

# B19-LU 5 re-evaluation for publication in Opel et al. (2026)

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## 1 Input

**Analysed file:** 1-Permafrost-1mm-63-100-Fsp-pIR290-sample\_B19-LU-5-24al.binx

Laboratory dose rate:  $0.0765 \pm 0.0038$  Gy/s

System ID: 190

Date of measurement: 290822

Date of analysis: 2025-10-29

Base name output files: 2025-10-29\_B19-LU 5 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	336	IRSL
3	420, 0.5	336	IRSL2
2	420, 0.238095238095238	144	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: 0.29 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 336 IRSL records reduced from 110 s to 100 s

(time needed: 0.7 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: 0.11 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 336 IRSL2 records reduced from 210 s to 200 s

(time needed: 1.76 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

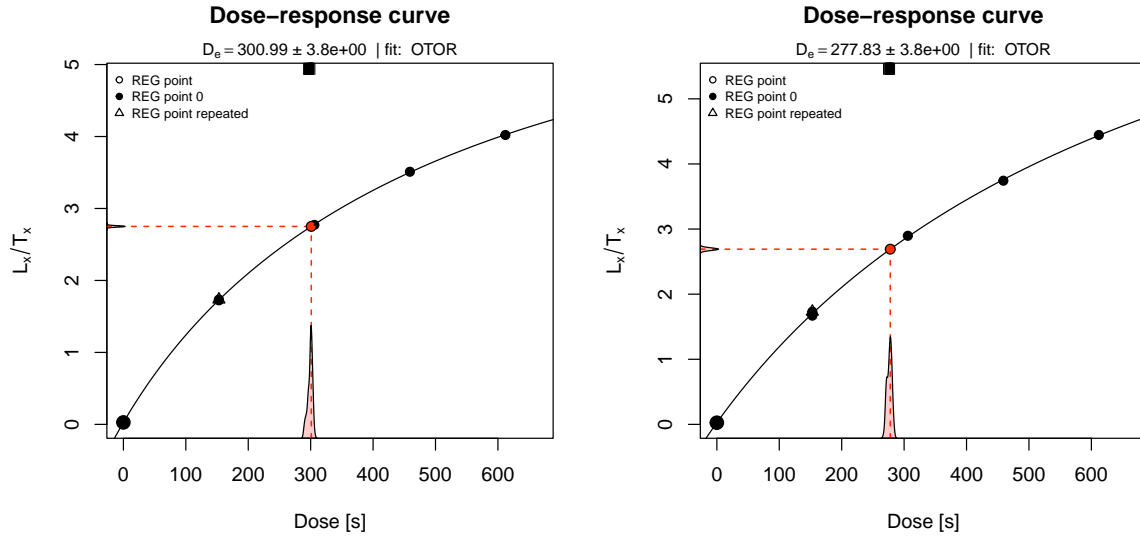
# Background limits (start channel, end channel)
# default: background_limits <- c(300, 400)
background_limits <- c(300, 400)

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

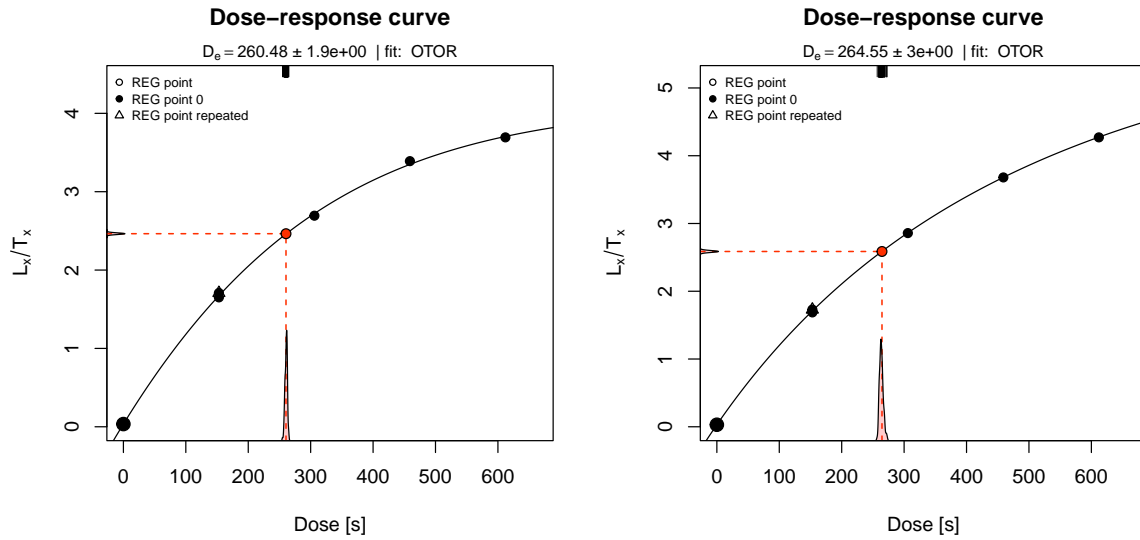
output_path <- paste(output_path, suffix)
```

## 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	300.99	3.57	OK
2	277.83	3.87	OK
3	260.48	2.34	OK
4	264.55	2.79	OK
5	347.56	1.94	OK
6	278.33	3.52	OK
7	278.19	3.06	OK
8	270.71	2.02	OK
9	273.94	3.15	OK
10	388.37	4.58	OK
11	346.56	5.27	OK
12	289.56	3.26	OK
13	346.81	5.39	OK
14	266.12	2.51	OK
15	318.12	3.86	OK
16	288.10	4.19	OK
17	306.22	2.72	OK
18	247.64	2.07	OK
19	307.66	3.46	OK
20	271.09	3.13	OK
21	245.85	2.07	OK
22	306.22	3.34	OK
23	310.79	3.72	OK
24	368.46	5.20	OK

24 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)

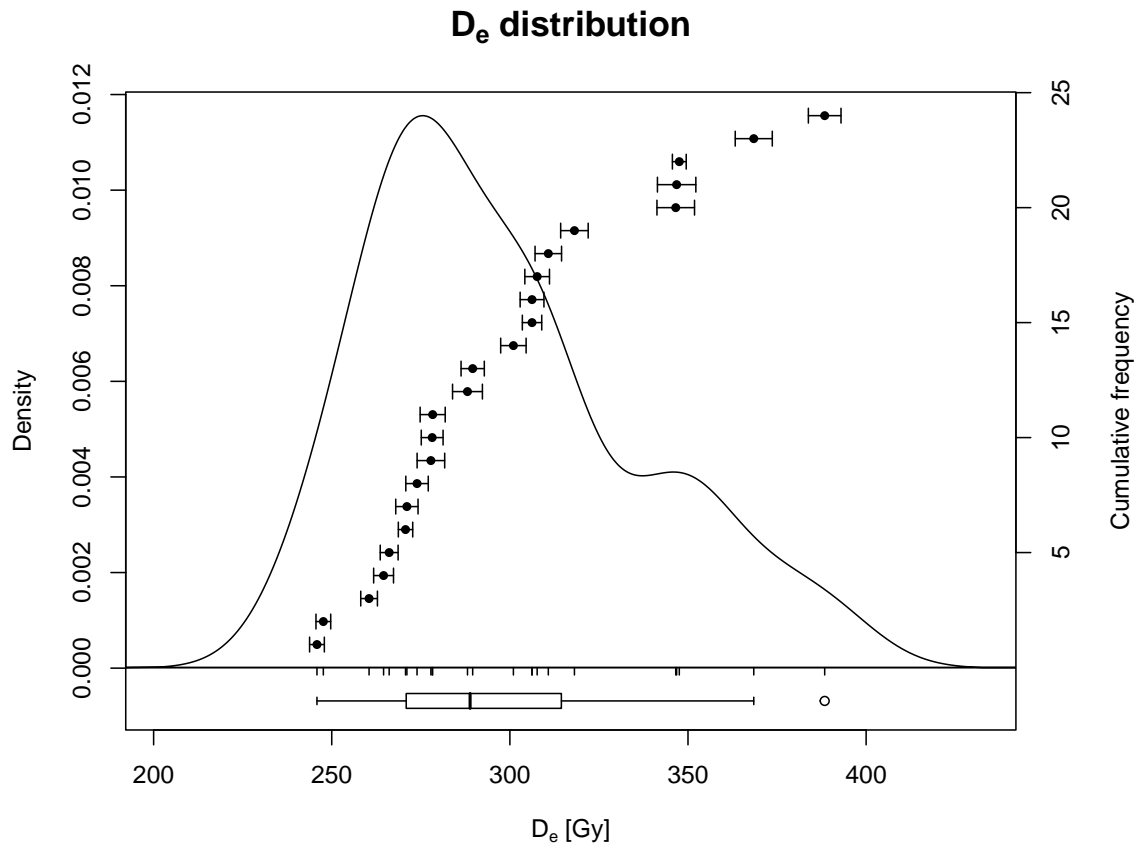
#	Criterium				Threshold
A	Recycling ratio (R6/R2)				0.1
B	Recuperation rate (Natural) 1				0.1
C	Testdose error				0.1
D	Palaeodose error				0.1
E	De > max. dose point				612.0

#	A	B	C	D	E
1	1.007	0.010	0.003	0.012	300.988
2	1.037	0.010	0.007	0.014	277.829
3	1.034	0.014	0.003	0.009	260.476
4	1.025	0.012	0.005	0.011	264.549
5	1.008	0.008	0.003	0.006	347.560
6	0.999	0.012	0.004	0.013	278.325
7	1.022	0.011	0.003	0.011	278.188
8	1.034	0.007	0.003	0.007	270.715
9	1.017	0.013	0.005	0.012	273.942
10	1.031	0.007	0.003	0.012	388.373
11	0.992	0.013	0.004	0.015	346.564
12	1.016	0.009	0.004	0.011	289.560
13	1.030	0.013	0.003	0.016	346.814
14	1.027	0.009	0.003	0.009	266.125
15	1.013	0.013	0.004	0.012	318.124
16	0.991	0.013	0.005	0.015	288.100
17	1.048	0.010	0.003	0.009	306.216
18	1.041	0.012	0.004	0.008	247.637
19	1.045	0.011	0.003	0.011	307.658
20	1.021	0.009	0.004	0.012	271.090
21	1.020	0.009	0.004	0.008	245.850
22	1.017	0.009	0.004	0.011	306.222
23	1.023	0.011	0.003	0.012	310.789
24	0.997	0.008	0.003	0.014	368.464

## 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.

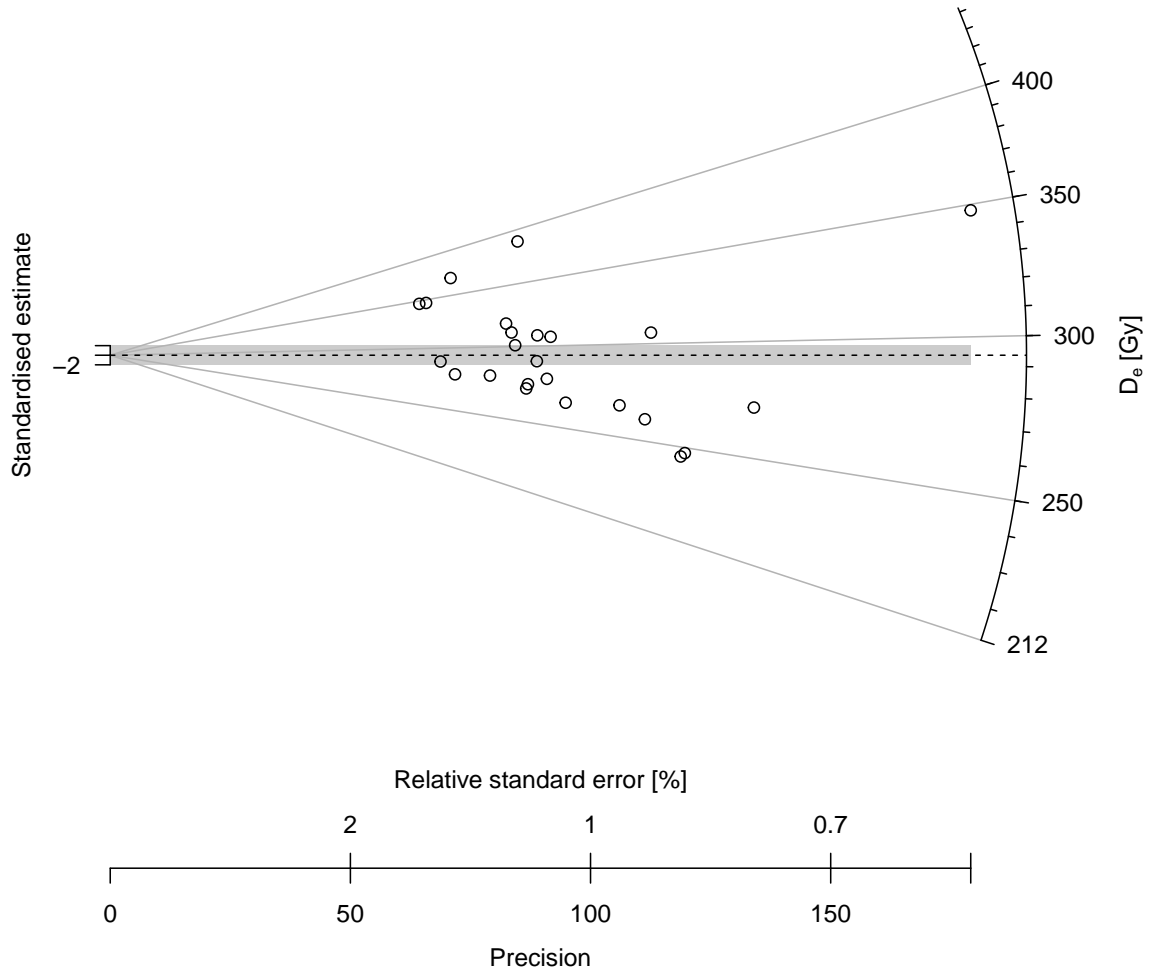


Skewness = 0.716



# D<sub>e</sub> distribution

n = 24 | in 2 sigma = 8.3 %

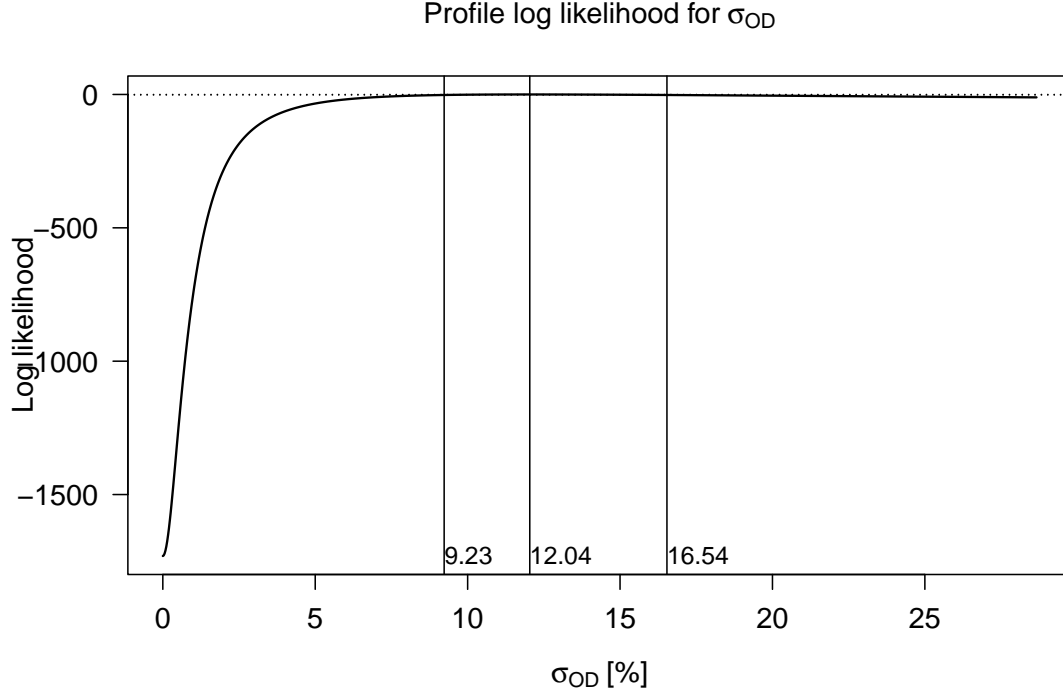


## 2.4 Central age model

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:                24
log:              TRUE
----- dose estimate -----
abs. central dose: 296.07
abs. SE:           7.30
rel. SE [%]:       2.47
----- overdispersion -----
abs. OD:           35.60
abs. SE:           5.19
OD [%]:            12.02
SE [%]:            1.75
-----
```



$\sigma$  = 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 7.3 to 16.505 Gy.