B19-LU 6 re-evaluation for publication in Opel et al. (2026)

Table of contents

1 Input

Analysed file: 3-Permafrost-1mm-63-100-Fsp-pIR290-sample_B19-LU-6-24al.binx

Laboratory dose rate: 0.1053 ± 0.0053 Gy/s

System ID: 306

Date of measurement: 141022

Date of analysis: 2025-10-29

Base name output files: 2025-10-29_B19-LU 6 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: 0.28 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: 0.82 s)
```

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

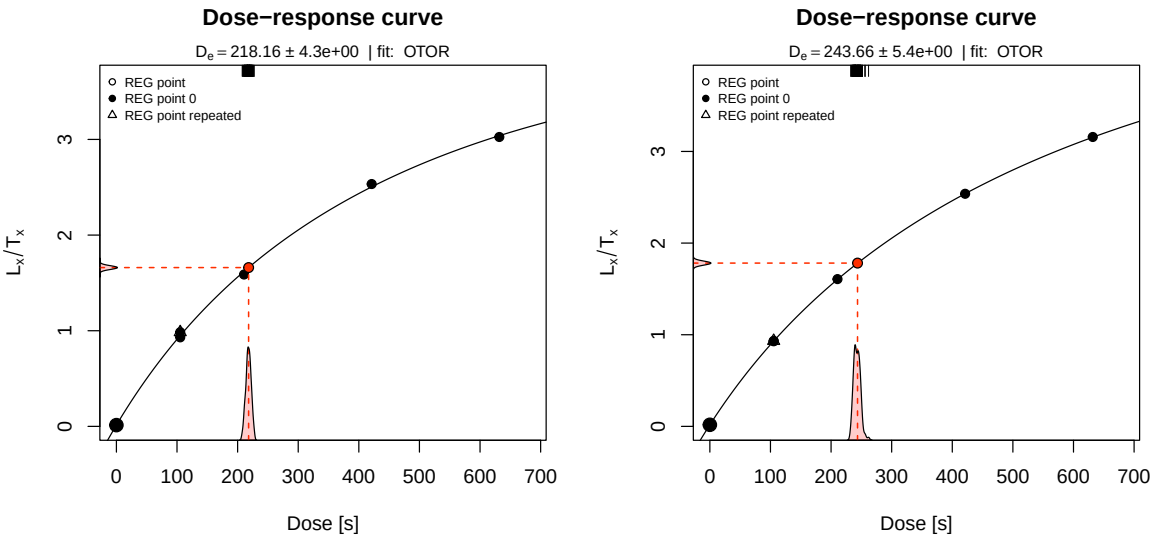
```
Data set was already manipulated by [RLum.OSL_correction()]. Old information in $CORRECTION w
CORRECTION STEP 1 ----- Check records for consistency in the detection settings -----
All IRSL2 records have the same detection settings
(time needed: 0.1 s)

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 336 IRSL2 records reduced from 210 s to 205 s
(time needed: 1.5 s)
```

1.2 Script settings

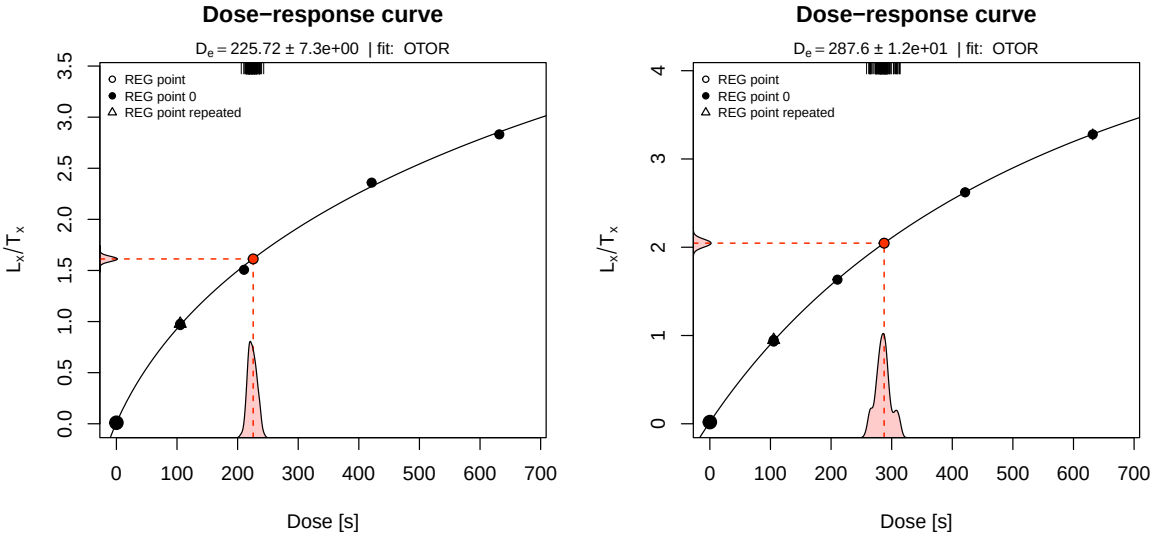
```
# Data set to evaluate?
IRSL_uncorrected <- IRSL_290_data

# 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	218.16	4.33	OK
2	243.66	5.63	OK
3	225.72	7.19	OK
4	287.60	12.52	OK
5	211.27	3.92	OK
6	268.94	6.86	OK
7	247.31	7.16	OK
8	257.46	7.11	OK
9	243.85	6.03	OK
10	268.34	6.55	OK
11	222.19	4.16	OK
12	251.82	5.56	OK
13	248.43	8.02	OK
14	258.56	3.47	OK
15	252.35	5.01	OK
16	223.90	6.46	OK
17	267.54	7.75	OK
18	251.75	7.77	OK
19	248.89	7.64	OK
20	217.38	4.58	OK
21	260.50	7.37	OK
22	268.36	5.02	OK
23	248.82	8.36	OK
24	238.39	6.47	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

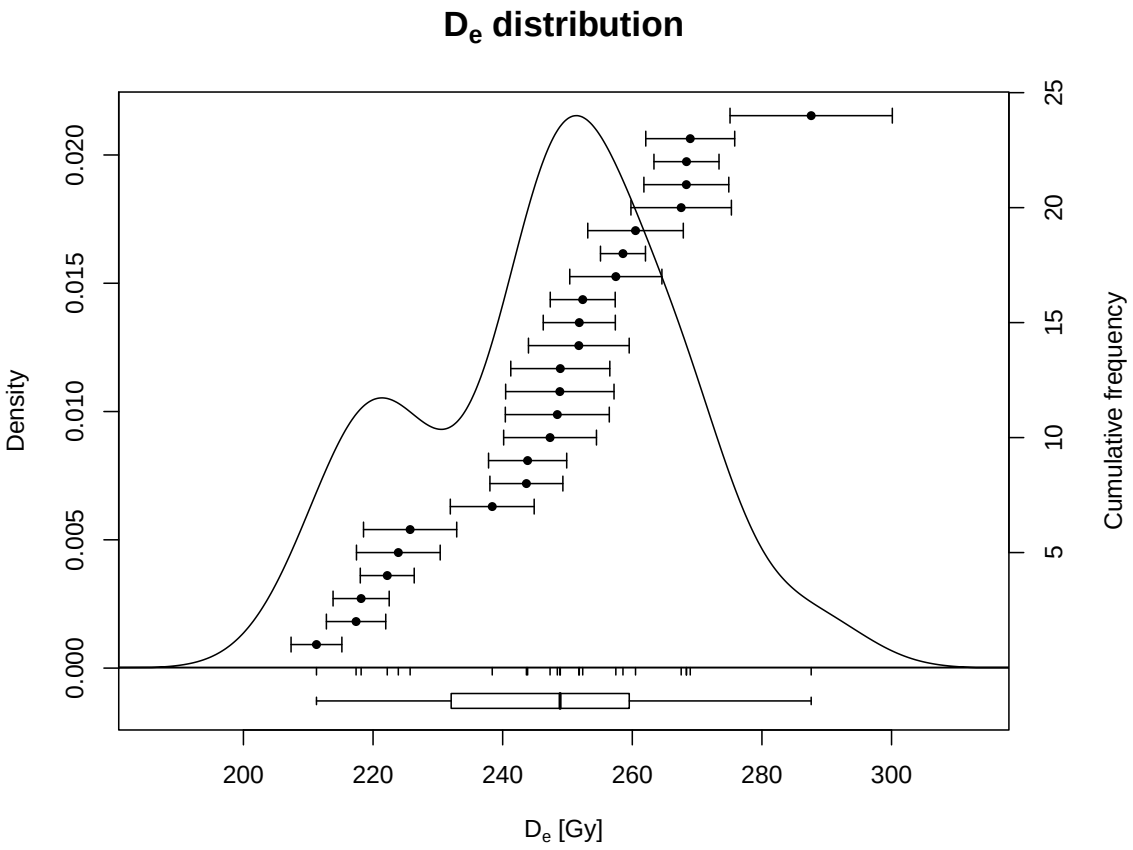
Table 2: Rejection criteria thresholds (left) and results (right)

#	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	631.8

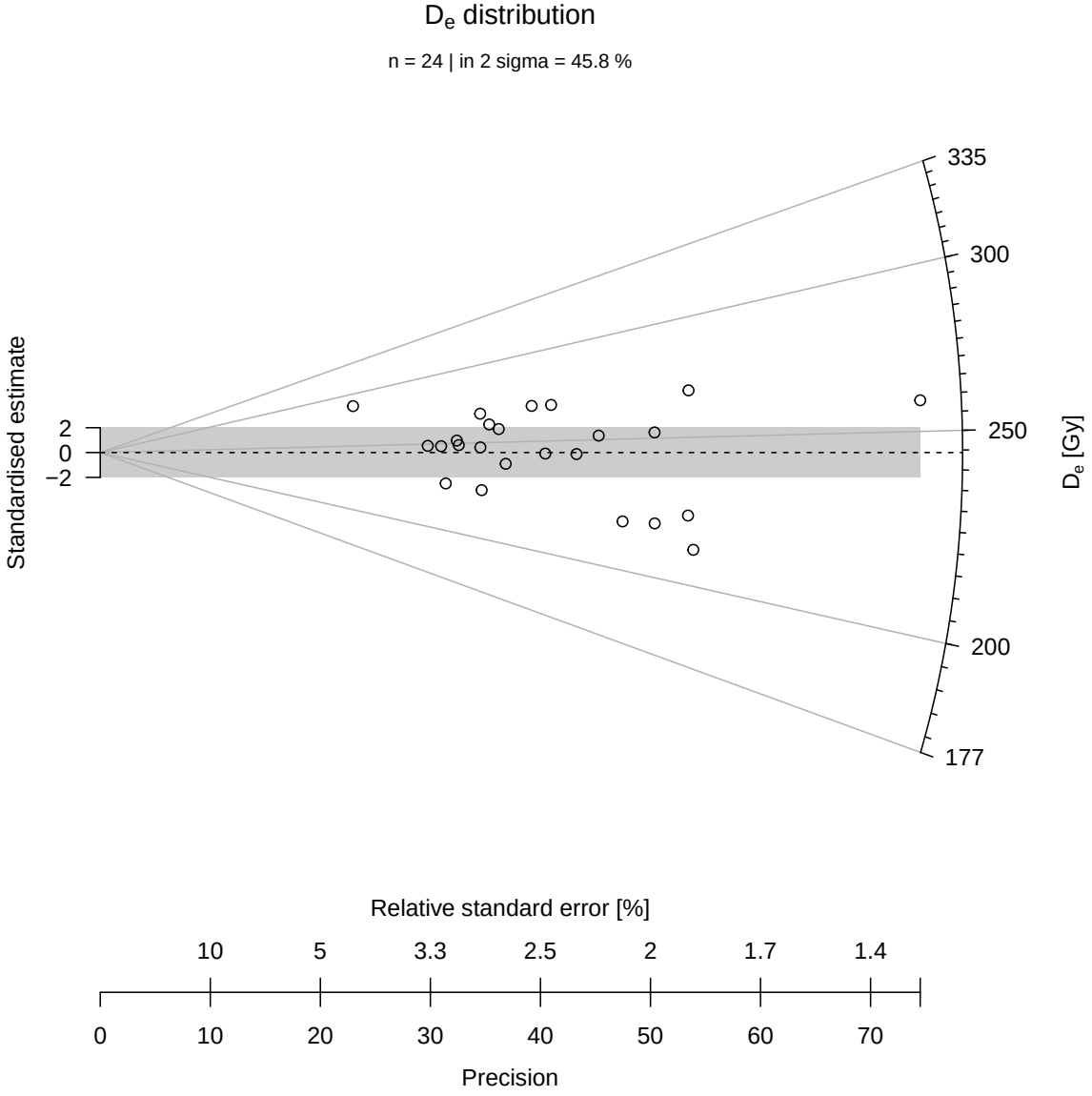
#	A	B	C	D	E
1	1.058	0.008	0.009	0.020	218.161
2	1.004	0.010	0.010	0.023	243.660
3	1.012	0.006	0.012	0.032	225.722
4	1.019	0.009	0.018	0.044	287.597
5	1.028	0.007	0.007	0.019	211.271
6	1.026	0.012	0.012	0.026	268.944
7	1.023	0.011	0.011	0.029	247.310
8	1.048	0.023	0.012	0.028	257.464
9	1.026	0.005	0.010	0.025	243.847
10	1.052	0.010	0.009	0.024	268.337
11	1.073	0.009	0.008	0.019	222.194
12	0.990	0.012	0.007	0.022	251.820
13	1.024	0.005	0.012	0.032	248.427
14	1.040	0.007	0.005	0.013	258.560
15	1.046	0.008	0.011	0.020	252.350
16	1.015	0.007	0.013	0.029	223.900
17	1.058	0.009	0.011	0.029	267.541
18	1.024	0.007	0.013	0.031	251.755
19	0.998	0.012	0.013	0.031	248.887
20	1.024	0.008	0.009	0.021	217.384
21	1.042	0.011	0.011	0.028	260.501
22	1.008	0.009	0.008	0.019	268.360
23	1.028	0.007	0.014	0.034	248.818
24	1.010	0.016	0.014	0.027	238.386

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.



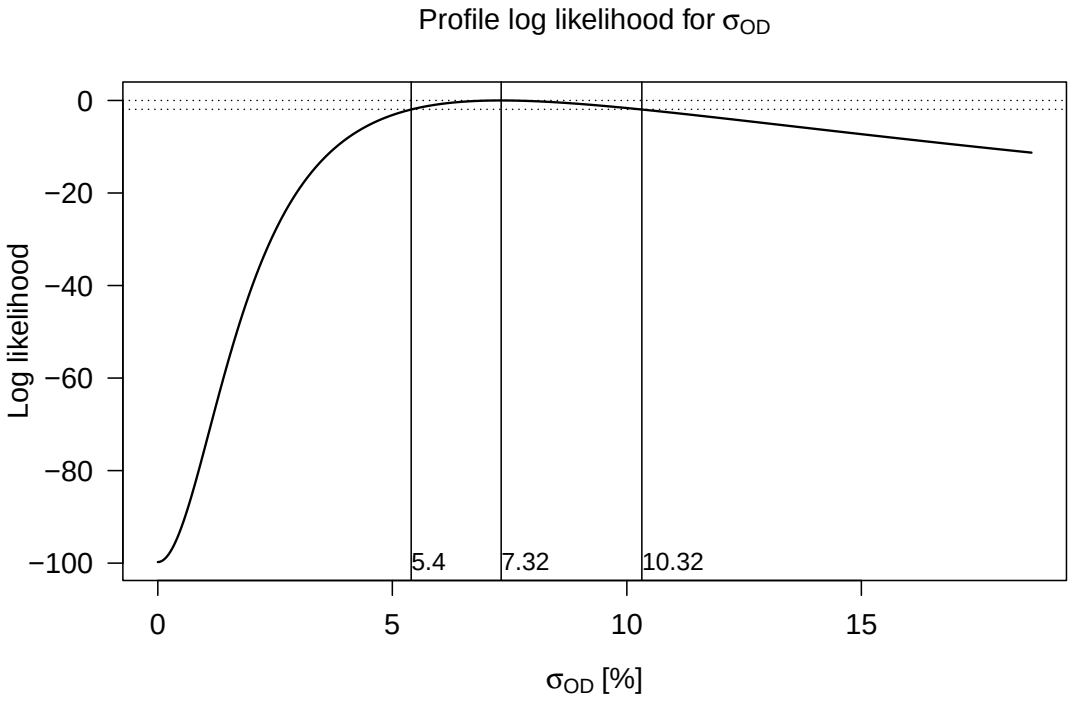

```
Skewness = -0.147
```


De distribution
n = 24 | in 2 sigma = 45.8 %
Standardised estimate
2
0
−2
335
300
250
200
177
De [Gy]
Relative standard error [%]
10
5
3.3
2.5
2
1.7
1.4
0
10
20
30
40
50
60
70
Precision

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:        245.99
 abs. SE:                  3.90
 rel. SE [%]:              1.59
---------- overdispersion -----------
 abs. OD:                  17.99
 abs. SE:                  2.93
 OD [%]:                   7.31
 SE [%]:                   1.19
-------------------------------------
```



σ = 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 3.904 to 12.904 Gy.