The integrand part can be solved using Gauss-*
42 *Hermite Quadrature. In numerical analysis, the method can be applied in the following form:*

$$\int_{-\infty}^\infty \exp(-x^2) f(x) dx \approx \sum_{i=1}^n \omega_i f(x_i) \quad (39)$$

43 where n is number of sample points used, and x_i is the roots of Hermite polynomial $H_n(x)$
44 such that $i = 1, \dots, n$, and the weights ω_i is

$$\omega_i = \frac{2^{n-1} n! \sqrt{\pi}}{n^2 [H_{n-1}(x_i)]^2} \quad (40)$$

45 Applying Definition 1, the integral of the Laplace transform is then

$$\phi(s)^d = \frac{1}{\sqrt{\pi}} \sum_{q=1}^{N_q} \omega_q \exp(-s \exp(\sqrt{2}\sigma y_q)) \exp(\sqrt{2}\sigma y_q)^d \quad (41)$$

46 where q denotes the q -th element of Gauss Hermite Quadrature, i.e., ω_q denotes the q -th
47 weight, y_q denotes the q -th node, and N_q denotes the total number of quadratures. Thus,

substituting into the log-likelihood:

$$\ell_j(\boldsymbol{\theta}) = \sum_{i=1}^{n_j} \delta_{ij} \log(h(t_{ij}|\mathbf{x}_{ij})) + \log \left(\frac{1}{\sqrt{\pi}} \sum_{q=1}^{N_q} \left[\omega_q \exp(\sqrt{2}\sigma y_q)^{d_j} \exp \left(- \sum_{i=1}^{n_j} H(t_{ij}|\mathbf{x}_{ij}) \exp(\sqrt{2}\sigma y_q) \right) \right] \right) \quad (42)$$

Similarly, the ascertainment correction in the log-normal frailty can be written as

$$A_j(\boldsymbol{\theta}) = \left[1 - \int_{-\infty}^{\infty} \exp(-zH(a_{p_j}|\mathbf{x}_{p_j}))f(z)dz \right]^{I(T_{p_j} < a_{p_j})} \left[\int_{-\infty}^{\infty} \exp(-zH(a_{p_j}|\mathbf{x}_{p_j}))f(z)dz \right]^{1-I(T_{p_j} < a_{p_j})} \quad (43)$$

$$= \left[1 - \sum_{q=1}^{N_q} \omega_q \exp \left(- \left(\sum_{i=1}^{n_j} H(a_{p_j}|\mathbf{x}_{p_j}) \exp(\sqrt{2}\sigma y_{q_p}) \right) \right) \right]^{I(T_{p_j} < a_{p_j})} \quad (44)$$

$$\times \left[\sum_{q=1}^{N_q} \omega_q \exp \left(- \left(\sum_{i=1}^{n_j} H(a_{p_j}|\mathbf{x}_{p_j}) \exp(\sqrt{2}\sigma y_{q_p}) \right) \right) \right]^{1-I(T_{p_j} < a_{p_j})} \quad (45)$$

7. Likelihood and Missing Data

7.1. Reviews on Missing Data

In this subsection, the notations are **distinct** to all other sections or subsections. The missing data problem was firstly brought by Rubin [7], and further targetted as a major statistical problem which many methodologists have developed different statistical tools to handle the missing data. Such as the practical book written by Rubin [8], and some comprehensive reviews on current missing data problems by Baraldi and Enders [9]. The missing data mechanism was introduced by Little and Rubin [10]. There are three missing data mechanisms, which are Missing Completely at Random (MCAR), Missing at Random (MAR), and Missing Not at Random (MNAR). There are some reviews on the missing data which rigorously present the statistical concept of three types of the missing mechanism [11].

Definition 2. (MCAR) Denote Y as the complete data matrix, and M as the missing data indicator matrix. Define y_{ij} and m_{ij} as i -th row (observation) and j -th column (variable) for the matrix Y and M . The conditional distribution of the missingness is said to be

$$f(m_i|y_i, \phi) = f(m_i|\phi) \quad (46)$$

That is, for the parameters of this distribution, m_i does not depend on any observed or missing data.

Example 1. (MCAR Example) There is a blind box with 500 indexed balls (No. 1 to 500) and their weights are unknown. We randomly draw 100 balls and measure their weights and record them in the Excel file. The Excel file contains two columns called Index and Weight, only those randomly selected balls will have Weights being filled. Those weights of unselected balls are called MCAR.

70 **Definition 3.** (MAR) Denote $y_{i,obs}$ as the observed y , and $y_{i,mis}$ as the missing y . Note
 71 that $y_i = (y_{i,obs}, y_{i,mis})$. The missing component is defined to be MAR if m only depends on
 72 $y_{i,obs}$. That is,

$$f(m_i|y_i, \phi) = f(m_i|y_{i,obs}, \phi) \quad (47)$$

73 **Example 2.** (MAR Example) In a psychological study, participants are asked to complete a
 74 survey so the scientist can profile their personalities. One question that asks participants to
 75 report their Mood status being good or bad. Male participants are typically too shy to answer
 76 this question, which yields some responses being missing. This is called the MAR, that the
 77 missingness on Mood status depends on the participant's gender, but not on the missing Mood
 78 itself.

79 **Definition 4.** (MNAR) In the MNAR, the missingness depends on the missing data itself,
 80 which is

$$f(m_i|y_i, \phi) = f(m_i|y_{i,mis}, y_{i,obs}, \phi) \quad (48)$$

81 In this case, the analysis needs to be conducted with caution. The missingness should be
 82 included in the likelihood construction.

83 **Example 3.** (MNAR Example) There is a study on participants' incomes. Person A makes
 84 \$200,000 per year, so they decide to report this amount without hesitancies. Person B makes
 85 \$10,000 per year, so they are not willing to provide this information, which this response is
 86 left as blank. This type of missing depends on the missing data itself, that Person B refuses
 87 to provide the response due to the response being comparatively low.

88 7.2. Multiple Imputation for the Continuous Variable without Considering the Family Struc- 89 ture

90 Again, to avoid overloaded mathematical notations, this subsection will not follow the
 91 previously defined notations. When making the imputation on the continuous variable, one
 92 easy way is to assume a conditionally normal model. Suppose y is the variable contains miss-
 93 ing values, \mathbf{x} are other variables are fully observed. We assume there are total p parameters
 94 being estimated in this linear regression. The conditionally normal model (linear regression)
 95 can be written as

$$y|\mathbf{x}, \boldsymbol{\beta} \sim N(\boldsymbol{\beta}\mathbf{x}, \sigma^2) \quad (49)$$

96 In the linear regression setting,

$$y = \mathbf{x}\boldsymbol{\beta} + \epsilon, \quad \epsilon \sim N(0, \sigma^2) \quad (50)$$

97 This simply corresponds to the likelihood

$$f(y|\mathbf{x}, \boldsymbol{\beta}, \sigma^2) \propto (\sigma^2)^{-n/2} \exp\left(-\frac{1}{2\sigma^2}(y - \mathbf{x}\boldsymbol{\beta})^\top(y - \mathbf{x}\boldsymbol{\beta})\right) \quad (51)$$

98 because of the conditional normality of y . We can solve that

$$\hat{\boldsymbol{\beta}} = (\mathbf{x}^\top \mathbf{x})^{-1} \mathbf{x}^\top y \quad (52)$$

In the Bayesian framework, we need to find the prior, which is the joint distribution $f(\sigma^2, \boldsymbol{\beta})$. Note that $(y - \mathbf{x}\boldsymbol{\beta})^\top(y - \mathbf{x}\boldsymbol{\beta})$ can be written as

$$(y - \mathbf{x}\boldsymbol{\beta})^\top(y - \mathbf{x}\boldsymbol{\beta}) = ((y - \mathbf{x}\boldsymbol{\beta}) + (\mathbf{x}\hat{\boldsymbol{\beta}} - \mathbf{x}\boldsymbol{\beta}))^\top((y - \mathbf{x}\boldsymbol{\beta}) + (\mathbf{x}\hat{\boldsymbol{\beta}} - \mathbf{x}\boldsymbol{\beta})) \quad (53)$$

$$= (y - \mathbf{x}\boldsymbol{\beta})^\top(y - \mathbf{x}\boldsymbol{\beta}) + (\boldsymbol{\beta} - \hat{\boldsymbol{\beta}})^\top(\mathbf{x}^\top \mathbf{x})(\boldsymbol{\beta} - \hat{\boldsymbol{\beta}}) + 2(\mathbf{x}\hat{\boldsymbol{\beta}} - \mathbf{x}\boldsymbol{\beta})^\top(\mathbf{x}\hat{\boldsymbol{\beta}} - \mathbf{x}\boldsymbol{\beta}) \quad (54)$$

$$= (y - \mathbf{x}\boldsymbol{\beta})^\top(y - \mathbf{x}\boldsymbol{\beta}) + (\boldsymbol{\beta} - \hat{\boldsymbol{\beta}})^\top(\mathbf{x}^\top \mathbf{x})(\boldsymbol{\beta} - \hat{\boldsymbol{\beta}}) \quad (55)$$

99 So Equation 51 will become

$$f(y|\mathbf{x}, \boldsymbol{\beta}, \sigma^2) \propto \underbrace{(\sigma^2)^{-v/2} \exp(-\frac{vs^2}{2\sigma^2})}_{f(\sigma)} \underbrace{(\sigma^2)^{-\frac{n-v}{2}} \exp\left(-\frac{1}{2\sigma^2}(\boldsymbol{\beta} - \hat{\boldsymbol{\beta}})^\top(\mathbf{x}^\top \mathbf{x})(\boldsymbol{\beta} - \hat{\boldsymbol{\beta}})\right)}_{f(\boldsymbol{\beta}|\sigma)} \quad (56)$$

100 where $vs^2 = (\mathbf{y} - \mathbf{x}\hat{\boldsymbol{\beta}})^\top(\mathbf{y} - \mathbf{x}\hat{\boldsymbol{\beta}}) = SSE$, such that $v = n_{obs} - p$. Then $f(\sigma^2)$ can be written
101 as a proportional density to the inverse gamma distribution,

$$f(\sigma^2) \propto (\sigma^2)^{-\frac{v}{2}-1} \exp(-\frac{vs^2}{2\sigma^2}) = (\sigma^2)^{-\frac{v}{2}-1} \exp(-\frac{SSE}{2\sigma^2}) \quad (57)$$

102 In this $\sigma^2 \sim \text{Inverse-Gamma}(\alpha, \phi)$, we have $\alpha = \frac{v}{2} = \frac{n_{obs}-p}{2}$ and $\phi = \frac{1}{2}vs^2 = \frac{SSE}{2}$. From the
103 inverse-gamma property, when

$$\sigma^2 \sim \text{Inverse-Gamma}\left(\frac{n_{obs}-p}{2}, \frac{SSE}{2}\right) \quad (58)$$

104 and $\exists \lambda$ such that

$$\sigma^2 = \frac{SSE}{2}/\lambda \quad (59)$$

105 then λ can be transformed

$$\lambda = \frac{\chi_{n_{obs}-p}^2}{2} \quad (60)$$

106 since $\chi_{df}^2 = \text{Gamma}(\frac{df}{2}, 2)$, so

$$\sigma^2 = \frac{\frac{SSE}{2}}{\frac{\chi_{n_{obs}-p}^2}{2}} = \frac{SSE}{\chi_{n_{obs}-p}^2} \quad (61)$$

107 Thus, we can sample the standard deviation of the missing data distribution from

$$\sigma^* = \hat{\sigma} \sqrt{\frac{SSE}{\chi_{n_{obs}-p}^2}} = \hat{\sigma} \sqrt{\frac{SSE}{g}} \quad (62)$$

108 from sampling $g \sim \chi_{n_{obs}-p}^2$. Moreover, we know

$$\text{Var}(\hat{\boldsymbol{\beta}}) = \sigma^2(\mathbf{x}^\top \mathbf{x}^{-1}) = \mathbf{V} \quad (63)$$

so the marginal distribution for β ,

$$\beta \sim N(\hat{\beta}, \sigma^2(\mathbf{x}^\top \mathbf{x})^{-1}) \quad (64)$$

Note that when a random variable $T \sim N(\mathbf{m}, \mathbf{c})$, then T can be generated from a standard normal variable \mathbf{u} with

$$T = \mathbf{m} + \mathbf{L}\mathbf{u} \quad (65)$$

where \mathbf{L} is the cholesky decomposition of \mathbf{c} such that $\mathbf{c} = \mathbf{L}\mathbf{L}^\top$. For β , from 64, it can be derived as

$$\beta = \hat{\beta} + \sigma(\mathbf{x}^\top \mathbf{x})^{-1/2} \mathbf{u}_1 \quad (66)$$

$$= \hat{\beta} + \mathbf{u}_1 \mathbf{V}^{-1/2} \quad (67)$$

Adjusting for σ^* to make sure β matches the variability implied by the random draw of σ^* ,

$$\beta^* = \hat{\beta} + \frac{\sigma^*}{\hat{\sigma}} \mathbf{u}_1 \mathbf{V}^{-1/2} \quad (68)$$

such that \mathbf{u}_1 is a row vector of p independent draws from a standard normal distribution, $u_{1k} \stackrel{iid}{\sim} N(0, 1)$, and $k = 1, \dots, p$. The imputation for y_i^* is computed as

$$y_i^* = \beta^* \mathbf{x}_i + u_{2i} \sigma^*, \text{ s.t. } u_{2i} \sim N(0, 1) \quad (69)$$

where u_{2i} adds the uncertainty to the imputation as well to ensure the imputation is not solely based on the predicted value of y_i^* . This prevents the underestimation of the variability. Therefore, the comprehensive steps of the multiple imputation on the continuous missing data can be summarized to the following steps:

1. Calculate $\hat{y} = \hat{\beta} \mathbf{x}$ using y_{obs} , and $\hat{\beta}$ can be obtained easily, as well as $\hat{\sigma}$, and $\text{Var}(\hat{\beta}) = \mathbf{V}$
2. Draw $g \sim \chi^2_{n_{obs}-p}$ for one random draw
3. Calculate $\sigma^* = \hat{\sigma} / \sqrt{SSE/g}$
4. Draw a p dimensional vector \mathbf{u}_1 such that $u_{1k} \stackrel{iid}{\sim} N(0, 1)$ and $k = 1, \dots, p$
5. Calculate $\beta^* = \hat{\beta} + \frac{\sigma^*}{\hat{\sigma}} \mathbf{u}_1 \mathbf{V}^{1/2}$ such that $\mathbf{V}^{1/2}$ is the cholesky decomposition of \mathbf{V}
6. Draw $u_{2i} \stackrel{iid}{\sim} N(0, 1)$
7. Impute $y_{mis,i} = \beta^* \mathbf{x}_i + u_{2i} \sigma^*$
8. Repeat 2. to 7. for M times to obtain M complete datasets

7.3. Multiple Imputation for the Continuous Variable Considering the Family Structure

In order to account for the kinship correlations, the conditional normal distribution needs to be adjusted where the variable contains the missing components are said to be multivariate

$$\mathbf{y}|\mathbf{x}, \beta \sim MVN(\beta \mathbf{x}, \sigma_g^2 K + \sigma_e^2) \quad (70)$$

where in the linear mixed effect regression form with flexible covariance matrix, the model can be written as

$$\mathbf{y} = \mathbf{x}\beta + \mathbf{u} + \mathbf{e} \quad (71)$$

where $\mathbf{u} \sim MVN(0, \sigma_g^2 K)$, and $\mathbf{e} \sim MVN(0, \sigma_e^2 I)$, such that K is the kinship matrix with the diagonal of 1 and I is the identity matrix. Denote that $\Sigma = \sigma_g^2 K + \sigma_e^2 I$. So in this multivariate version of linear mixed effects model. With unknown mean and covariance matrix, the prior of the covariance matrix can be selected as an Inverse Wishart distribution with some degrees of freedom and the scale parameter. However, in this case, the covariance matrix is not fully unknown. Therefore, some steps of this multiple imputation will be based on the empirical estimates rather than the prior distributions. The step can be concluded as follows:

1. Obtain the kinship matrix K among all individuals
2. Calculate the estimates of $\hat{y} = \mathbf{x}\beta$, obtain estimates of $\hat{\beta}$, $\hat{\sigma}_g^2$, $\hat{\sigma}_e^2$, $\text{Var}(\hat{\beta}) = \mathbf{V}$. In this step, naturally, $\hat{\Sigma}$ is obtained.
3. Obtain the conditional variance of y_i ,

$$\text{Var}(y_i | \mathbf{y}_{-i}) = \hat{\Sigma}_{ii} - \hat{\Sigma}_{i,-i} \hat{\Sigma}_{-i,-i}^{-1} \hat{\Sigma}_{-i,i} = \hat{\sigma}_i^2 \quad (72)$$

4. Draw p -dimensional vector w_1 such that $w_{1k} \stackrel{iid}{\sim} N(0, 1)$ where $k = 1, \dots, p$
5. Calculate $\beta^* = \hat{\beta} + w_1 \mathbf{V}^{1/2}$ such that $\mathbf{V}^{1/2}$ is the cholesky decomposition of \mathbf{V}
6. Obtain $\mu_i^* = \beta^* \mathbf{x}_i$
7. Obtain the conditional expectations

$$E(y_{mis,i} | \mathbf{y}_{-i}) = \mu_i^* + \hat{\Sigma}_{i,-i} \hat{\Sigma}_{-i,-i}^{-1} (\mathbf{y}_{-i} - \boldsymbol{\mu}_{-i}^*) \quad (73)$$

8. Draw $w_{2i} \sim N(0, 1)$
9. Impute $y_{mis,i} = E(y_{mis,i} | \mathbf{y}_{-i}) + w_{2i} \hat{\sigma}_i$
10. Repeat 4. to 9. for M times to obtain M complete datasets.

8. Variance Estimation

Based on the Rubin's rule, the pooling step of the analysis is defined as

$$\bar{\theta} = \frac{1}{M} \sum_{i=1}^M \theta_i \quad (74)$$

where θ_i is the parameter estimate that we are making the inference in a study for i -th imputation after M imputations. So $\bar{\theta}$ is the pooled parameter estimates. Based on Barnard and Rubin [12], the variance estimation is also defined in a two-level structure, which are within imputation variance and between imputation variance. The within imputation variance is similar to the pooled parameter estimation, where

$$V_W = \frac{1}{M} \sum_{i=1}^m SE_i^2 \quad (75)$$

such that V_W determines the within-imputation variance, and it's simply "pooled" variance among all analyses from the imputed dataset i . The between-imputation variance, on the

other hand, accounts for the extra variances caused by the missing data. The between-imputation variance V_B is defined as

$$V_B = \frac{\sum_{i=1}^M (\theta_i - \bar{\theta})^2}{M - 1} \quad (76)$$

where V_B is the unbiased estimation. Note that θ is estimated using the only finite M imputed datasets, according to Van Buuren [13], V_B is the approximation when $M \rightarrow \infty$. Therefore, the total variance can be written as

$$V_{\text{Total}} = V_W + V_B + \frac{V_B}{M} \quad (77)$$

when M is large enough, V_{Total} tends to have the only two components of within and between variances. The test statistic (Wald statistic) is

$$\frac{(\bar{\theta} - \theta_0)^2}{V_{\text{Total}}} \sim F_{1, df_{adj}} \quad (78)$$

which

$$\frac{\bar{\theta} - \theta_0}{\sqrt{V_{\text{Total}}}} \sim t_{df_{adj}, \frac{1-\alpha}{2}} \quad (79)$$

such that α is the significance level. Define

$$\rho = \frac{V_B + \frac{V_B}{M}}{V_{\text{Total}}} \quad (80)$$

and

$$r = \frac{V_B + \frac{V_B}{M}}{V_W} \quad (81)$$

where ρ is the fraction of missing information, which quantifies the proportion of the total variance that is attributable to the fact that the data have been imputed M times. Also, r is the relative increase in variance due to non-responses (missing data), which measures the increase in variance due to the missing data compared to if there were no missing data. In the interpretation, ρ gives the proportion of the total variance that is due to the uncertainty introduced by the missing data. A higher ρ indicates a larger fraction of the total uncertainty comes from the fact that the data were imputed. A higher r indicates that the missing data have a larger impact on the overall variance. In the first MI literature by Rubin [14], the degrees of freedom was defined as

$$df_{old} = (M - 1) \times \left(1 + \frac{1}{r}\right)^2 \quad (82)$$

The estimated degrees of freedom for the observed data, adjusted for the missing information, are

$$df_{obs} = \frac{(n - k) + 1}{(n - k) + 3} (n - k)(1 - \rho) \quad (83)$$

181 where n is the number of observations in each imputed data, and k is the number of pa-
 182 rameters to be estimated. Barnard and Rubin [12] further alternated the calculation of the
 183 degrees of freedom by combining Equations 82 and 83

$$df_{adj} = \frac{df_{old}df_{obs}}{df_{old} + df_{obs}} \quad (84)$$

184 When conducting the statistical tests on the pooled estimates, df_{adj} is used for the t-
 185 distribution degrees of freedom. The confidence interval is straightforward, where we obtain

$$SE_{pooled} = \sqrt{V_{Total}} \quad (85)$$

186 then we simply calculate

$$CI = \bar{\theta} \pm t_{df_{adj}, \frac{1-\alpha}{2}} \times SE_{pooled} \quad (86)$$

187 9. Simulation Study (Temporary)

188 9.1. Generating Missing at Random

189 From the MICE (Multivariate Imputation by Chained Equations) package in R authored
 190 by Van Buuren and Groothuis-Oudshoorn [15], there is one function add-on that is very
 191 helpful in generating the missingness of a data while considering the missing mechanism.
 192 The function was introduced by Schouten et al. [16] that on the opposite of imputation, the
 193 amputation is designed to simulate the missing data.

References

- [1] Jacqueline E Rudolph, Stephen R Cole, and Jessie K Edwards. Parametric assumptions equate to hidden observations: comparing the efficiency of nonparametric and parametric models for estimating time to aids or death in a cohort of hiv-positive women. *BMC medical research methodology*, 18:1–5, 2018.
- [2] Roger L Berger and George Casella. *Statistical inference*. Duxbury, 2001.
- [3] Amy H Herring, Joseph G Ibrahim, and Stuart R Lipsitz. Frailty models with missing covariates. *Biometrics*, 58(1):98–109, 2002.
- [4] Suyeon Park, Sungyoung Lee, Young Lee, Christine Herold, Basavaraj Hooli, Kristina Mullin, Taesung Park, Changsoon Park, Lars Bertram, Christoph Lange, et al. Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. *BMC medical genetics*, 16:1–12, 2015.
- [5] Andrew G Clark, Melissa J Hubisz, Carlos D Bustamante, Scott H Williamson, and Rasmus Nielsen. Ascertainment bias in studies of human genome-wide polymorphism. *Genome research*, 15(11):1496–1502, 2005.
- [6] Theodor A Balan and Hein Putter. A tutorial on frailty models. *Statistical methods in medical research*, 29(11):3424–3454, 2020.
- [7] Donald B Rubin. Inference and missing data. *Biometrika*, 63(3):581–592, 1976.
- [8] Donald B Rubin. *Multiple imputation for nonresponse in surveys*. John Wiley & Sons, New York, 1987. doi: 10.1002/9780470316696.
- [9] Amanda N Baraldi and Craig K Enders. An introduction to modern missing data analyses. *Journal of school psychology*, 48(1):5–37, 2010.
- [10] Roderick JA Little and Donald B Rubin. *Statistical analysis with missing data*, volume 793. John Wiley & Sons, 2019.
- [11] Miriam Seoane Santos, Ricardo Cardoso Pereira, Adriana Fonseca Costa, Jastin Pompeu Soares, João Santos, and Pedro Henriques Abreu. Generating synthetic missing data: A review by missing mechanism. *IEEE Access*, 7:11651–11667, 2019.
- [12] John Barnard and Donald B Rubin. Miscellanea. small-sample degrees of freedom with multiple imputation. *Biometrika*, 86(4):948–955, 1999.
- [13] Stef Van Buuren. *Flexible imputation of missing data*. CRC press, 2018.
- [14] D.B. Rubin. *Multiple Imputation for Nonresponse in Surveys*. John Wiley & Sons, 1987.
- [15] Stef Van Buuren and Karin Groothuis-Oudshoorn. mice: Multivariate imputation by chained equations in r. *Journal of statistical software*, 45:1–67, 2011.
- [16] Rianne Margaretha Schouten, Peter Lugtig, and Gerko Vink. Generating missing values for simulation purposes: a multivariate amputation procedure. *Journal of Statistical Computation and Simulation*, 88(15):2909–2930, 2018.