

# B19-LU 13 re-evaluation for publication in Opel et al. (2026)

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## 1 Input

**Analysed file:** 3-Permafrost-1mm-63-90-Fsp\_LU-13\_24al.binx

Laboratory dose rate:  $0.104 \pm 0.0052$  Gy/s

System ID: 306

Date of measurement: 260423

Date of analysis: 2025-10-29

Base name output files: 2025-10-29\_B19-LU 13 re-eval

R version 4.5.1 (2025-06-13 ucrt)

Luminescence package 1.1.1

OSLdecomposition package 1.1.0

## 1.1 Data preparation

First, the records are checked for consistency and records with different measurement settings are separated. Second, the unstimulated parts of the measurements are removed.

```
CORRECTION STEP 1 ----- Check records for consistency in the detection settings -----
```

```
Frequency table of different sets of detection settings (Channels, Channel width):
```

|   | settings               | frequency | record_type |
|---|------------------------|-----------|-------------|
| 1 | 220, 0.5               | 384       | IRSL        |
| 3 | 420, 0.5               | 384       | IRSL2       |
| 2 | 420, 0.238095238095238 | 168       | IRSL3       |

```
RLum.Data.Curve@RecordType changed to IRSL2 or IRSL3 in sequence: 1, 2, 3, 4, 5, 6, 7, 8, 9,
```

```
Further data manipulations are performed just on IRSL records
```

```
(time needed: 0.34 s)
```

```
CORRECTION STEP 2 ----- Remove not stimulated measurement parts -----
```

```
Measurement parts with stimulation light turned off detected and removed:
```

```
5 s at the beginning and 5 s at the end.
```

```
-> Length of 384 IRSL records reduced from 110 s to 100 s
```

```
(time needed: 0.94 s)
```

We perform the code again but only for IRSL2 records to clean also 290°C IRSL records.

```
Data set was already manipulated by [RLum.OSL_correction()]. Old information in $CORRECTION v
```

```
CORRECTION STEP 1 ----- Check records for consistency in the detection settings -----
```

```
All IRSL2 records have the same detection settings
```

```
(time needed: 0.13 s)
```

```
CORRECTION STEP 2 ----- Remove not stimulated measurement parts -----
```

```
Measurement parts with stimulation light turned off detected and removed:
```

```
5 s at the beginning and 0 s at the end.
```

```
-> Length of 384 IRSL2 records reduced from 210 s to 205 s
```

```
(time needed: 2.65 s)
```

## 1.2 Script settings

```
# Data set to evaluate?
IRSL_uncorrected <- IRSL_290_data

# Integration area (channels)
# default: signal_window_width <- 7
signal_window_width <- 7

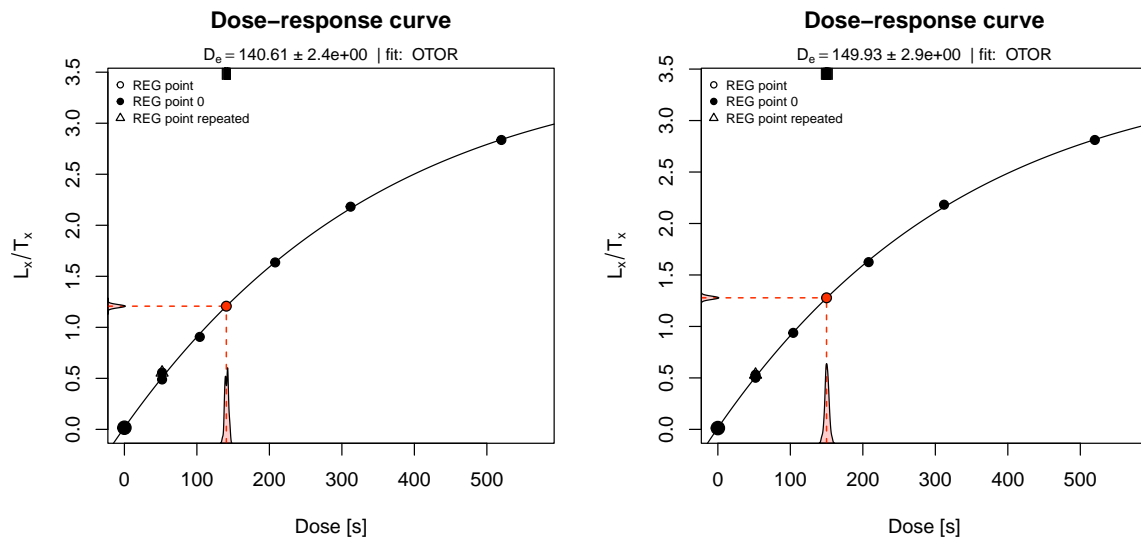
# Background limits (start channel, end channel)
# default: background_limits <- c(300, 400)
background_limits <- c(300, 400)

# File suffix
# default: suffix <- ""
suffix <- paste0(signal_window_width, "ch late bg")

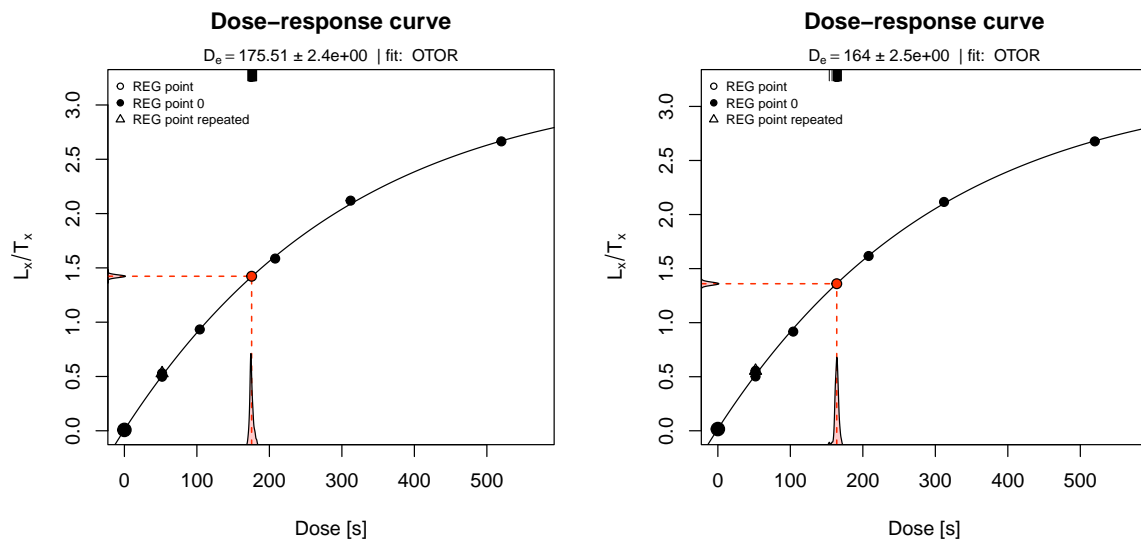
output_path <- paste(output_path, suffix)
```

## 2 Output

--- Dose response curve for aliquot 1 (left) and aliquot 2 (right) ---



--- Dose response curve for aliquot 3 (left) and aliquot 4 (right) ---



## 2.1 De calculation result table

The De values are calculated using the `analyse_SAR.CWOSL()` function of the `Luminescence` package.

Table 1: Equivalent doses

| #  | De [Gy] | De error [Gy] | Rejection criteria |
|----|---------|---------------|--------------------|
| 1  | 140.61  | 2.60          | FAILED             |
| 2  | 149.93  | 3.09          | OK                 |
| 3  | 175.51  | 2.54          | OK                 |
| 4  | 164.00  | 2.80          | FAILED             |
| 5  | 149.38  | 2.97          | FAILED             |
| 6  | 131.82  | 2.08          | FAILED             |
| 7  | 166.67  | 1.82          | OK                 |
| 8  | 147.88  | 2.64          | OK                 |
| 9  | 149.96  | 2.16          | OK                 |
| 10 | 156.67  | 2.71          | OK                 |
| 11 | 167.92  | 1.71          | OK                 |
| 12 | 166.77  | 4.06          | FAILED             |
| 13 | 169.74  | 2.99          | OK                 |
| 14 | 153.06  | 2.91          | OK                 |
| 15 | 134.07  | 7.26          | FAILED             |
| 16 | 138.71  | 2.70          | OK                 |
| 17 | 167.96  | 2.90          | OK                 |
| 18 | 160.05  | 3.12          | OK                 |
| 19 | 151.86  | 2.03          | OK                 |
| 20 | 167.10  | 2.39          | OK                 |
| 21 | 147.23  | 3.91          | OK                 |
| 22 | 143.37  | 2.42          | OK                 |
| 23 | 182.00  | 3.51          | FAILED             |
| 24 | 146.51  | 2.61          | OK                 |

17 of all aliquots passed the rejection criteria. The results of all aliquots in the table above include the dose rate errors.

## 2.2 Rejection criteria

Table 2: Rejection criteria thresholds (left) and results (right)

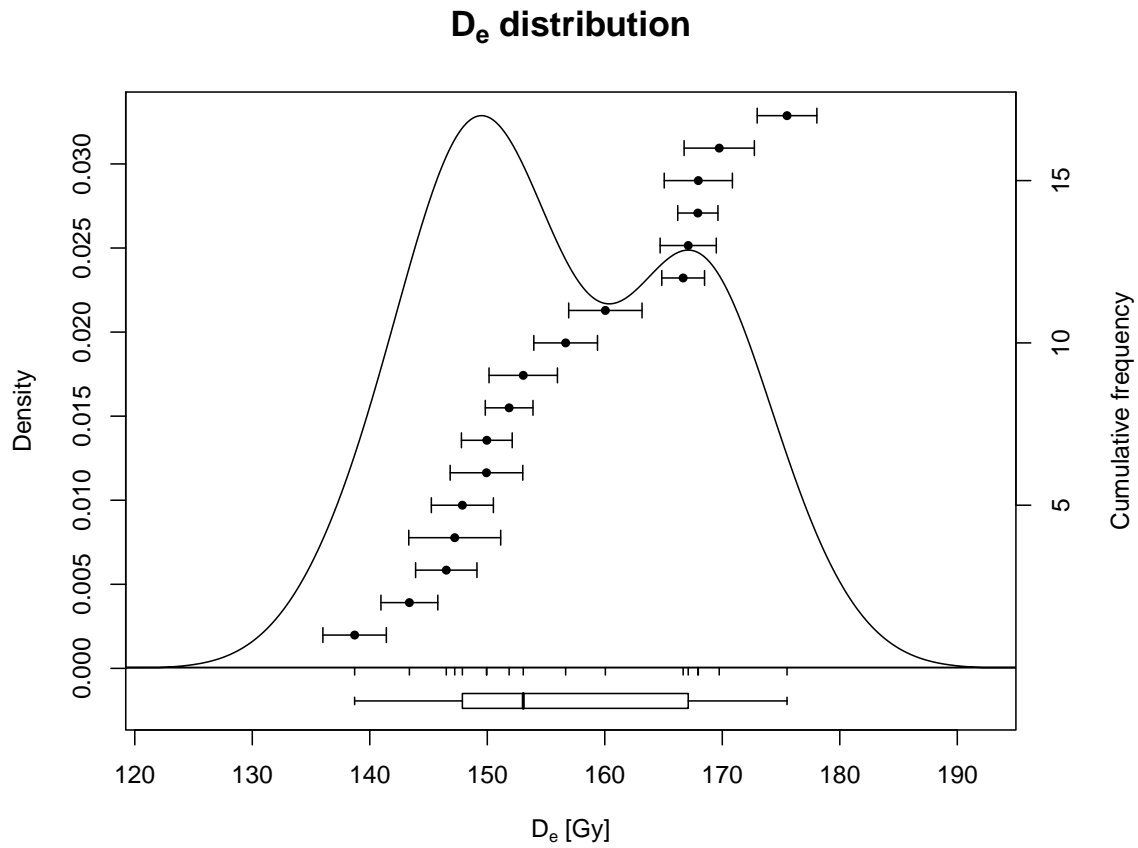
| # | Criterium                     |  |  |  | Threshold |
|---|-------------------------------|--|--|--|-----------|
| A | Recycling ratio (R7/R2)       |  |  |  | 0.1       |
| B | Recuperation rate (Natural) 1 |  |  |  | 0.1       |
| C | Testdose error                |  |  |  | 0.1       |
| D | Palaeodose error              |  |  |  | 0.1       |
| E | De > max. dose point          |  |  |  | 520.0     |

| #  | A     | B     | C     | D     | E       |
|----|-------|-------|-------|-------|---------|
| 1  | 1.138 | 0.013 | 0.010 | 0.018 | 140.607 |
| 2  | 1.059 | 0.010 | 0.009 | 0.021 | 149.934 |
| 3  | 1.064 | 0.006 | 0.007 | 0.014 | 175.510 |
| 4  | 1.104 | 0.012 | 0.008 | 0.017 | 164.000 |
| 5  | 1.110 | 0.011 | 0.010 | 0.020 | 149.378 |
| 6  | 1.126 | 0.012 | 0.008 | 0.016 | 131.817 |
| 7  | 1.062 | 0.017 | 0.005 | 0.011 | 166.666 |
| 8  | 1.084 | 0.013 | 0.011 | 0.018 | 147.879 |
| 9  | 1.093 | 0.015 | 0.007 | 0.014 | 149.962 |
| 10 | 1.076 | 0.012 | 0.008 | 0.017 | 156.665 |
| 11 | 1.072 | 0.011 | 0.005 | 0.010 | 167.917 |
| 12 | 1.154 | 0.028 | 0.012 | 0.024 | 166.765 |
| 13 | 1.076 | 0.010 | 0.009 | 0.018 | 169.744 |
| 14 | 1.096 | 0.013 | 0.008 | 0.019 | 153.060 |
| 15 | 1.140 | 0.024 | 0.026 | 0.054 | 134.074 |
| 16 | 1.086 | 0.013 | 0.009 | 0.019 | 138.714 |
| 17 | 1.072 | 0.013 | 0.008 | 0.017 | 167.959 |
| 18 | 1.051 | 0.022 | 0.010 | 0.019 | 160.047 |
| 19 | 1.059 | 0.010 | 0.007 | 0.013 | 151.862 |
| 20 | 1.075 | 0.012 | 0.007 | 0.014 | 167.100 |
| 21 | 1.076 | 0.011 | 0.013 | 0.027 | 147.226 |
| 22 | 1.082 | 0.006 | 0.008 | 0.017 | 143.373 |
| 23 | 1.126 | 0.009 | 0.009 | 0.019 | 181.996 |
| 24 | 1.097 | 0.013 | 0.009 | 0.018 | 146.512 |

## 2.3 Dose distribution

The dose distribution is plotted below with the functions `plot_KDE()` and `plot_RadialPlot()` of the `Luminescence` package. Those aliquots which did not passed the rejection criteria, where not included in any of the dose distribution calculations.

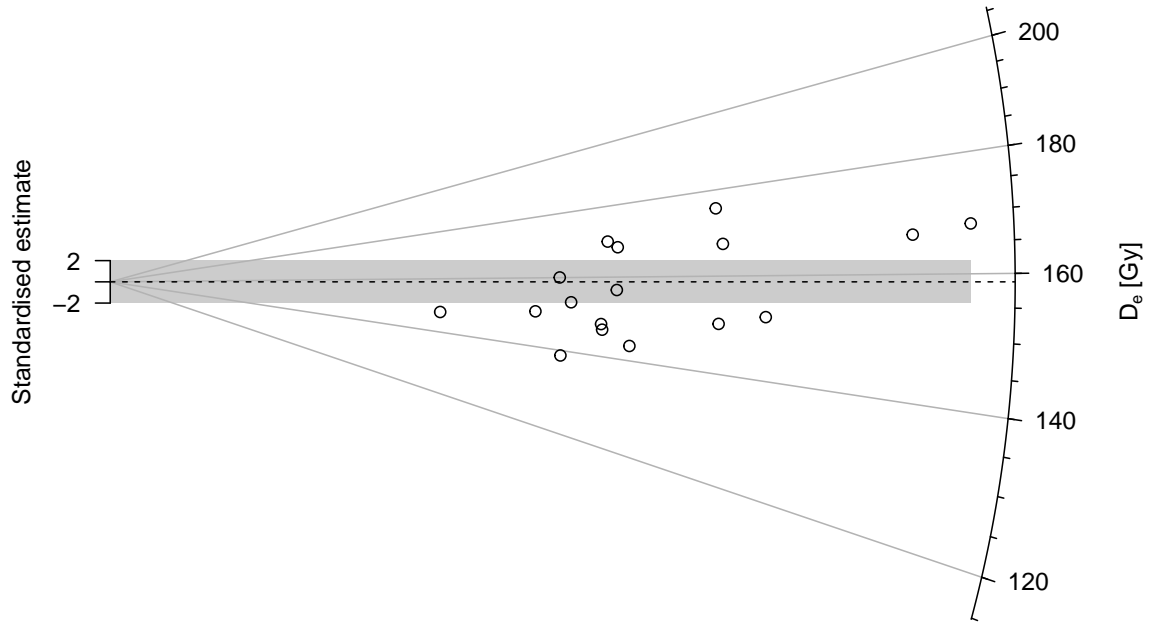


Skewness = 0.163

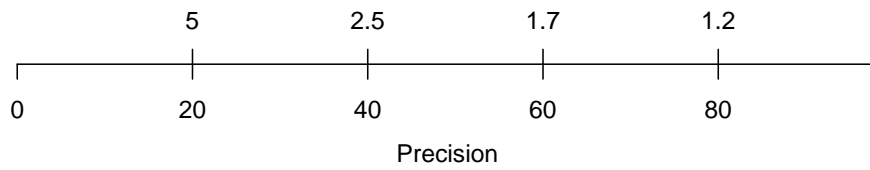


# D<sub>e</sub> distribution

n = 17 | in 2 sigma = 17.6 %



Relative standard error [%]

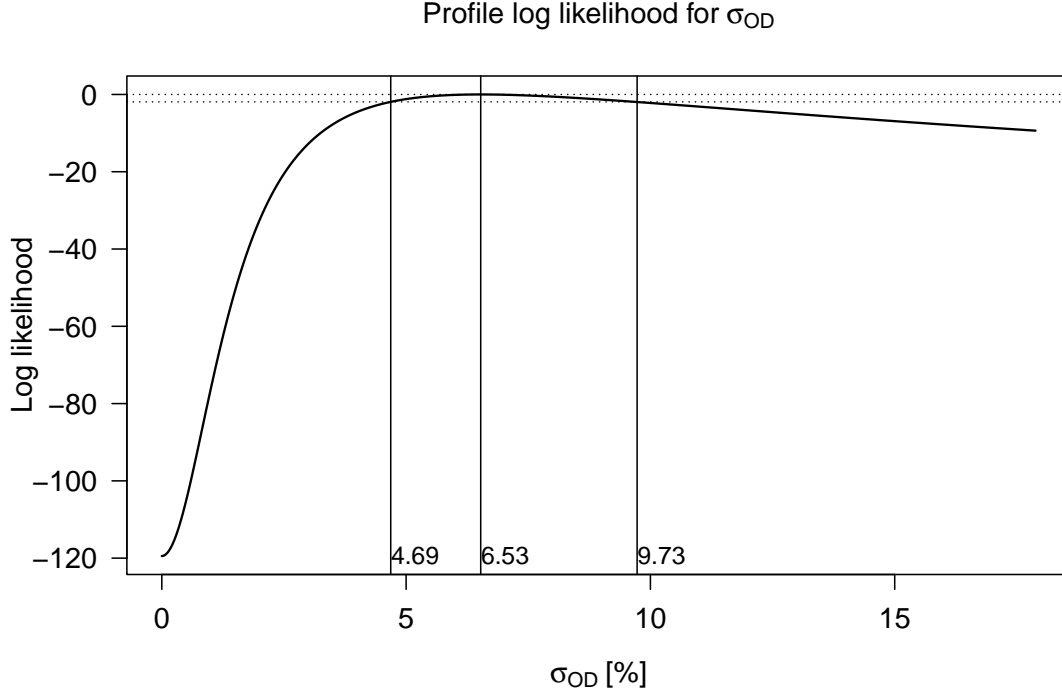


## 2.4 Central age model

Below is output of the function `calc_CentralDose()` of the `Luminescence` package shown, which calculates the central dose and the over-dispersion of the  $D_e$  distribution.

```
[calc_CentralDose]

----- meta data -----
n:                        17
log:                      TRUE
----- dose estimate -----
abs. central dose:       156.27
abs. SE:                  2.56
rel. SE [%]:             1.64
----- overdispersion -----
abs. OD:                  10.19
abs. SE:                  1.87
OD [%]:                   6.52
SE [%]:                   1.20
-----
```



$\sigma$  = standard error,  $OD$  = over-dispersion

## 2.5 Paleodose result

We assume that the dose rate error of the beta-source affects all  $D_e$  values systematically the same way. Thus, we increase the CAM paleodose error result by the assumed relative dose rate error of  $rel.err = 0.05$  using the formula:

$$\sigma = \sqrt{\sigma_{CAM}^2 + (rel.err_{source} D_{CAM})^2}$$

This increases the paleodose error from 2.556 to 8.221 Gy.