

**Prolonged Grief Disorder Symptoms and its Relationship with Kinship, Type of Loss
and Biological Sex in Bereaved Individuals**

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Abstract

Introduction

One out of ten bereaved individuals, and one out five traumatically bereaved individuals, develop Prolonged Grief Disorder (PGD). Factors heightening chances of experiencing more severe PGD symptoms are being female, traumatic loss and loss of a child or partner. The current study explored associations and interaction effects between kinship, type of loss and biological sex on PGD symptoms. The study aimed to distinguish between traumatically and non-traumatically bereaved individuals, noting that PGD symptoms are more severe in the traumatically bereaved.

Method

Two samples were assessed in the current research, of which sample one mainly consisted of non-traumatically bereaved individuals and sample two included traumatically bereaved individuals. Participants in sample one ($N = 80$) were recruited through social media advertisements and bereavement support websites. Participants in sample two ($N = 52$) were recruited via the "rouwmeter" (grief meter) website. Data on kinship, type of loss, biological sex, and PGD symptoms was gathered through interviews (sample 1) or questionnaires (sample 2). A three-way ANOVA was conducted to test for associations and interactions. The partial eta squared was used to determine the effect size.

Results

The associations of kinship ($F(1, 119) = 87.55, p < .001$), type of loss ($F(1, 119) = 68.48, p < .001$) and biological sex ($F(1, 119) = 6.50, p = .012$) on the total PGD score were found to be significant. For kinship and type of loss, a strong association was found, whilst biological sex showed a weak association with the total PGD score. No significant interaction effects were found between the three variables.

Discussion

The results provide additional support on existing literature regarding the association of kinship, type of loss, biological sex and PGD symptoms. No significant interaction effects were found, possibly due to the unequal distribution of participants among the levels of each category. Future studies could replicate the findings of this study while using stratified sampling.

Keywords: Prolonged Grief Disorder, Kinship, Type of Loss, Biological Sex, Traumatic Loss

Introduction

Dealing with the loss of a loved one is one of the most challenging experiences that people may face in their lifetime (Szuhany et al., 2021). The most frequently found grief trajectory following the loss of a loved one starts with intense acute grief which develops into a more integrated form of grief with time, where the bereaved finds pleasure and interest in reengaging in everyday activities (Shear et al., 2013). However, one out of ten individuals do not follow this typical trajectory (Lundorff et al., 2017) and experience more severe symptoms of distress, which can be referred to as Prolonged Grief Disorder (PGD) (Mughal et al., 2024). PGD is characterized by responses following loss that result in functional impairment in social, occupational, or other vital areas of functioning exceeding cultural norms (Eisma, 2023; Szuhany et al., 2021). PGD manifests through symptoms like pervasive and intense yearning or longing for the deceased and persistent preoccupation with the lost individual for at least a month, occurring at least twelve months post-loss according to the Diagnostic and Statistical Manual of Mental Disorders, Fifth edition, Text Revision (DSM-5-TR) (APA, 2022; Eisma, 2023; Treml et al., 2020),.

Several risk factors are known to increase the risk of experiencing more severe PGD symptoms, for instance, traumatic circumstances of the loss. The likelihood of experiencing PGD symptoms following traumatic loss has been reported to be considerably higher, five out of ten individuals who lose a loved one following a traumatic event are likely to experience PGD symptoms (Djelantik et al., 2020). Examples of traumatic losses encompass death due to suicides, accidents, murder, acts of terror, natural disasters and combat (Kristensen et al., 2012). Traumatically bereaved individuals may undergo a distinct grieving process compared to those facing non-violent losses. Apart from dealing with the loss of their loved one, they must also deal with the shock and horror of the traumatic incident (Hibberd et al., 2010). The traumatic nature of the loss can trigger vivid visual images of the final moments of the deceased's life, along with thoughts about what their loved one endured. Consequently, these individuals may try to avoid these vivid images (Heeke et al., 2017) and triggers which are associated with the traumatic incident (Hibberd et al., 2010). The abruptness of a violent death often leaves survivors confronted with feelings injustice and a sense of meaninglessness (Currier et al., 2008). Additionally, traumatically bereaved individuals might be more likely to ruminate about the death and consider actions that might have prevented the death of their loved one (Morina, 2011).

Another risk factor which is associated with experiencing more severe PGD symptoms is the relationship with the deceased, also referred to as kinship (Buur et al., 2024). Research has shown that the loss of a closely related family member was associated with more severe grief reactions than the loss of a distantly related family member (Heeke et al., 2017). For example, parents who have lost a child are more likely to experience more intense yearning and preoccupation with the deceased as opposed to those experiencing other losses (Morris et al., 2019). Corroborating these findings, Doering et al. (2022) showed that individuals who have lost a child, followed by those who had lost their spouse, are likely to experience more severe PGD symptoms as compared to individuals who have lost their parent, friend or other type of kinship.

The risk of experiencing more severe PGD symptoms is also increased if the bereaved is female (Heeke et al., 2017; Thimm et al., 2020). Females have been reported to be six times more likely to develop PGD compared to males (Steil et al., 2019). The symptoms experienced by females are characterized by an increasing grief reaction, while males often show a decreasing grief reaction (Lundorff et al., 2020). Heeke et al. (2017) proposed that women scoring higher on personality traits linked to adverse mental health outcomes could offer a potential explanation for these gender disparities. Moreover, women tend to react to stressful situations with anxiety and avoidant behaviour, increasing their vulnerability to develop mental health problems (Heeke et al., 2017). Females have also been shown to be less able to withstand or rebound from a crisis compared to males (Yalcin-Siedentopf et al., 2021).

Additionally, research has indicated that the difference in bereavement between the two sexes is also shaped by kinship to the deceased (Stroebe et al., 2007). The loss of a child has been reported to have a greater effect on the mother than the father (Kersting & Kroker, 2010; Li et al., 2003). Women deal with higher depression levels following the loss of their spouse, yet, men report higher mortality rates (Stroebe et al., 2007). Elevated rates of suicidal ideations were reported for men who had lost their female spouse (Smith & Zick, 1996). The rates remained high over the years after bereavement, in comparison to suicidal ideation rates among women which were mostly restricted to the first year after the loss (Schaefer et al., 1995). It was also found that widows seem to adjust better to spousal loss, compared to widowers (Stroebe et al., 2007). It remains unclear whether the influence of kinship on PGD symptoms is also influenced by biological sex, and if so, which combination of groups is at risk of experiencing more severe PGD symptoms.

Additionally, Heeke et al. (2017) found a small positive association between female sex and prolonged grief in individuals experiencing traumatic loss. An interaction effect between biological sex and type of loss was also established in other research (Kokou-Tchri, 2024). Contrary, a study researching complicated grief, which is another conceptualization of PGD, found no significant differences between traumatic and non-traumatic bereaved considering gender, indicating gender and type of loss do not interact (Tal et al., 2017). The findings regarding biological sex and type of loss interaction are not uniform, thus necessitating further research in this area.

Studies have investigated the relationship between kinship PGD symptoms, generally finding that the loss of a child or partner is associated with experiencing more severe PGD symptoms among both normally and traumatically bereaved individuals (Buur et al., 2024; Heeke et al., 2017; Morris et al., 2019). However, some studies present contradictory findings. For instance, Schaal et al. (2010) reported no significant association between kinship and grief reactions in traumatically bereaved individuals, challenging the consensus that the kinship to the deceased increases the risk of experiencing more severe PGD symptoms in traumatically bereaved individuals. These discrepancies suggest the need for further research to explore the underlying reasons for these inconsistencies regarding the relationship between type of loss and kinship.

The Present Study

This study investigates the association of kinship, type of loss, and biological sex on PGD symptoms in bereaved individuals. A distinction will be made between traumatic and non-traumatic bereavement, since existing literature highlights the heightened severity of PGD symptoms among traumatically bereaved individuals (Djelantik et al., 2020). Despite this, research often lacks a clear delineation between these groups. For instance, studies on factors influencing PGD frequently involve a single sample that includes both traumatically and non-traumatically bereaved individuals (Neria & Litz, 2004). This is problematic since it has been shown that those who are traumatically bereaved experience a distinct type of bereavement compared to those who are non-traumatically bereaved (Djelantik et al., 2020). The first research question is: “To what extent are kinship, type of loss, and biological sex associated with PGD symptoms among bereaved individuals?”, with hypotheses that individuals who lost a partner or child, those experiencing traumatic bereavement, and females experience more severe PGD symptoms. Additionally, the study will explore two-

way interaction effects between the variables to address inconsistencies in grief-related research (Heeke et al., 2017; Schaal et al., 2010; Stroebe et al., 2007; Tal et al., 2017). Given the potential for two-way interactions among the three variables based on prior research, the study will also examine three-way interaction effects. The second research question is: “To what extent do the interaction effects between kinship, type of loss, and biological sex influence PGD symptoms among bereaved individuals?” with the hypothesis that these variables interact, leading to heightened PGD scores in certain combinations.

Method

Participants

Sample 1

The participants of the study were recruited in two samples. Sample one consisted of 80 participants (Lenferink et al., 2022). Recruitment of sample one took place between January and March 2022. All study participants were proficient in the Dutch or German language. Participation was voluntary and participants had the opportunity to withdraw at any time during the study. Informed consent was obtained from all participants.

The participants in the study were selected through non-probability sampling, specifically purposive sampling. Participants were recruited using social media advertisements and by posting materials for recruitment on websites aimed at bereaved people. Participants could win a gift card worth 50 euros for their participation.

First, participants responded to questions regarding their demographic characteristics. Following, they answered a question regarding a possible diagnosis of a psychotic disorder, as this is one of the exclusion criteria. Participants were asked about loss-related characteristics, such as information about kinship. One of the questions in the interview was about suicidal ideations, as this was the second exclusion criterion. Participants proceeded to complete the Traumatic Grief Inventory – Clinician Administered (TGI-CA). The main inclusion criterion for sample one was that individuals must have lost their loved one at least three months prior to the participation in the study. Additionally, the participants needed to have a smartphone and be older than eighteen years old.

Sample 2

Sample 2 consisted of 52 participants. Recruitment of sample two took place between April and May 2024. All study participants were proficient in the Dutch language. Participation was voluntary and participants had the opportunity to withdraw at any time during the study. Informed consent was obtained from all participants.

The participants in sample two were recruited through the “Rouwmeter” (“Grief meter”), which is a tool that individuals can use to determine whether professional help would be beneficial in their process of dealing with bereavement. After filling in the “Rouwmeter”, participants were asked about their willingness to participate in future studies regarding the loss of their loved ones. If so, the participants were approached via email and invited to enrol in the study. Participants in sample two could win a gift card worth 50 euros.

The participants were asked for loss- and background characteristics in a questionnaire. The participants filled in the Traumatic Grief Inventory – Self-Report Plus (TGI-SR+) At the end of the questionnaires, they were given the option to request an individualized report of their scores.

The main inclusion criteria were that individuals must have lost their loved one following a traumatic event at least twelve months prior to the participation in the study. Additionally, the participants needed to have a smartphone and be older than seventeen years old. Exclusion criteria encompassed the participant being diagnosed with a psychotic disorder or experiencing suicidal ideation.

Measures

Sample 1

TGI-CA

The primary measure to assess PGD symptoms in sample one was the TGI-CA. It is a 22-item interview with options on a 5-point Likert scale ranging from 1 (never) to 5 (always). The questionnaire assesses how often specific grief reactions occurred during the past month, however, the timeframe was adjusted to two weeks for the study (e.g., “In the past two weeks, did you feel alone or detached from others?”). The questionnaire is in line with the symptoms provided by the DSM-5-TR (Lenferink et al., 2023). The total score was determined by summing the answers to each item. A cut-off point of ≥ 71 was used to indicate

disturbed grief. Although the cut-off score for the 22-item TGI-CA has not been established, this assumption was made based on the similarity of its items to those in the TGI-SR+ (Lenferink et al., 2022). The TGI-CA has been reported to have good psychometric properties (Lenferink et al., 2023).

Kinship, Type of Loss and Biological Sex

To gather data on kinship, type of loss and biological sex of the participant, a section of the survey included questions addressing these variables.

When asked about kinship, the participant could answer one of the following options: “partner”, “child”, “father/mother”, “brother/sister”, “grandfather/grandmother”, “grandchild”, “friend”, or “other, namely”. As prior research has shown, PGD symptoms are more severe among those who lost a child or partner (Heeke et al., 2019). Therefore, kinship was treated as a categorical variable, in which all answers were divided into either “child/partner” or “other”. The remaining options falling under “other” encompassed the response options: “father/mother”, “brother/sister”, “grandfather/grandmother”, “grandchild”, and “friend”. To gather data on the type of loss, participants were asked about the cause of death. The answer options were: “natural cause”, “suicide”, “accident”, “homicide” and “other”. Since research has shown that traumatically bereaved individuals experience more severe PGD symptoms (Hibberd et al., 2010), the type of loss variable was treated as a categorical variable with two levels; 1 = traumatically bereaved and 0 = non-traumatically bereaved. The answer options “suicide”, “accident” and “homicide” are part of the traumatically bereaved category. Obtaining data on biological sex involved asking the participant about their gender. The answer options were “male” and “female”. Thus, biological sex was treated as a categorical variable which included two levels (male and female).

Sample 2

TGI-SR+

The primary measure used to determine PGD symptoms in sample two was the Traumatic Grief Inventory – Self Report Plus (TGI-SR+). The TGI-SR+ is the questionnaire version of the TGI-CA. It is a 22-item questionnaire with a 5-point Likert scale answer option for each item. The TGI-SR+ is an extension of the 18-item TGI-SR measure. The answer options and calculation of the total score, and the cut-off score are the same as the ones used

in sample one. A cut-off point for disturbed grief is reported to be ≥ 71 (Lenferink et al., 2022). The TGI-SR+ has been reported to have high construct validity (Lenferink et al., 2023) and excellent internal reliability (Kokou-Kpolou et al., 2022), specifically good internal consistency (Lenferink et al., 2023).

Kinship, Type of Loss and Biological Sex

The collection of data on kinship and biological sex, as well as the treatment of these variables, in sample two was conducted using an identical methodology as employed in sample one. All participants in the second sample were traumatically bereaved due to either suicide, homicide, or an accident.

Procedure

Sample 1

The sample 1 study is part of the research conducted in the study "Rouw in het dagelijks leven," ("Grief in daily life"). During a telephone interview, participants completed assessments for PGD, PTSD, and depression symptoms at Timepoint 1 (T1), they also provided information on background and loss-related characteristics. Participants then completed ESM-based (Experience Sampling Methodology) grief reaction assessments five times a day for 14 days within the app "Ethica". At Timepoint 2 (T2), participants repeated similar assessments as in T1 via telephone interview.

This study only used use the TGI-CA results from T1 and information gathered on kinship, type of loss and biological sex during T1. Ethical approval was obtained by the researchers at the University of Twente before data collection.

Sample 2

The sample 2 study is also part of the main study "Grief in Daily Life", employing two sets of questionnaires and an ESM part, following the same time phases as in sample one. Assessments in both studies are similar, however, sample two used the TGI-SR+ questionnaire instead of the TGI-CA interview version.

This study only used use the TGI-SR+ results from T1 and information gathered on kinship, type of loss and biological sex during T1. Ethical approval was obtained by the researchers at the University of Twente before data collection.

Data Analysis

The statistical analyses were conducted using the software RStudio version 2023.12.1+402. The data in the current study was computed from two datasets. Thus prior to data analysis, these datasets were combined.

The independent categorical variables were kinship, type of loss and biological sex, the dependent continuous variable was PGD symptoms.

To test whether an association existed between kinship, type of loss, biological sex and PGD symptoms, each relationship was initially examined individually. Subsequently, a three-way ANOVA analysis was performed to explore the interactions between these variables in relation to PGD symptoms. This type of analysis was chosen due to the combination of three independent categorical variables and one dependent continuous variable.

To be able to conduct a three-way ANOVA, the data needed to meet certain assumptions. First, detection of significant outliers was done upon visual inspection of a boxplot graph. Second, to test whether the dependent variable was normally distributed, the Shapiro-Wilk test was performed, alongside of visual inspection of a Q-Q plot. To test for homoscedasticity, the Levene's test was performed, along with a visual inspection of a residuals vs. predicted plot. After assumption testing, the three-way ANOVA was performed.

Results

Descriptive Statistics

The combined sample of the study consisted of 132 participants. However, the final sample excluded 5 participants due to suicidal ideations. The remaining sample consisted of 127 participants. The participants' age in sample one ranged from 20 to 84. The participants' age in sample two ranged from 29 to 76. Around 78% (N = 62) of the participants in sample one identified as female and 23% (N = 18) as male. Around 85% (N = 40) of the participants in sample two identified as female, 15% (N = 7) as male.

The total PGD score ranged between 22 and 101 (M = 50.7, SD = 21.5), whilst possible scores could range between 22 and 110. Of the 127 participants, 28 participants had a score above or equal to the cut-off score of 71, indicative of disturbed grief. See Table 1 for an overview of participant and loss characteristics.

Table 1*Characteristics of Bereaved People (N = 127)*

Characteristics	M (SD)	N (%)
Gender		
Male		25 (19.7)
Female		102 (80.3)
Age	46.9 (15.3)	
Country of birth		
The Netherlands		70 (55.1)
Germany		46 (36.2)
Other		11 (8.7)
Level of education		
High school		19 (15.0)
Vocational education		32 (25.2)
College/ university		76 (59.8)
Kinship		
Child / partner		42 (23.1)
Other		85 (76.9)
Type of loss		
Traumatically bereaved		54 (42.8)
Non-traumatically bereaved		73 (57.2)
Time since loss	6.4 (7.7)	
Age deceased	53.4 (22.6)	

Checking Assumptions Three-way ANOVA

The assumptions of the three-way ANOVA were met. An examination of a Q-Q plot indicated no significant outliers. The Shapiro-Wilk test proved the normality of the residuals of the dependent variable, $W = .990$, $p = .508$. This finding is supported by a Q-Q plot, which suggests the normality of residuals. The Levene's test did not prove homoscedasticity, $F = 2.50$, $p = .020$. A visual inspection of a residuals vs. predicted plot suggests that the assumption is not violated. However, the generalizability of the results needs to be considered with caution.

Results ANOVA analysis for Total PGD Score

A three-way ANOVA was conducted to examine the relationship between kinship, type of loss and biological sex and their interaction effects, on the total PGD score. Table 2 shows the results of the ANOVA model.

Table 2

ANOVA Results for Total PGD Score

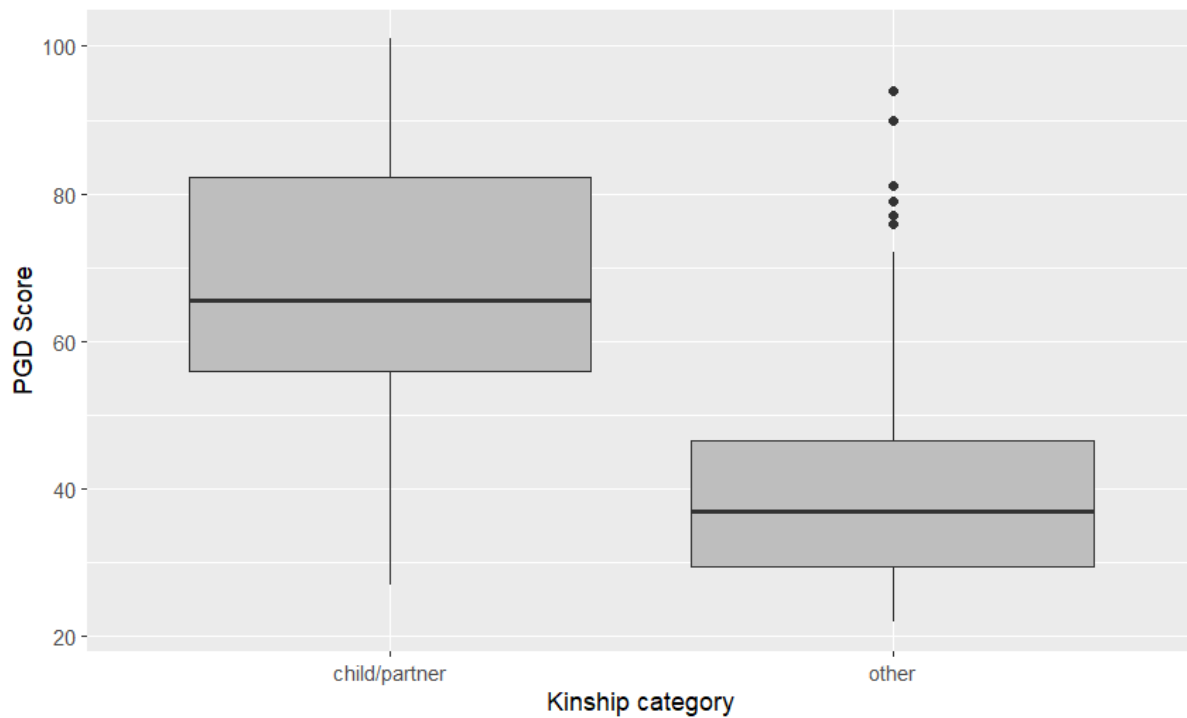
Predictor	Sum of Squares	<i>df</i>	Mean Square	<i>F</i>	<i>p</i>
Kinship	17905	1	17905	87.55	<.001
Type of loss	14003	1	14003	68.48	<.001
Biological sex	1330	1	1330	6.50	.012
Type of loss x kinship	13	1	13	0.06	.804
Kinship x biological sex	26	1	26	0.13	.724
Biological sex x type of loss	416	1	416	2.04	.156
Type of loss x biological sex x kinship	176	1	176	0.86	.356
Residuals	24336	119	205		

Note. ANOVA = Analysis of Variance PGD = Prolonged Grief Disorder

Association Kinship and PGD Score

The results indicated a significant association between kinship and the total PGD score, $F(1, 119) = 87.55, p < .001$. Due to the p -value $< .05$, the null hypothesis can be rejected, which states that kinship is not associated with the total PGD score. The effect of kinship on the total PGD score was significant, with a partial eta squared value of 0.42, 95% CI [0.32, 1.00], indicating a large effect. As shown in Figure 1, a significant difference in PGD score exists between the two categories child/partner and other. Individuals who lost a child or partner have a higher PGD score. The boxplot in Figure 1 shows a few outliers for the level “other” within the factor “kinship”. After rerunning the results, excluding these outliers, the same conclusion can be drawn; kinship is associated with the total PGD score, $F(1, 112) = 142.92, p < .001$. After excluding the outliers, the effect of kinship on the total PGD score remains significant, with a partial eta squared value of 0.56, 95% CI [0.46, 1.00], indicating a large effect.

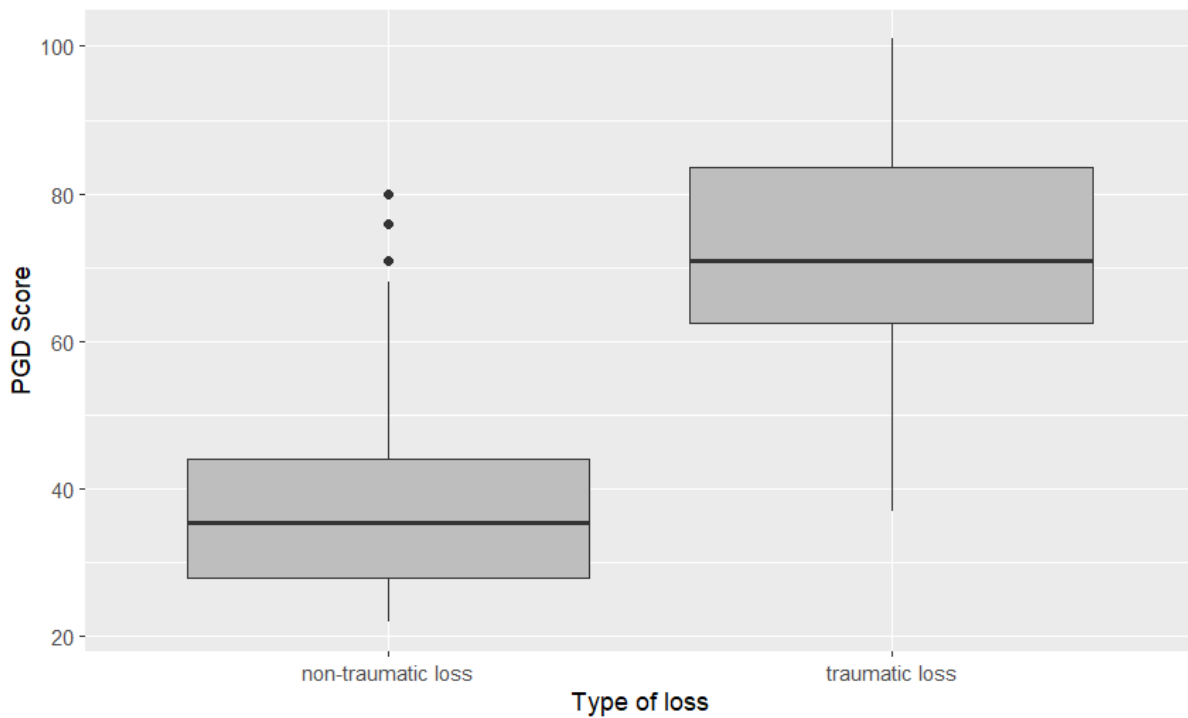
Figure 1
Boxplot of PGD Total Scores by Kinship



Association Type of Loss and PGD Symptoms

The results indicated a significant association between the type of loss and the total PGD score, $F(1, 119) = 68.48, p < .001$. Due to the p -value $< .05$, the null hypothesis can be rejected, which states that the type of loss is not associated with the total PGD score. The effect of type of loss on the total PGD score was significant, with a partial eta squared value of 0.37, 95% CI [0.26, 1.00], indicating a large effect. As shown in Figure 2, a significant difference in PGD score exists between the two categories of traumatic and non-traumatic loss. Individuals who lost a loved one following a traumatic event have a higher PGD score. The boxplot in Figure 2 shows a few outliers for the level “non-traumatic loss” within the factor “type of loss”. After rerunning the results, excluding these outliers, the same conclusion can be drawn; type of loss is associated with the total PGD score, $F(1, 112) = 96.72, p < .001$. After excluding the outliers, the effect of type of loss on the total PGD score remains significant, with a partial eta squared value of 0.46, 95% CI [0.35, 1.00], indicating a large effect.

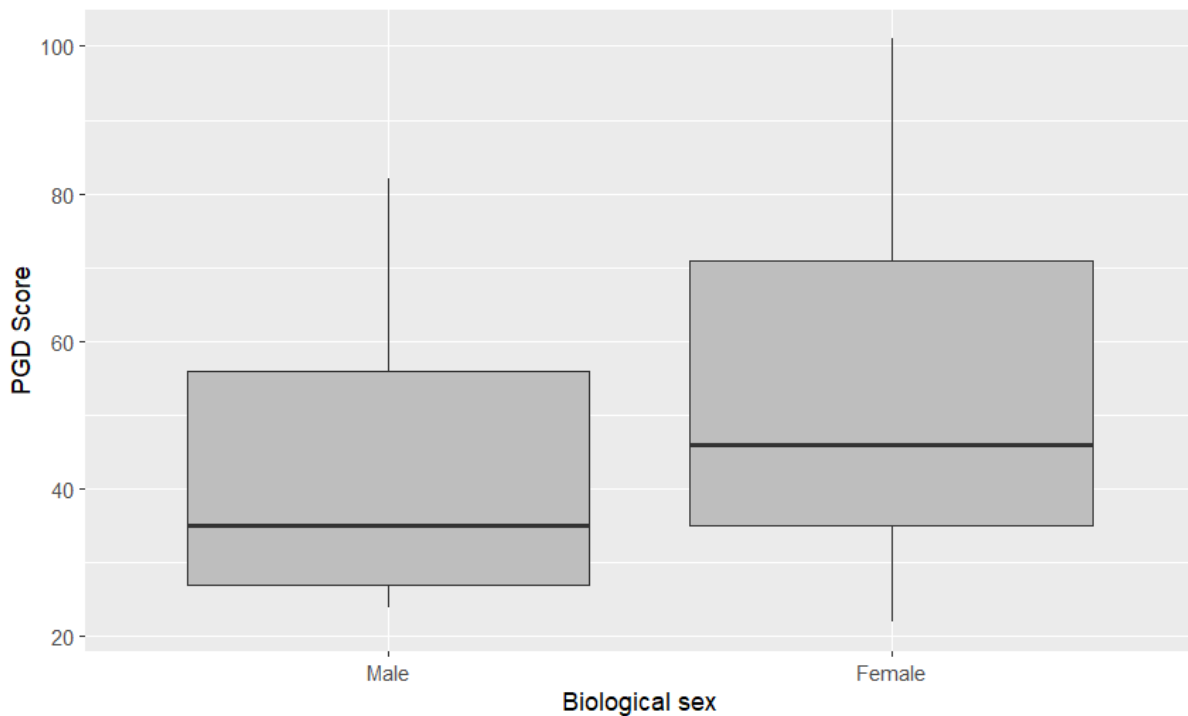
Figure 2
Boxplot of PGD Total Scores by Type of Loss



Association Biological Sex and PGD Score

The results indicated a significant association between biological sex and the total PGD score, $F(1, 119) = 6.50, p = .012$. Due to the p -value $< .05$, the null hypothesis can be rejected, which states that biological sex is not associated with PGD symptoms. The effect of biological sex on the total PGD score was significant, with a partial eta squared value of 0.06, 95% CI [0.01, 1.00], indicating a medium effect. As shown in Figure 3, a significant difference in PGD score exists between the two biological sexes male and female. Female individuals who lost a loved one have a higher PGD score.

Figure 3
Boxplot of PGD Total Scores by Biological Sex



Interaction Kinship and Type of Loss on PGD Score

The results indicated no significant interaction effect of kinship and type of loss on the total PGD score, $F(1, 119) = 0.06, p = .804$. Due to the p -value $>.05$, the null hypothesis cannot be rejected, which states that there is no interaction effect between kinship and type of loss on the total PGD score. The partial eta squared value is $<.001$, 95% CI [0.00, 1.00], indicating a small effect.

Interaction Biological Sex and Kinship on PGD Score

The results indicated no significant interaction effect of biological sex and kinship on the total PGD score, $F(1, 119) = 0.13, p = .724$. Due to the p -value $>.05$, the null hypothesis cannot be rejected, which states that there is no interaction effect between biological sex and kinship on the total PGD score. The partial eta squared value is $.001$, 95% CI [0.00, 1.00], indicating a small effect.

Interaction Type of Loss and Biological Sex on PGD Score

The results indicated no significant interaction effect of type of loss and biological sex on the total PGD score, $F(1, 119) = 2.04, p = .156$. Due to the p -value $>.05$, the null hypothesis cannot be rejected, which states that there is no interaction effect between the type

of loss and biological sex on the total PGD score. The partial eta squared value is 0.02, 95% CI [0.00, 1.00], indicating a small effect.

Interaction Kinship, Type of Loss and Biological Sex on PGD Score

The results indicated no significant three-way interaction effect of kinship, type of loss and biological sex on the total PGD score, $F(1, 119) = 0.86, p = .356$. Due to the p -value $>.05$, the null hypothesis cannot be rejected, which states that there is no three-way interaction effect between kinship, type of loss and biological sex on the total PGD score. The partial eta squared value is .007, 95% CI [0.00, 1.00], indicating a small effect. The results of the three-way interaction testing should be interpreted with caution due to uneven distribution of participants across the levels of each category, as illustrated in Table 3.

Table 3

Distribution of Data per Category

Gender	Male		Female	
	Traumatic loss	Non-traumatic loss	Traumatic loss	Non-traumatic loss
Type of loss				
Kinship				
Child/partner	7	2	28	7
Other	1	15	19	48

Discussion

This research explored the association between kinship, type of loss, biological sex, and their interaction effects, on PGD symptoms. The study explored differences in traumatically and non-traumatically bereaved individuals, as a clear delineation between these two groups is often lacking in grief-related research. Making a distinction between these two groups is of importance as individuals experiencing traumatic loss exhibit more severe PGD symptoms, and underlying causes are important to investigate (Djelantik et al., 2020). Findings showed a strong association of kinship and type of loss with the total PGD score. A weak association was found for biological sex and the total PGD score. No significant interaction effects were found between two or three factors on the total PGD score.

Association Kinship and PGD Score

The results of this study found that kinship is strongly associated with the total PGD score. Individuals having lost a child or partner have significantly higher PGD scores compared to individuals who lost a loved one such as a sibling or grandparent. The findings are in line with the expectations, stating that the loss of a child or partner are associated with elevated risk of experiencing more severe PGD symptoms, compared to other types of kinship (Fernández-Alcántara & Zech, 2017; Thieleman et al., 2023). A possible reason for the fact that losing a child or partner results in more severe grief reactions is that the bereaved individual, being a parent or partner, usually have spent a lot of time in life with their deceased loved one and often in the same home, which can lead to a heightened sense of loss in their lives (Fernández-Alcántara & Zech, 2017). Additionally, the loss of a child feels unnatural, as it is opposed to the natural cycle of life (Osterweis et al., 1984). Research has also shown that individuals who lost a child or spouse can be blamed for the death by others, leading to increased social isolation (Yuan et al., 2024). This in turn can increase the risk of developing more severe PGD symptoms.

Association Type of Loss and PGD Score

The results found an association between type of loss and an elevated risk of experiencing more severe PGD symptoms. Participants who have lost their loved one due to a traumatic event, being murder, suicide, or an accident, have a significantly higher PGD score compared to non-traumatic losses. These findings support the hypothesis that traumatically bereaved individuals experience more severe grief reactions. The finding that the type of loss is associated with the total PGD score is in line with the expectations (Djelantik et al., 2020; Hibberd et al., 2010). A possible explanation for this finding is that traumatic losses cause more emotional distress because of more intrusive and negative memories, along with a disruption of positive and self-evident assumptions about the world, for example that the world is a safe place (Djelantik et al., 2020). The element of suddenness in traumatic losses is also associated with experiencing more severe PGD symptoms (Schaal et al., 2010). Additionally, a reason for this finding could be that people who have lost a loved one following a traumatic event, mainly due to an accident, feel as if someone else is responsible for the death (Melhem et al., 2007).

Association Biological Sex and PGD Score

The results found a weak association between biological sex and the total PGD score, being that female participants have higher PGD scores. The findings are in line with the expectations that females tend to have higher levels of traumatic grief (Chen et al., 1999). A potential explanation for the gender differences could be that women score higher on personality traits linked to adverse mental health outcomes (Heeke et al., 2017). For example, women tend to react with anxiety and avoidant behaviour when they experience stressful situations, which may make them more prone to develop mental health problems following bereavement.

Interaction Effects of Kinship, Type of Loss, Biological Sex and PGD score

The results found no two- or three-way significant interaction effects between any of the three independent variables: kinship, type of loss and biological sex. This means that the combined effect of all three variables on the PGD score is not significant. It is a possibility that no significant interaction effects were found because the variables do not interact. This finding shows that the influence of kinship and biological sex on PGD symptoms is not dependent on the type of loss.

Another possible reason for not finding interaction effects, even though they were expected based on previous research (Buur et al., 2024; Heeke et al., 2017; Kokou-Tchri, 2024; Stroebe et al., 2007), could be due to the unequal distribution of participants among levels of each factor. As an example, there was only one male participant who lost a loved one in the category “other” following a traumatic event and only two male participants lost a child/partner following a non-traumatic event.

After reviewing the mean squares of the main effects and interaction effects, which are far smaller for the interaction effect, it could be possible that the interaction effects might not have enough power to reach statistical significance (Leon & Heo, 2009). This suggests that to determine whether significant interaction effects exist, a larger sample size would be necessary.

Limitations and Future Directions

This study, while contributing important findings regarding the relationship between kinship, type of loss, biological sex and PGD symptoms, has several limitations that warrant discussion for future research. First, the study has a relatively small sample size and the

distribution among factor levels is uneven, see Table 3. As can be seen in the results, the degree of uncertainty around the estimates of the effect size for the confidence interval is high, which is likely an effect of the smaller sample size. The sample distribution is not equal among factor levels, considering the high number of female participants and the low number of male participants. A possible explanation for this would be that research has shown that acceptance rates for grief-related studies are higher for women, since women who are more emotionally disturbed feel in greater need of support, and would therefore be more likely to participate (Stroebe & Stroebe, 1990). An equal distribution among factor levels is important as a population-representative sample is uniquely important in the field of grief research (Doering et al., 2022). Thus, future research should conduct a similar study, however, make use of stratified sampling. When dividing the total population over various strata, e.g. gender, one could select individuals from each stratum for participation to ensure equal distribution among factor levels.

Second, the nature of the recruitment strategy of both samples might have led to sampling bias, to be more specific self-selection bias. The participants were given the opportunity to participate in the study after filling in the grief meter or on recruitment posts online. Thus, it is likely that participants who are more willing to discuss their grief reactions, participate in the study, leading to a possible misrepresentation of the actual PGD scores among the total population (Stroebe & Stroebe, 1990). Additionally, research has also shown that participants in studies focussed on psychopathology often experience more severe symptoms compared to those who do not participate (Kaźmierczak et al., 2023). Future studies should ensure a more representable sample through recruitment via more diverse channels. Next to the grief meter and social media sites, recruitment strategies should focus on, for example, healthcare facilities and local organizations to approach participants. Ruling out self-selection bias in grief-related research is an obstacle, however, diversifying recruitment channels as much as possible will likely result in targeting participants with more varying levels of willingness to discuss their grief reactions. This could lead to a better representation of the actual population experiencing PGD symptoms. Another option to minimize self-selection bias would be to use a similar recruitment strategy as Kersting et al. (2011), where they selected a great number of participants in a country and excluded those who did not lose a significant other. However, to utilize this strategy, resources in terms of researcher capacity and time are a necessity.

Another possible explanation for the differences in PGD symptoms related to gender could be that low income and low socioeconomic status, which are often associated with being female (APA, 2010), are also associated with higher levels of PGD (Steil et al., 2019). This could explain why women, in general, might be more at risk for experiencing more severe PGD symptoms. Future studies should aim to establish possible interaction effects, in the research field of PGD, to be able to conclude the interactions between being female, low socioeconomic status and low income, since they are interesting variables to understand the underlying causes of the differences in experiencing PGD symptoms.

Conclusion

This study explored how kinship, type of loss, and biological sex relate to the severity of PGD symptoms. The findings showed that each of these factors individually affects how severe an individual's grief symptoms are. However, there was no evidence that these factors influence each other in how they affect PGD severity, meaning that the influence of kinship and biological sex on the PGD symptoms is not dependent on the type of loss. One limitation of the study was that the participants were not evenly spread across all groups, which might explain why no interactions were found. Future research should ensure participants are evenly distributed across all categories to test for interaction effects, optimize recruitment strategies and test for the influence of income and socioeconomic status in relation to gender.

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Appendix

```
#rscript psy thesis

#installing packages

install.packages("tidyverse")
install.packages("ggplot2")
install.packages("readr")
install.packages("dplyr")
install.packages("foreign")
install.packages("lubridate")
install.packages("anytime")
install.packages("car")
install.packages("rstatix")
install.packages("effectsize")

#library packages

library(tidyverse)
library(ggplot2)
library(readr)
library(dplyr)
library(foreign)
library(lubridate)
library(anytime)
library(car)
library(rstatix)
library(effectsize)

#downloading data files

ESM1 <- read.spss("ESM1_T1_T2_Wide.sav", to.data.frame = TRUE)
ESM3 <- read.spss("ESM3_T1.sav", to.data.frame = TRUE)

#removing suicidal ideations in ESM3

yes_responses_suicidal <- subset(ESM3, suicidal1.1 == "Ja")
```

```

ESM3_nosuic <- ESM3[!(ESM3$suicidal1.1 == "Ja" & !is.na(ESM3$suicidal1.1)),
]

#selecting variables of interest

ESM1_interestingvariables <- ESM1[, c("T1_ResponseId", "T1_Home_country",
"T1_Education", "T1_DoB", "T1_Gender", "T1_kinship",
"T1_kinship_8_TEXT","T1_cause", "T1_cause_5_TEXT", "T1_age_deceased",
"T1_DoD", "T1_TGI_CA_1_1", "T1_TGI_CA_1_2", "T1_TGI_CA_1_3",
"T1_TGI_CA_1_4", "T1_TGI_CA_1_5", "T1_TGI_CA_1_6", "T1_TGI_CA_1_7",
"T1_TGI_CA_1_8", "T1_TGI_CA_1_9", "T1_TGI_CA_1_10", "T1_TGI_CA_1_11",
"T1_TGI_CA_1_12", "T1_TGI_CA_1_13", "T1_TGI_CA_1_14", "T1_TGI_CA_1_15",
"T1_TGI_CA_1_16", "T1_TGI_CA_1_17", "T1_TGI_CA_1_18", "T1_TGI_CA_1_19",
"T1_TGI_CA_1_20", "T1_TGI_CA_1_21", "T1_TGI_CA_1_22")]

ESM3_nosuic_interestingvariables <- ESM3_nosuic[,c("ResponseId",
"Home_country", "Education", "DoB", "Gender", "kinship", "kinship_8_TEXT",
"cause", "cause_5_TEXT", "age_deceased", "DoD", "TGI_1","TGI_2", "TGI_3",
"TGI_4", "TGI_5", "TGI_6", "TGI_7", "TGI_8", "TGI_9", "TGI_10", "TGI_11",
"TGI_12", "TGI_13", "TGI_14", "TGI_15", "TGI_16", "TGI_17", "TGI_18",
"TGI_19", "TGI_20", "TGI_21", "TGI_22")]

#merging data sets

merged_ESM <- merge(ESM1_interestingvariables,
ESM3_nosuic_interestingvariables, by.x = c("T1_ResponseId",
"T1_Home_country", "T1_Education", "T1_DoB", "T1_Gender", "T1_kinship",
"T1_kinship_8_TEXT","T1_cause", "T1_cause_5_TEXT", "T1_age_deceased",
"T1_DoD", "T1_TGI_CA_1_1", "T1_TGI_CA_1_2", "T1_TGI_CA_1_3",
"T1_TGI_CA_1_4", "T1_TGI_CA_1_5", "T1_TGI_CA_1_6", "T1_TGI_CA_1_7",
"T1_TGI_CA_1_8", "T1_TGI_CA_1_9", "T1_TGI_CA_1_10", "T1_TGI_CA_1_11",
"T1_TGI_CA_1_12", "T1_TGI_CA_1_13", "T1_TGI_CA_1_14", "T1_TGI_CA_1_15",
"T1_TGI_CA_1_16", "T1_TGI_CA_1_17", "T1_TGI_CA_1_18", "T1_TGI_CA_1_19",
"T1_TGI_CA_1_20", "T1_TGI_CA_1_21", "T1_TGI_CA_1_22"),

by.y = c("ResponseId", "Home_country", "Education",
"DoB", "Gender", "kinship", "kinship_8_TEXT", "cause", "cause_5_TEXT",
"age_deceased", "DoD", "TGI_1","TGI_2", "TGI_3", "TGI_4", "TGI_5", "TGI_6",
"TGI_7", "TGI_8", "TGI_9", "TGI_10", "TGI_11", "TGI_12", "TGI_13",
"TGI_14", "TGI_15", "TGI_16", "TGI_17", "TGI_18", "TGI_19", "TGI_20",
"TGI_21", "TGI_22"),

all = TRUE)

#adding type of loss as variable (traumatic / general loss)

traumatic_id <- c(ESM3_nosuic_interestingvariables$ResponseId)

merged_ESM$loss_classification <- ifelse(merged_ESM$T1_ResponseId %in%
traumatic_id, "traumatic loss", "non-traumatic loss")

# traumatic in ESM1 = "R_2R1FMnWazq9vweC", "R_rpwZpvYD7nbnAYV",
"R_yKDGVPda34NRZMR","R_5upKzyRnmvuaO89", "R_1pXAcPilRXWae4i",
"R_3rIoMqwmTdnWJOA", "R_3gSGpbAlmtFrGfI", "R_3HYR89Xn22KSEy0")

rows_to_change <- c(38, 119, 126, 88, 18, 73, 57, 60)

# Change "non-traumatic loss" to "traumatic loss" for the specified rows

```

```

merged_ESM$loss_classification[rows_to_change] <- "traumatic loss"
#translating values to same language (gender)
translate <- function(value) {
  if (value == "Vrouw") {
    return("Woman")
  } else if (value == "Man") {
    return("Man")
  } else if (value == "Woman") {
    return("Woman")
  } else {
    return(value)
  }
}

merged_ESM$T1_Gender <- sapply(merged_ESM$T1_Gender, translate)
#translating values to same language (kinship)
translate2 <- function(value) {
  if (value == "Kind") {
    return("Child")
  } else if (value == "Broer/zus") {
    return("Brother/sister")
  } else if (value == "Friend") {
    return("Friend")
  } else if (value == "Child") {
    return("Child")
  } else if (value == "Grandchild") {
    return("Grandchild")
  } else if (value == "Partner") {
    return("Partner")
  } else if (value == "Grandparent") {
    return("Grandparent")
  } else if (value == "None of the above, namely") {
    return("None of the above, namely")
  }
}

```

```

} else if (value == "Geen van bovenstaande, namelijk mijn:") {
  return("None of the above, namely")
} else if (value == "Vader/moeder") {
  return("Father/mother")
} else if (value == "Sibling") {
  return("Sibling")
} else if (value == "Parent") {
  return("Parent")
} else if (value == "Vriend(in)") {
  return("Friend")
} else {
  return(value)
}
}

merged_ESM$T1_kinship <- sapply(merged_ESM$T1_kinship, translate2)
#translating values to same language (kinship_other)
translate3 <- function(value) {
  if (value == "Moeder en broer
") {
    return("Mother and brother")
  } else if (value == "Tante
") {
    return("Aunt")
  } else if (value == "ex-vrouw
") {
    return("Ex-wife")
  } else if (value == "tante
") {
    return("Aunt")
  } else if (value == "schoonmoeder
") {
    return("Mother in law")
  } else if (value == "Neef
") {

```

```

    return("Nephew")
  } else if (value == "Onkel
") {
    return("Uncle")
  } else if (value == "neefje als kind
") {
    return("Nephew")
  } else if (value == "Geliefde (wij woonden niet samen)
") {
    return("Lover")
  } else if (value == "Geliefde (maar nog geen partner)
") {
    return("Lover")
  } else if (value == "Oom
") {
    return("Uncle")
  } else if (value == "Nicht
") {
    return("Niece")
  } else {
    return(value)
  }
}

```

```
merged_ESM$T1_kinship_8_TEXT <- sapply(merged_ESM$T1_kinship_8_TEXT,
translate3)
```

```
#translating values to same language (TGI_CA_1_)
```

```
translate4 <- function(value) {
  if (value == "1. Nooit") {
    return("1. Never")
  } else if (value == "Nooit") {
    return("1. Never")
  } else if (value == "2. Zelden") {
    return("2. Rarely")
  } else if (value == "Zelden") {

```

```

    return("2. Rarely")
  } else if (value == "3. Soms") {
    return("3. Sometimes")
  } else if (value == "Soms") {
    return("3. Sometimes")
  } else if (value == "4. Vaak") {
    return("4. Often")
  } else if (value == "Vaak") {
    return("4. Often")
  } else if (value == "5. Altijd") {
    return("5. Always")
  } else if (value == "Altijd") {
    return("5. Always")
  } else {
    return(value)
  }
}
translate5 <- function(value) {
  if (value == "1.Never") {
    return("1. Never")
  } else if (value == "2.Rarely") {
    return("2. Rarely")
  } else if (value == "3.Sometimes") {
    return("3. Sometimes")
  } else if (value == "4.Often") {
    return("4. Often")
  } else if (value == "5.Always") {
    return("5. Always")
  } else {
    return(value)
  }
}

```

```
merged_ESM$T1_TGI_CA_1_1 <- sapply(merged_ESM$T1_TGI_CA_1_1, translate4)
merged_ESM$T1_TGI_CA_1_2 <- sapply(merged_ESM$T1_TGI_CA_1_2, translate4)
merged_ESM$T1_TGI_CA_1_3 <- sapply(merged_ESM$T1_TGI_CA_1_3, translate4)
merged_ESM$T1_TGI_CA_1_4 <- sapply(merged_ESM$T1_TGI_CA_1_4, translate4)
merged_ESM$T1_TGI_CA_1_5 <- sapply(merged_ESM$T1_TGI_CA_1_5, translate4)
merged_ESM$T1_TGI_CA_1_6 <- sapply(merged_ESM$T1_TGI_CA_1_6, translate4)
merged_ESM$T1_TGI_CA_1_7 <- sapply(merged_ESM$T1_TGI_CA_1_7, translate4)
merged_ESM$T1_TGI_CA_1_8 <- sapply(merged_ESM$T1_TGI_CA_1_8, translate4)
merged_ESM$T1_TGI_CA_1_9 <- sapply(merged_ESM$T1_TGI_CA_1_9, translate4)
merged_ESM$T1_TGI_CA_1_10 <- sapply(merged_ESM$T1_TGI_CA_1_10, translate4)
merged_ESM$T1_TGI_CA_1_11 <- sapply(merged_ESM$T1_TGI_CA_1_11, translate4)
merged_ESM$T1_TGI_CA_1_12 <- sapply(merged_ESM$T1_TGI_CA_1_12, translate4)
merged_ESM$T1_TGI_CA_1_13 <- sapply(merged_ESM$T1_TGI_CA_1_13, translate4)
merged_ESM$T1_TGI_CA_1_14 <- sapply(merged_ESM$T1_TGI_CA_1_14, translate4)
merged_ESM$T1_TGI_CA_1_15 <- sapply(merged_ESM$T1_TGI_CA_1_15, translate4)
merged_ESM$T1_TGI_CA_1_16 <- sapply(merged_ESM$T1_TGI_CA_1_16, translate4)
merged_ESM$T1_TGI_CA_1_17 <- sapply(merged_ESM$T1_TGI_CA_1_17, translate4)
merged_ESM$T1_TGI_CA_1_18 <- sapply(merged_ESM$T1_TGI_CA_1_18, translate4)
merged_ESM$T1_TGI_CA_1_19 <- sapply(merged_ESM$T1_TGI_CA_1_19, translate4)
merged_ESM$T1_TGI_CA_1_20 <- sapply(merged_ESM$T1_TGI_CA_1_20, translate4)
merged_ESM$T1_TGI_CA_1_21 <- sapply(merged_ESM$T1_TGI_CA_1_21, translate4)
merged_ESM$T1_TGI_CA_1_22 <- sapply(merged_ESM$T1_TGI_CA_1_22, translate4)
```

```
merged_ESM$T1_TGI_CA_1_1 <- sapply(merged_ESM$T1_TGI_CA_1_1, translate5)
merged_ESM$T1_TGI_CA_1_2 <- sapply(merged_ESM$T1_TGI_CA_1_2, translate5)
merged_ESM$T1_TGI_CA_1_3 <- sapply(merged_ESM$T1_TGI_CA_1_3, translate5)
merged_ESM$T1_TGI_CA_1_4 <- sapply(merged_ESM$T1_TGI_CA_1_4, translate5)
merged_ESM$T1_TGI_CA_1_5 <- sapply(merged_ESM$T1_TGI_CA_1_5, translate5)
merged_ESM$T1_TGI_CA_1_6 <- sapply(merged_ESM$T1_TGI_CA_1_6, translate5)
merged_ESM$T1_TGI_CA_1_7 <- sapply(merged_ESM$T1_TGI_CA_1_7, translate5)
merged_ESM$T1_TGI_CA_1_8 <- sapply(merged_ESM$T1_TGI_CA_1_8, translate5)
merged_ESM$T1_TGI_CA_1_9 <- sapply(merged_ESM$T1_TGI_CA_1_9, translate5)
```



```

merged_ESM$T1_TGI_CA_1_10 <- sapply(merged_ESM$T1_TGI_CA_1_10, translate5)
merged_ESM$T1_TGI_CA_1_11 <- sapply(merged_ESM$T1_TGI_CA_1_11, translate5)
merged_ESM$T1_TGI_CA_1_12 <- sapply(merged_ESM$T1_TGI_CA_1_12, translate5)
merged_ESM$T1_TGI_CA_1_13 <- sapply(merged_ESM$T1_TGI_CA_1_13, translate5)
merged_ESM$T1_TGI_CA_1_14 <- sapply(merged_ESM$T1_TGI_CA_1_14, translate5)
merged_ESM$T1_TGI_CA_1_15 <- sapply(merged_ESM$T1_TGI_CA_1_15, translate5)
merged_ESM$T1_TGI_CA_1_16 <- sapply(merged_ESM$T1_TGI_CA_1_16, translate5)
merged_ESM$T1_TGI_CA_1_17 <- sapply(merged_ESM$T1_TGI_CA_1_17, translate5)
merged_ESM$T1_TGI_CA_1_18 <- sapply(merged_ESM$T1_TGI_CA_1_18, translate5)
merged_ESM$T1_TGI_CA_1_19 <- sapply(merged_ESM$T1_TGI_CA_1_19, translate5)
merged_ESM$T1_TGI_CA_1_20 <- sapply(merged_ESM$T1_TGI_CA_1_20, translate5)
merged_ESM$T1_TGI_CA_1_21 <- sapply(merged_ESM$T1_TGI_CA_1_21, translate5)
merged_ESM$T1_TGI_CA_1_22 <- sapply(merged_ESM$T1_TGI_CA_1_22, translate5)

```

```
#translating values to same language (home country)
```

```

translate6 <- function(value) {
  if (value == "België") {
    return("Belgium")
  } else if (value == "Deutschland") {
    return("Germany")
  } else if (value == "Indonesië") {
    return("Indonesia")
  } else if (value == "nederland") {
    return("Netherlands")
  } else if (value == "Nederland") {
    return("Netherlands")
  } else if (value == "nederlandse antillen") {
    return("Netherlands")
  } else if (value == "Nl") {

```

```

    return("Netherlands")
  } else if (value == "Oekraïne
") {
    return("Ukraine")
  } else if (value == "paramaribo
") {
    return("Surinam")
  } else {
    return(value)
  }
}

merged_ESM$T1_Home_country <- sapply(merged_ESM$T1_Home_country,
translate6)

#translating values to same language (education)
translate7 <- function(value) {
  if (value == "High school") {
    return("High school")
  } else if (value == "Vocational education") {
    return("Vocational education")
  } else if (value == "College/university") {
    return("College/university")
  } else if (value == "middelbare school") {
    return("High school")
  } else if (value == "MBO (MEAO, MTS)") {
    return("Vocational education")
  } else if (value == "HBO, WO, universiteit (HTS, HEAO)") {
    return("College/university")
  } else {
    return(value)
  }
}

merged_ESM$T1_Education <- sapply(merged_ESM$T1_Education, translate7)

```

```

#translating values to same language (cause of death)
translate8 <- function(value) {
  if (value == "Physical disease") {
    return("Physical disease")
  } else if (value == "Accident") {
    return("Accident")
  } else if (value == "Suicide") {
    return("Suicide")
  } else if (value == "Homicide/murder") {
    return("Homicide/murder")
  } else if (value == "Ongeval (bijvoorbeeld ongeluk, verkeersongeval,
verdrinking, vergifting)") {
    return("Accident")
  } else if (value == "Zelfdoding") {
    return("Suicide")
  } else if (value == "Moord of doodslag") {
    return("Homicide/murder")
  } else if (value == "Other, namely") {
    return("Other, namely")
  } else if (value == "Anders, namelijk") {
    return("Other, namely")
  } else if (value == "9") {
    return("Other, namely")
  } else {
    return(value)
  }
}

merged_ESM$T1_cause <- sapply(merged_ESM$T1_cause, translate8)

#translating values to same language (cause of death TEXT)
translate9 <- function(value) {
  if (value == "ungeklärt
") {
    return("Unknown")
  }
}

```

```

    } else if (value == "onbekend
") {
        return("Unknown")
    } else if (value == "Mijn moeder (63) op 20-1-2021 en mijn broer op 1-1-
2018
") {
        return("Unknown")
    } else if (value == "Hartstilstand
") {
        return("Physical disease")
    } else if (value == "cva
") {
        return("Physical disease")
    } else if (value == "euthanasie
") {
        return("Euthanasia")
    } else {
        return(value)
    }
}

```

```

merged_ESM$T1_cause_5_TEXT <- sapply(merged_ESM$T1_cause_5_TEXT,
translate9)

```

```

#assigning numeric values to TGI scores

```

```

Assign_numeric_value <- function(value) {
    if (value == "1. Never") {
        return(1)
    } else if (value == "2. Rarely") {
        return(2)
    } else if (value == "3. Sometimes") {
        return(3)
    } else if (value == "4. Often") {
        return(4)
    } else if (value == "5. Always") {
        return(5)
    }
}

```

```
}  
  
}  
  
merged_ESM$Num_TGI1 <- sapply(merged_ESM$T1_TGI_CA_1_1,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI2 <- sapply(merged_ESM$T1_TGI_CA_1_2,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI3 <- sapply(merged_ESM$T1_TGI_CA_1_3,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI4 <- sapply(merged_ESM$T1_TGI_CA_1_4,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI5 <- sapply(merged_ESM$T1_TGI_CA_1_5,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI6 <- sapply(merged_ESM$T1_TGI_CA_1_6,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI7 <- sapply(merged_ESM$T1_TGI_CA_1_7,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI8 <- sapply(merged_ESM$T1_TGI_CA_1_8,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI9 <- sapply(merged_ESM$T1_TGI_CA_1_9,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI10 <- sapply(merged_ESM$T1_TGI_CA_1_10,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI11 <- sapply(merged_ESM$T1_TGI_CA_1_11,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI12 <- sapply(merged_ESM$T1_TGI_CA_1_12,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI13 <- sapply(merged_ESM$T1_TGI_CA_1_13,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI14 <- sapply(merged_ESM$T1_TGI_CA_1_14,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI15 <- sapply(merged_ESM$T1_TGI_CA_1_15,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI16 <- sapply(merged_ESM$T1_TGI_CA_1_16,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI17 <- sapply(merged_ESM$T1_TGI_CA_1_17,  
Assign_numeric_value)  
  
merged_ESM$Num_TGI18 <- sapply(merged_ESM$T1_TGI_CA_1_18,  
Assign_numeric_value)
```

```

merged_ESM$Num_TGI19 <- sapply(merged_ESM$T1_TGI_CA_1_19,
Assign_numeric_value)

merged_ESM$Num_TGI20 <- sapply(merged_ESM$T1_TGI_CA_1_20,
Assign_numeric_value)

merged_ESM$Num_TGI21 <- sapply(merged_ESM$T1_TGI_CA_1_21,
Assign_numeric_value)

merged_ESM$Num_TGI22 <- sapply(merged_ESM$T1_TGI_CA_1_22,
Assign_numeric_value)

#kinship value distribution
print(table(merged_ESM$T1_kinship))
print(table(merged_ESM$T1_kinship_8_TEXT))

#cause of death distribution
print(table(merged_ESM$T1_cause))
print(table(merged_ESM$T1_cause_5_TEXT))

#combining DoB columns into one
merged_ESM$DoBcomb <- ifelse(is.na(merged_ESM$DoB),
as.character(merged_ESM$T1_DoB),
                                paste(merged_ESM$DoB, merged_ESM$T1_DoB))

#age, select all dd-mm-yy from DoBcomb in merged_ESM
DoB_dd_mm_yy <- grepl("\\d{2}-\\d{2}-\\d{4}", merged_ESM$DoBcomb)
Date_stripe <- merged_ESM[DoB_dd_mm_yy,]
Date_stripe$DoBcomb <- as.Date(Date_stripe$DoBcomb, format = "%d-%m-%Y")
Date_stripe <- Date_stripe[!is.na(Date_stripe$DoBcomb),]

DoB.dd.mm.yy <- grepl("\\d{2}\\d{2}\\d{4}", merged_ESM$DoBcomb)
Date_dot <- merged_ESM[DoB.dd.mm.yy,]
Date_dot$DoBcomb <- as.Date(Date_dot$DoBcomb, format = "%d.%m.%Y")
Date_dot <- Date_dot[!is.na(Date_dot$DoBcomb),]

DoBddmmyy <- grepl("\\d{2}\\d{2}\\d{4}", merged_ESM$DoBcomb)
Date_slash <- merged_ESM[DoBddmmyy,]
Date_slash$DoBcomb <- as.Date(Date_slash$DoBcomb, format = "%d/%m/%Y")
Date_slash <- Date_slash[!is.na(Date_slash$DoBcomb),]

```

```

Date_stripe$Age <- as.numeric(difftime(Sys.Date(), Date_stripe$DoBcomb,
units = "days") / 365.25)

Date_dot$Age <- as.numeric(difftime(Sys.Date(), Date_dot$DoBcomb, units =
"days") / 365.25)

Date_slash$Age <- as.numeric(difftime(Sys.Date(), Date_slash$DoBcomb, units
= "days") / 365.25)

combined_ESM <- cbind(Date_stripe, Date_slash$Age, Date_dot$Age)

#combining age sets again

all_ages <- c(Date_dot$Age, Date_stripe$Age, Date_slash$Age)

View(all_ages)

mean_age <- mean(all_ages, na.rm = TRUE)

print(mean_age)

sd_age <- sd(all_ages, na.rm = TRUE)

print(sd_age)

min_value_age <- min(all_ages)

print(min_value_age)

max_value_age <- max(all_ages)

print(max_value_age)

#mean age deceased

mean_agedeceased <- mean(merged_ESM$T1_age_deceased, na.rm = TRUE)

print(mean_agedeceased)

sd_agedeceased <- sd(merged_ESM$T1_age_deceased, na.rm = TRUE)

print(sd_agedeceased)

#calculating time since loss

calculate_time_since_loss <- function(T1_DoD) {
  formats <- c("%d-%m-%Y", "%d.%m.%Y", "%d/%m/%Y")
  for (fmt in formats) {
    parsed_date <- as.Date(T1_DoD, format = fmt)
    if (!is.na(parsed_date)) {
      time_since_loss <- as.numeric(difftime(Sys.Date(), parsed_date, units
= "days") / 365.25)
      return(time_since_loss)
    }
  }
}

```

```

    return(NA)
  }

merged_ESM$TimeSinceLoss <- sapply(merged_ESM$T1_DoD,
  calculate_time_since_loss)

merged_ESM <- merged_ESM[!is.na(merged_ESM$TimeSinceLoss), ]

mean_tsl <- mean(merged_ESM$TimeSinceLoss, na.rm = TRUE)
sd_tsl <- sd(merged_ESM$TimeSinceLoss, na.rm = TRUE)
print(mean_tsl)
print(sd_tsl)

#sum score TGI
columns_to_sum <- c("Num_TGI1", "Num_TGI2", "Num_TGI3", "Num_TGI4",
  "Num_TGI5", "Num_TGI6", "Num_TGI7", "Num_TGI8", "Num_TGI9", "Num_TGI10",
  "Num_TGI11", "Num_TGI12", "Num_TGI13", "Num_TGI14", "Num_TGI15",
  "Num_TGI16", "Num_TGI17", "Num_TGI18", "Num_TGI19", "Num_TGI20",
  "Num_TGI21", "Num_TGI22")

merged_ESM$PGDscore <- rowSums(merged_ESM[, columns_to_sum], na.rm = TRUE)
merged_ESM$PGDscore <- as.numeric(merged_ESM$PGDscore)

#calculating mean & SD PGD score& above cut-off score
mean_pgd <- mean(merged_ESM$PGDscore, na.rm = TRUE)
print(mean_pgd)

sd_pgd <- sd(merged_ESM$PGDscore, na.rm = TRUE)
print(sd_pgd)

min_pgd <- min(merged_ESM$PGDscore)
max_pgd <- max(merged_ESM$PGDscore)

sum(merged_ESM$PGDscore > 70)

#grouping kinship
merged_ESM <- merged_ESM %>%
  mutate(kinship_category = case_when(
    T1_kinship %in% c("Child", "Partner") |

```



```

      (!is.na(T1_kinship_8_TEXT) & T1_kinship_8_TEXT %in% c("Lover")) ~
"child/partner",
      TRUE ~ "other"
    ))

kin_Cat <- table(merged_ESM$kinship_category)
print(kin_Cat)

#making variables as factors
merged_ESM$T1_Gender <- as.factor(merged_ESM$T1_Gender)
merged_ESM$loss_classification <- as.factor(merged_ESM$loss_classification)
merged_ESM$kinship_category <- as.factor(merged_ESM$kinship_category)

#checking assumptions of ANOVA
#fitting the anova model
anova_model <- aov(PGDscore ~ kinship_category * loss_classification *
T1_Gender, data = merged_ESM)

anova_nointeraction <- aov(PGDscore ~ kinship_category +
loss_classification + T1_Gender, data = merged_ESM)

summary(anova_nointeraction)

#checking for outliers
merged_ESM %>%
  group_by(T1_Gender, loss_classification, kinship_category) %>%
  identify_outliers(PGDscore)
ggplot(merged_ESM, aes(y = PGDscore)) +
  geom_boxplot() +
  ggtitle("Boxplot of pgd_score") +
  xlab("pgd_score")

#checking normality
qqnorm(anova_model$residuals)
qqline(anova_model$residuals)

shapiro_test <- shapiro.test(anova_model$residuals)
print(shapiro_test)

```

```

#homogeneity of variances
leveneTest(PGDscore ~ kinship_category * T1_Gender * loss_classification,
data = merged_ESM)

fitted_values <- fitted(anova_model)
residuals <- resid(anova_model)

plot_data <- data.frame(Fitted = fitted_values, Residuals = residuals)
residuals_data <- data.frame(Residuals = residuals)

ggplot(residuals_data, aes(x = Residuals)) +
  geom_histogram(binwidth = 0.5, fill = "blue", color = "black", alpha =
0.7) +
  labs(title = "Histogram of Residuals", x = "Residuals", y = "Frequency")
+
  theme_minimal()
ggplot(plot_data, aes(x = Fitted, y = Residuals)) +
  geom_point() +
  geom_hline(yintercept = 0, linetype = "dashed", color = "red") +
  labs(title = "Residuals vs Fitted Values", x = "Fitted Values", y =
"Residuals") +
  theme_minimal()
hist(residuals,
  main = "Histogram of Residuals",
  xlab = "Residuals",
  ylab = "Frequency",
  col = "skyblue")

#three way anova
summary(anova_model)

#showing distribution of levels for three-way interaction
with(merged_ESM, table(kinship_category, loss_classification, T1_Gender))
with(ESM1_interestingvariables, table(T1_Gender))
with(ESM3_nosuic_interestingvariables, table(Gender))

#effect size
print(partial_eta_squared(anova_model))
partial_eta_squared_result <- eta_squared(anova_model, partial = TRUE)
print(partial_eta_squared_result)

```

```

#removing outliers and rerunning anova model
#outliers in loss_classification
R_3qEcKLeqKssdgDs
R_3itd00lmLN0eEzY
R_3HYR89Xn22KSEy0

#outliers in kinship
R_5plFONJKTmn0FSZ
R_5hr6QwJ1VjmbG5X
R_4fcSNQMXV6983uw
R_4CEBrJhYuBreJ9B
R_3qEcKLeqKssdgDs
R_1B5lAqqvGj8lyqB

#new data set without outliers
merged_ESM_noutliers <- merged_ESM %>%
  filter(!(row_number() %in% c(72, 62, 60, 87, 83, 77, 76, 2)))

anova_model_noutliers <- aov(PGDscore ~ kinship_category *
loss_classification * T1_Gender, data = merged_ESM_noutliers)
summary(anova_model_noutliers)

#partial eta squared no outlier for kinship and type of loss
print(partial_eta_squared(anova_model_noutliers))
partial_eta_squared_result_nout <- eta_squared(anova_model_noutliers,
partial = TRUE)
print(partial_eta_squared_result_nout)

#boxplots to show differences in scores
merged_ESM$T1_Gender <- fct_recode(merged_ESM$T1_Gender,
  Male = "Man",
  Female = "Woman")

ggplot(merged_ESM, aes(x = T1_Gender, y = PGDscore, fill = T1_Gender)) +

```

```
geom_boxplot(width = 0.8, fill = "grey", position = position_dodge(width = 5))+
```

```
labs(x = "Biological sex", y = "PGD Score")
```

```
ggplot(merged_ESM, aes(x = kinship_category, y = PGDscore, fill = kinship_category)) +
```

```
geom_boxplot(width = 0.8, fill = "grey", position = position_dodge(width = 5))+
```

```
labs(x = "Kinship category", y = "PGD Score")
```

```
ggplot(merged_ESM, aes(x = loss_classification, y = PGDscore, fill = loss_classification)) +
```

```
geom_boxplot(width = 0.8, fill = "grey", position = position_dodge(width = 5))+
```

```
labs(x = "Type of loss", y = "PGD Score")
```