**Table 1. Descriptive statistics.**

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| --- | --- | --- | --- | --- | --- |
|  | **Total (N=4071)** | **Rotterdam (N=566)** | **Berlin (N=1343)** | **Warsaw (N=1179)** | **Amsterdam (N=983)** |
| **Positive SN status** | 889 (21.8%) | 170 (30.0%) | 259 (19.3%) | 224 (19.0%) | 236 (24.0%) |
| **Males** | 1996 (49.0%) | 273 (48.2%) | 753 (56.1%) | 473 (40.1%) | 497 (50.6%) |
| **Age** |  |  |  |  |  |
| Median (Q1, Q3) | 55.0 (43.0, 66.0) | 52.0 (40.0, 62.0) | 62.0 (48.0, 71.0) | 51.0 (42.0, 62.0) | 55.0 (43.0, 65.0) |
| Min - Max | 13.0 - 94.0 | 13.0 - 88.0 | 13.0 - 94.0 | 15.0 - 83.0 | 15.0 - 89.0 |
| **Ulceration** |  |  |  |  |  |
| No | 2759 (70.2%) | 332 (66.7%) | 1049 (80.0%) | 690 (59.1%) | 688 (72.2%) |
| Yes | 1171 (29.8%) | 166 (33.3%) | 263 (20.0%) | 477 (40.9%) | 265 (27.8%) |
| Missing | 141 | 68 | 31 | 12 | 30 |
| **Location** |  |  |  |  |  |
| Arm | 615 (15.6%) | 86 (15.2%) | 217 (16.2%) | 184 (17.0%) | 128 (13.5%) |
| Leg | 1189 (30.2%) | 218 (38.5%) | 324 (24.2%) | 370 (34.3%) | 277 (29.2%) |
| Trunk | 1815 (46.1%) | 242 (42.8%) | 654 (48.9%) | 512 (47.4%) | 407 (42.8%) |
| Head and neck | 314 (8.0%) | 20 (3.5%) | 142 (10.6%) | 14 (1.3%) | 138 (14.5%) |
| Missing | 138 | 0 | 6 | 99 | 33 |
| **Histology** |  |  |  |  |  |
| SSM | 2164 (58.2%) | 285 (55.9%) | 910 (70.0%) | 371 (39.0%) | 598 (62.6%) |
| NM | 1226 (33.0%) | 195 (38.2%) | 290 (22.3%) | 465 (48.8%) | 276 (28.9%) |
| ALM | 126 (3.4%) | 16 (3.1%) | 54 (4.2%) | 27 (2.8%) | 29 (3.0%) |
| LMM | 153 (4.1%) | 5 (1.0%) | 45 (3.5%) | 85 (8.9%) | 18 (1.9%) |
| Other | 49 (1.3%) | 9 (1.8%) | 1 (0.1%) | 4 (0.4%) | 35 (3.7%) |
| Missing | 353 | 56 | 43 | 227 | 27 |
| **Breslow** |  |  |  |  |  |
| Mean (SD) | 2.8 (3.3) | 2.8 (2.3) | 2.3 (2.5) | 3.6 (4.9) | 2.6 (2.0) |
| Min - Max | 0.1 - 90.0 | 0.3 - 20.0 | 0.1 - 30.0 | 0.1 - 90.0 | 0.5 - 22.0 |
| Missing | 59 | 6 | 16 | 28 | 9 |
| **Multiple fields** | 374 (9.2%) | 87 (15.4%) | 41 (3.1%) | 23 (2.0%) | 223 (22.7%) |
| **Total number of negative SN** |  |  |  |  |  |
| Mean (SD) | 1.7 (1.4) | 1.6 (1.4) | 1.6 (1.3) | 1.2 (1.0) | 2.2 (1.6) |
| Min - Max | 0.0 - 15.0 | 0.0 - 10.0 | 0.0 - 13.0 | 0.0 - 9.0 | 0.0 - 15.0 |
| Missing | 162 | 1 | 27 | 134 | 0 |
| **Total number of positive SN** |  |  |  |  |  |
| Mean (SD) | 0.3 (0.6) | 0.4 (0.7) | 0.2 (0.4) | 0.3 (0.6) | 0.3 (0.6) |
| Min - Max | 0.0 - 5.0 | 0.0 - 4.0 | 0.0 - 2.0 | 0.0 - 5.0 | 0.0 - 4.0 |
| Missing | 1 | 0 | 1 | 0 | 0 |
| **SN tumour burden** |  |  |  |  |  |
| Mean (SD) | 1.2 (1.3) | 1.1 (1.3) | 1.0 (0.5) | 1.4 (2.0) | 1.1 (0.8) |
| Min - Max | 0.0 - 38.0 | 0.0 - 15.0 | 0.0 - 8.0 | 0.0 - 38.0 | 0.0 - 8.0 |
| Missing | 301 | 18 | 163 | 0 | 120 |
| **Location metastasis in lymph** |  |  |  |  |  |
| Subcap | 3319 (88.1%) | 440 (80.3%) | 1123 (95.2%) | 963 (81.7%) | 793 (92.1%) |
| Combined | 213 (5.7%) | 43 (7.8%) | 27 (2.3%) | 104 (8.8%) | 39 (4.5%) |
| Parenchymal | 86 (2.3%) | 19 (3.5%) | 11 (0.9%) | 51 (4.3%) | 5 (0.6%) |
| Multifocal | 45 (1.2%) | 21 (3.8%) | 9 (0.8%) | 9 (0.8%) | 6 (0.7%) |
| Extensive | 105 (2.8%) | 25 (4.6%) | 10 (0.8%) | 52 (4.4%) | 18 (2.1%) |
| Missing | 303 | 18 | 163 | 0 | 122 |
| **Recurrence** | 862 (21.2%) | 160 (28.3%) | 175 (13.0%) | 319 (27.1%) | 208 (21.2%) |
| **Deaths** | 606 (14.9%) | 115 (20.3%) | 148 (11.0%) | 216 (18.3%) | 127 (12.9%) |
| **Melanoma specific mortality** | 504 (12.4%) | 102 (18.0%) | 101 (7.5%) | 203 (17.2%) | 98 (10.0%) |

**Table 2. Coefficients of the full model for recurrence, model selected by backward selection with α=0.05 and α=0.01.**

|  |  |  |  |
| --- | --- | --- | --- |
|  | Full | BS5 | BS1 |
| **Positive SN status** | 0.179 | 1.268 | 1.299 |
| **Male** | 0.206 |  |  |
| Positive SN status \* Male | -0.226 |  |  |
| **Age** | 0.141 | 0.33 | 0.344 |
| Positive SN status \* Age | 0.335 |  |  |
| **Ulceration** | 0.561 | 0.459 | 0.494 |
| Positive SN status \* Ulceration | -0.25 |  |  |
| **Location** |  |  |  |
| Arm | (ref) | (ref) | (ref) |
| Leg | 0.332 | 0.273 | 0.271 |
| Trunk | 0.415 | 0.397 | 0.392 |
| Head and neck | 0.841 | 0.739 | 0.697 |
| Positive SN status \* Arm | (ref) |  |  |
| Positive SN status \* Leg | -0.189 |  |  |
| Positive SN status \* Trunk | -0.238 |  |  |
| Positive SN status \* Head and neck | -0.385 |  |  |
| **Histology** |  |  |  |
| SSM | (ref) |  |  |
| NM | 0.217 | 0.229 |  |
| ALM | 0.511 | 0.484 |  |
| LMM | 0.085 | 0.068 |  |
| Other | -0.146 | -0.209 |  |
| Positive SN status \* SSM | (ref) |  |  |
| Positive SN status \* NM | 0.039 |  |  |
| Positive SN status \* ALM | -0.138 |  |  |
| Positive SN status \* LMM | -0.021 |  |  |
| Positive SN status \* other | -0.372 |  |  |
| **Breslow** | 0.757 | 0.769 | 0.816 |
| Positive SN status \* Breslow | -0.334 | -0.375 | -0.396 |
| **Multiple fields** | 0.273 | 0.251 |  |
| Positive SN status \* Multiple fields | 0.027 |  |  |
| **Total number of negative SN** | -0.028 |  |  |
| **Total number of positive SN** | -0.03 |  |  |
| **SN tumour burden (Rdamcrit)** | 0.18 | 0.208 | 0.213 |
| **Location metastasis in lymph node (Dewar)** |  |  |  |
| Subcap | (ref) |  |  |
| Combined | 0.369 |  |  |
| Parenchymal | 0.106 |  |  |
| Multifocal | 0.009 |  |  |
| Extensive | 0.177 |  |  |

**Figure 1.** Log relative hazard of the covariates included in the full model, model resulting from backward selection with .05 and .

|  |  |  |
| --- | --- | --- |
| **Full model** | **Backward selection** | **Backward selection** |
| **C:\Users\056424\AppData\Local\Microsoft\Windows\INetCache\Content.Word\plot.predict.full.png** | **C:\Users\056424\AppData\Local\Microsoft\Windows\INetCache\Content.Word\plot.predict.BS.05.png** | **C:\Users\056424\AppData\Local\Microsoft\Windows\INetCache\Content.Word\plot.predict.BS.01.png** |

**Figure 2.** Log relative hazard of Breslow in the full model, model resulting from backward selection with critical value 0.05 and 0.01.

|  |  |  |
| --- | --- | --- |
| **Full model** | **Backward selection** | **Backward selection** |
|  |  |  |

**Figure 3.** Calibration of full model and models selected by backward selection predicting Recurrence for each center.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Full model** |  |  |  |  |
| **Backward selection** |  |  |  |  |
| **Backward selection** |  |  |  |  |