

1 ProtoDrift: Evaluating the impact of small-to-big 2 adjustments to chemotherapy protocols

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24 **Abstract**

25 Adjustments to chemotherapy protocols are common to adapt treatments to individual patient needs,
26 yet consensus on the impact of such adjustments is lacking. We introduce ProtoDrift, a novel met-
27 ric that quantifies time and dose adjustments in chemotherapies. This weighted distance enables an
28 assessment of their impact on patient outcomes, offering more detailed analyses than the traditional
29 Relative Dose Intensity (RDI). We compared ProtoDrift and RDI prediction performances through
30 survival analyses on 20,808 patients across 38 groups, categorised by cancer location and treatment
31 line at two hospitals. Without optimisation, ProtoDrift achieves either comparable or better predic-
32 tion results in 71% of patient groups (27 out of 38). Once optimised, ProtoDrift surpasses the RDI
33 C-index predictions in 89% (16 out of 18) of patient groups from the first hospital. This study con-
34 firms ProtoDrift as an advanced tool for refining chemotherapy regimen design, highlighting the
35 critical role of time adjustments in patient outcomes.

36 **1 Introduction**

37 Chemotherapy aims at finding the delicate balance between tumour reduction and minimised side
38 effects through the use of cytotoxic drugs. A common strategy to achieve this trade-off is to combine
39 various drugs in a timely manner.¹ Indeed, chemotherapy regimens are precisely designed to specify
40 the molecules, their dosages, modes and timing of administration in the form of cycles of treatment,
41 aligned with cancer cell life cycles.^{2,3} While regimens are usually defined by their prototypical cycle,
42 the overall chemotherapy protocol consists in the repetition of this cycle over time.
43 Despite the fact that protocols are precisely defined, their implementation in patient treatment often
44 undergo modifications, which arise for various reasons such as toxicity, accommodations for patient
45 convenience, or operational constraints within healthcare facilities.^{4,5,6} Figure 1 depicts an example
46 of chemotherapy protocol and how its implementation in a patient may drift over time for various
47 reasons.

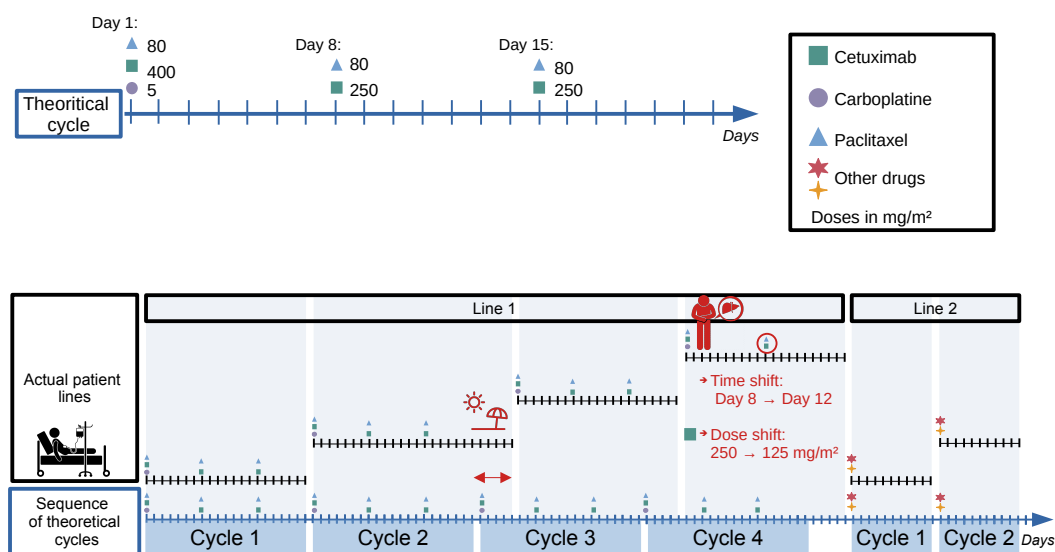


Figure 1: (Top) Graphical description of the regimen 1465 used to treat head and neck cancer. It is 21 days long and composed of various administrations including Cetuximab at day 1 (400mg/m²) day 8 (250), day 15 (250) and Paclitaxel at day 1, day 8, day 15 (80mg/m²). (Bottom) Comparison between lines (Line 1 and Line 2) followed by a fictive patient and the protocol (*i.e.* the sequence of theoretical cycles defined by the regimen itself). In this scenario, cycle 3 is delayed because the patient is in family holidays. In cycle 4, the oncologist decides to change the day of Cetuximab and Paclitaxel administrations, and to reduce the dose of Cetuximab, due to an hepatotoxicity. Both drugs are administrated only twice, instead of three times during this cycle. At the end of cycle 4, after noticing that the tumour is not shrinking fast enough, the medical expert team decides to change the regimen. Thus, a new line of treatment (Line 2) is started.

48 Adjustment to the protocols are also motivated by empirical hypotheses and vary depending on cancer
 49 locations, patient demographics, and other factors. For instance, research on early breast cancer
 50 suggests that reducing intervals between treatment cycles can improve patient outcomes.⁷ Mean-
 51 while, other studies have explored how dose reductions for specific cancer treatments can maintain
 52 efficacy, while reducing costs, illustrating the range of strategies that might be employed.⁸ Within
 53 the diversity of possible adjustments, some are well evaluated but others that are based on clinical
 54 experience or habits might lack of consensus.⁹ This highlights the necessity for tools capable of providing
 55 fine-grained description of the various types of adjustments and thus enabling the evaluation
 56 of their impact on the clinical evolution of patients.

57 The Relative Dose Intensity (RDI) is the current and standard way to assess the adherence to chemo-
 58 therapy protocols.^{10,11,12} RDI relies on the dose intensity, denoted DI, that is defined for a given anti-
 59 cancer drug d as the total dose delivered on a defined period of time in weeks since the start of the
 60 treatment line.¹³ In other terms:

$$DI(d) = \frac{\text{Total dose received of drug } d}{\text{duration in weeks}}. \quad (1)$$

61 The RDI itself is the ratio of the DI received by a patient on the planned DI, *i.e.*, the DI that would
 62 have been received in the case of a full adherence to the protocol, or

$$RDI(d) = \frac{\text{Actual } DI(d)}{\text{Planned } DI(d)}. \quad (2)$$

63 The All Drugs Relative Dose Intensity (ADRDI) is defined for a protocol as the arithmetic mean of
64 the RDIs of the anti-cancer drugs administrated in this protocol:

$$\text{ADRDI} = \frac{1}{|\mathcal{M}|} \sum_{i=1}^{|\mathcal{M}|} \text{RDI}(d_i) \quad (3)$$

65 with \mathcal{M} the set of administrated drugs. Many studies employ the RDI, in combination with a
66 threshold, usually set to 80%, to distinguish adherent from non-adherent patients in survival anal-
67 yses.^{14,15,16,17} However, this RDI approach oversimplifies the complex dynamics of chemotherapy
68 treatment, focusing on dosage without fully accounting for the timing of administrations and its po-
69 tential impacts on patient outcomes.

70 We propose in this article ProtoDrift, a more nuanced approach to quantify treatment deviations
71 from the planned treatment, assigning weighted dissimilarities to each type of variance, aiming at
72 small-to-large variations from the protocol, which could have been motivated by medical care. The
73 finding of the optimal weights offers a detailed view of the relative importance of the various type of
74 adjustments made during chemotherapy. In this sense ProtoDrift may enhance our understanding
75 of treatment responses and guide more effective patient management.

76 2 Results

77 2.1 Patient group characteristics

78 We computed ADRDI and Naive ProtoDrift (NP) (ProtoDrift without optimised weights) across 38
79 patient groups from two French University hospitals, the European Hospital Georges Pompidou
80 (HEGP) and the University Hospital of Bordeaux (UHB). Patients groups are formed based on tu-
81 mour location and treatment line number. The study is composed of 18 patient groups from HEGP
82 hospital, and 20 patients groups from UHB (see Data sources and study design Section in Methods).
83 Tables 1 and 2 present the mean, standard deviation (SD) and violin plots of the distribution of 1-
84 ADRDI and Naive ProtoDrift (NP), ProtoDrift without optimised weights, in our two hospitals and
85 in each of their subgroups. Although 1-ADRDI and NP share similar means across most subgroups,
86 their distinct distributions suggest that each metric capture different aspect of treatment adjustments.

	Demographic characteristics				Overall Survival		Metrics					
	Sex Count (%)		Age at line start		Mortality count (%)		NP		1-ADRDI		Distribution	
	M	F	Mean	SD	3 years	5 years	Mean	SD	Mean	SD	NP	1-ADRDI
All locations												
1 st line (8787)	4717 (53.7%)	4072 (46.3%)	64.16	13.42	5047 (57.4%)	5605 (63.8%)	0.14	0.12	0.19	0.19		
1 st line (12021)	7429 (61.8%)	4592 (38.2%)	62.9	15.89	4630 (38.5%)	5058 (42.1%)	0.2	0.14	0.31	0.31		
2 nd line (4318)	2252 (52.2%)	2066 (47.8%)	63.9	12.96	2821 (65.3%)	3089 (71.5%)	0.13	0.12	0.22	0.22		
2 nd line (5578)	3329 (59.7%)	2249 (40.3%)	62.42	15.3	1975 (35.4%)	2137 (38.3%)	0.21	0.15	0.39	0.32		
Respiratory and Thoracic												
1 st line (2030)	1339 (66%)	691 (34%)	64.62	11.61	1442 (71%)	1550 (76.4%)	0.14	0.11	0.18	0.18		
1 st line (918)	587 (63.9%)	331 (36.1%)	56.74	20.26	516 (56.2%)	548 (59.7%)	0.17	0.12	0.27	0.27		
2 nd line (850)	540 (63.5%)	310 (36.5%)	63.87	11.06	645 (75.9%)	689 (81.1%)	0.14	0.13	0.21	0.21		
2 nd line (346)	215 (62.1%)	131 (37.9%)	59.78	13.22	213 (61.6%)	229 (66.2%)	0.2	0.14	0.33	0.27		
Colon												
1 st line (1298)	730 (56.2%)	568 (43.8%)	65.39	13.13	720 (55.5%)	836 (64.4%)	0.13	0.1	0.22	0.2		
1 st line (507)	304 (60%)	203 (40%)	65.33	12.45	295 (58.2%)	316 (62.3%)	0.15	0.13	0.39	0.24		
2 nd line (748)	407 (54.4%)	341 (45.6%)	65.86	13.16	484 (64.7%)	555 (74.2%)	0.13	0.1	0.25	0.2		
2 nd line (216)	132 (61.1%)	84 (38.9%)	64.9	13.07	143 (66.2%)	150 (69.4%)	0.21	0.18	0.46	0.33		
Lymphoid and Hematologic												
1 st line (495)	286 (57.8%)	209 (42.2%)	64.73	21.11	219 (44.2%)	245 (49.5%)	0.16	0.12	0.23	0.23		
1 st line (4816)	2767 (57.5%)	2049 (42.5%)	61.5	17.09	1455 (30.2%)	1622 (33.7%)	0.25	0.14	0.46	0.3		
2 nd line (227)	137 (60.4%)	90 (39.6%)	63.19	20.02	98 (43.2%)	115 (50.7%)	0.18	0.15	0.31	0.29		
2 nd line (2741)	1575 (57.5%)	1166 (42.5%)	61.42	16.47	724 (26.4%)	812 (29.6%)	0.25	0.13	0.48	0.28		
Bladder and Urothelial												
1 st line (727)	563 (77.4%)	164 (22.6%)	69.12	11.88	419 (57.6%)	471 (64.8%)	0.13	0.11	0.2	0.23		
1 st line (601)	485 (80.7%)	116 (19.3%)	66.9	11.34	144 (24%)	160 (26.6%)	0.15	0.12	0.17	0.27		
2 nd line (217)	174 (80.2%)	43 (19.8%)	67.34	12.97	161 (74.2%)	169 (77.9%)	0.13	0.12	0.21	0.23		
2 nd line (131)	109 (83.2%)	22 (16.8%)	64.6	12.95	44 (33.6%)	46 (35.1%)	0.14	0.15	0.22	0.29		
ENT (Ear, Nose, Throat)												
1 st line (1365)	1096 (80.3%)	269 (19.7%)	62.67	11.42	736 (53.9%)	836 (61.2%)	0.13	0.13	0.16	0.19		
1 st line (762)	576 (75.6%)	186 (24.4%)	59.11	12.96	305 (40%)	336 (44.1%)	0.09	0.08	0.08	0.18		
2 nd line (750)	610 (81.3%)	140 (18.7%)	63.08	11.13	492 (65.6%)	532 (70.9%)	0.13	0.14	0.18	0.22		
2 nd line (294)	229 (77.9%)	65 (22.1%)	59.44	13.06	163 (55.4%)	173 (58.8%)	0.09	0.1	0.14	0.22		
Pancreas and Biliary Tract												
1 st line (991)	540 (54.5%)	451 (45.5%)	68.35	11.53	741 (74.8%)	786 (79.3%)	0.19	0.12	0.24	0.19		
1 st line (803)	461 (57.4%)	342 (42.6%)	67.91	11	622 (77.5%)	640 (79.7%)	0.15	0.09	0.26	0.2		
2 nd line (510)	268 (52.5%)	242 (47.5%)	67.68	11.4	408 (80%)	426 (83.5%)	0.18	0.12	0.31	0.21		
2 nd line (271)	152 (56.1%)	119 (43.9%)	66.61	11.7	209 (77.1%)	212 (78.2%)	0.19	0.12	0.36	0.24		

Table 1: Demographic, overall survival, and distribution of ProtoDrift (NP) and 1-ADRDI in our two cohorts and each group of the study. 1-ADRDI is used to facilitate comparison with ProtoDrift (NP), as ADRDI is high when treatment closely aligns with the planned protocol, whereas ProtoDrift (NP) is low. Blue is used for data of the first hospital (HEGP) and red for the second (UHB) (1/2)

	Demographic characteristics				Overall Survival		Metrics				Distribution	
	Sex Count (%)		Age at line start		Mortality count (%)		NP		1-ADRDI		NP	1-ADRDI
	M	F	Mean	SD	3 years	5 years	Mean	SD	Mean	SD		
Breast												
1 st line (1235)	51 (4.1%)	1184 (95.9%)	57.27	13.71	398 (32.2%)	486 (39.4%)	0.09	0.09	0.11	0.17		
2 nd line (563)	23 (4.1%)	540 (95.9%)	57.36	13.16	258 (45.8%)	296 (52.6%)	0.1	0.11	0.16	0.19		
Ovary												
1 st line (502)	0 (0%)	502 (100%)	65.42	13.13	251 (50%)	291 (58%)	0.17	0.14	0.16	0.15		
2 nd line (313)	0 (0%)	313 (100%)	66.22	11.69	167 (53.4%)	199 (63.6%)	0.12	0.11	0.15	0.17		
Stomach												
1 st line (433)	279 (64.4%)	154 (35.6%)	62.73	13.5	288 (66.5%)	302 (69.7%)	0.13	0.09	0.23	0.2		
2 nd line (207)	135 (65.2%)	72 (34.8%)	61.75	13.1	150 (72.5%)	156 (75.4%)	0.13	0.1	0.24	0.21		
Liver												
1 st line (848)	723 (85.3%)	125 (14.7%)	68.3	10.1	391 (46.1%)	451 (53.2%)	0.22	0.11	0.16	0.28		
2 nd line (152)	131 (86.2%)	21 (13.8%)	70.47	9.68	74 (48.7%)	80 (52.6%)	0.21	0.17	0.36	0.36		
Neurology												
1 st line (685)	317 (46.3%)	368 (53.7%)	54.65	17.23	52 (7.6%)	66 (9.6%)	0.27	0.13	0.44	0.41		
2 nd line (411)	198 (48.2%)	213 (51.8%)	54.8	16.01	27 (6.6%)	28 (6.8%)	0.27	0.17	0.54	0.41		
Melanoma												
1 st line (1473)	882 (59.9%)	591 (40.1%)	67.04	14.57	689 (46.8%)	731 (49.6%)	0.13	0.14	0.05	0.11		
2 nd line (628)	371 (59.1%)	257 (40.9%)	65.84	14.07	274 (43.6%)	295 (47%)	0.1	0.14	0.07	0.14		
Myeloma												
1 st line (609)	328 (53.9%)	281 (46.1%)	67.22	10.84	162 (26.6%)	189 (31%)	0.18	0.13	0.35	0.27		
2 nd line (389)	217 (55.8%)	172 (44.2%)	68.43	10.77	105 (27%)	113 (29%)	0.21	0.13	0.46	0.26		

Table 2: Demographic, overall survival, and distribution of ProtoDrift (NP) and 1-ADRDI in our two cohorts and each group of the study. 1-ADRDI is used to facilitate comparison with ProtoDrift (NP), as ADRDI is high when treatment closely aligns with the planned protocol, whereas ProtoDrift (NP) is low. Blue is used for data of the first hospital (HEGP) and red for the second (UHB) (2/2)

87 2.2 Optimised ProtoDrift Results

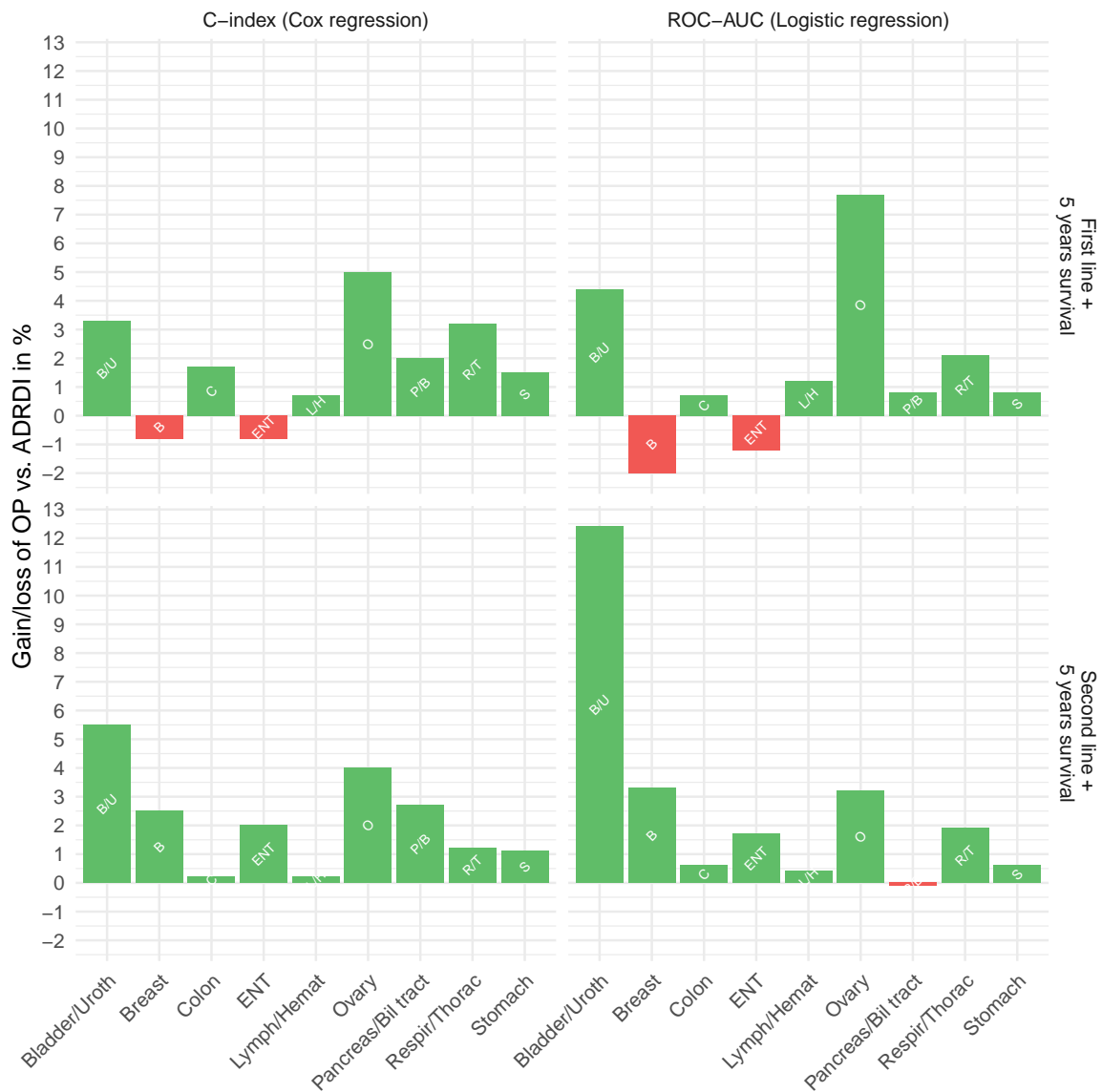


Figure 2: 5-year overall survival prediction score gains when using OP_{Cox} (on the left) or OP_{Logit} (on the right) vs. ADRDI. Relative gains are in green, losses are in red.

88 The optimisation of ProtoDrift weights with Cox regression (OP_{Cox}) results in notable improvements
 89 of the C-index with regards to ADRDI across 16 out of 18 (89%) groups at HEGP. In 13 of them (72%)
 90 C-index increases with at least 1%. This trend is also observed when optimising the weights with
 91 the logistic regression (OP_{Logit}), with gains in 15 groups (83%), and gains of at least 1% in 9 groups
 92 (50%). These results are summarised in Figure 2.
 93 We observe a smaller SD of gains with OP_{Cox} with regards to OP_{Logit} that reaches the higher gains
 94 with over 7.5% and 12% for Ovary, first line and Bladder/Urothelial, second line, respectively.

95 2.3 Naïve ProtoDrift results

96 To evaluate the performance of Naïve ProtoDrift (NP) against the baseline ADRDI, we computed
97 and compared three Cox-based performance indicators: significance of the regression coefficient,
98 C-index, and LogRank p-values (see section 4.3 in Methods).

99 We find that NP performs comparably or better than ADRDI in a substantial proportion of patient
100 groups. Specifically, 50% of groups at both HEGP and UHB (9/18 and 10/20, respectively) show at
101 least one performance gain and no loss across the three indicators. Overall, 67% of HEGP groups
102 and 75% of UHB groups have either comparable or improved results with NP.

103 Notably, a subset of groups demonstrate consistent improvements across all three indicators. At
104 HEGP, these include Respiratory/Thoracic, Colon, and Ovary (first line), as well as ENT (second
105 line). At UHB, they include Colon, ENT, and Melanoma (first line), and Colon and Melanoma (sec-
106 ond line). Conversely, ADRDI outperforms NP (i.e., at least one loss and no gain) in 18% of the total
107 groups.

108 These results suggest that ProtoDrift, even without optimisation, offers a more nuanced capture of
109 treatment adherence compared to ADRDI.

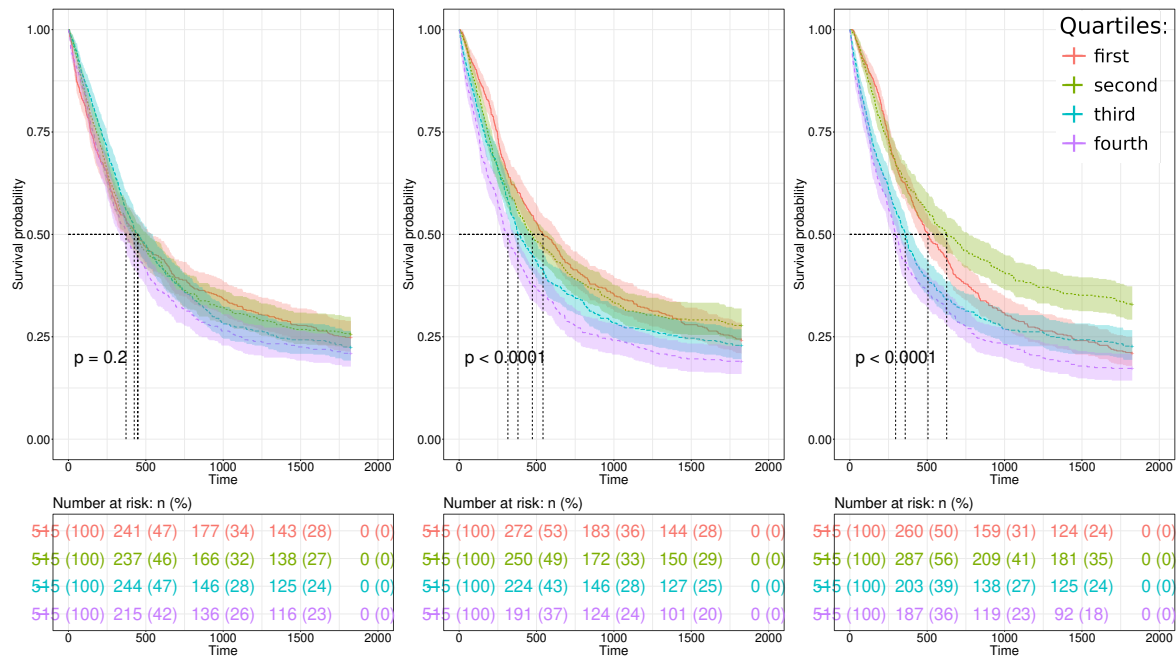
110 For a visual overview, we refer the reader to the UpSet-style summaries and per-group bar plots
111 provided in Appendix Figures 10 and 11, which synthesize the comparative performance across
112 patient subgroups. For full transparency, the complete numerical results—covering all three Cox-
113 based indicators and additional logistic regression metrics—are available in Appendix Tables B.3

114 2.4 Illustration with the prediction of the 5-year overall survival in the Respira- 115 tory/Thoracic group

116 NP and OP have been computed for each group of the first hospital (HEGP), and in one group only
117 (Respiratory/Thoracic) in the second hospital for external validation. The complete results of the
118 comparative analysis are available at <https://files.inria.fr/protodrift-surv/>. Here,
119 we focus on results obtained on the illustrative group for which ProtoDrift was optimised in both
120 hospitals: patients with Respiratory/Thoracic cancer, in their first line of treatment, using Cox re-
121 gression prediction.

122 Figure 3 shows that, in patients treated in HEGP hospital, both NP and OP_{Cox} models demonstrate
123 superior performance to ADRDI across the three considered indicators (see Figure 3b). Firstly, both
124 NP and OP_{Cox} show significant contributions to the Cox regression models (p -values < 0.01 and $= 0.01$,
125 respectively), indicating a reliable prediction of the mortality risk, which is not observed with ADRDI
126 (p -value $= 0.23$). Secondly, the two models outperform ADRDI in predictive performance, evidenced
127 by higher C-index scores. Lastly, the discriminative power analysis, using Kaplan-Meier survival
128 curves (see Figure 3a), confirmed that OP_{Cox} , and to a lower extent NP, effectively differentiate be-
129 tween patient survival outcomes across quartiles, validated by significant LogRank test results (see
130 Figure 3b). Interestingly, we observe with OP_{Cox} , which best align with the outcomes, an inversion
131 of second and first quartiles that can not be observed with other approaches.

132
133 Figure 4 shows that in patients treated in UHB, none of the metric shows a significant contribution
134 in the Cox regressions models (see Figure 4b). However, we qualitatively observe that the Kaplan
135 Meier curves are more spaced apart with NP or OP_{Cox} than with ADRDI quartiles, underscoring a
136 better overall discriminative power (see Figure 4a).



(a) Kaplan-Meier curves constructed on 1 – ADRDI (left), NP (middle), and OP_{Cox} (right) quartiles.

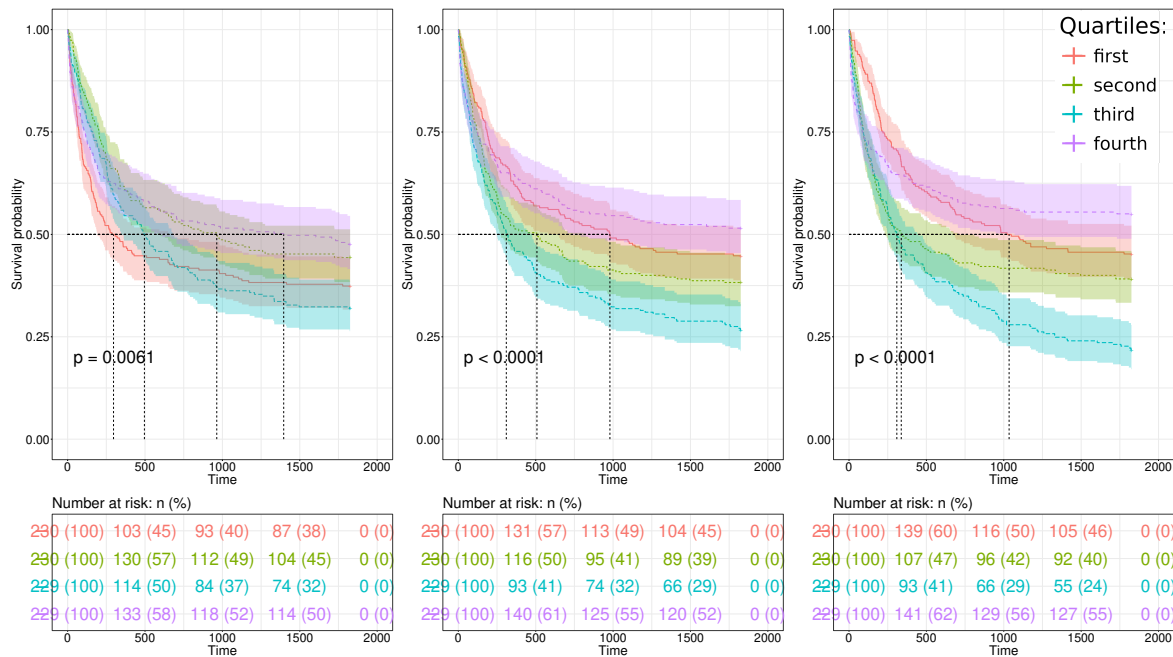
Cox regression models comparison

$h(t) = h_0 * \exp(\theta_1 * \text{metric} + \theta_2 * \text{age} + \theta_3 * \text{sex})$

	Significance of the explanatory variable				Prediction score (C-index)			Discriminative power analysis between quartiles (LogRank test p-values)						
	θ_1	CI	sd	p-value	Value	CI	sd	1 st vs. 2 nd	1 st vs. 3 rd	2 nd vs. 3 rd	1 st vs. 4 th	2 nd vs. 4 th	3 rd vs. 4 th	
OP_{Cox}	1.10	(0.72 - 1.49)	0.23	0.01	0.55	(0.52 - 0.58)	0.02	0.01	0.04	0.01	0.01	0.01	0.01	0.03
NP	1.44	(0.76 - 2.10)	0.40	0.01	0.54	(0.51 - 0.57)	0.02	0.89	0.05	0.06	0.01	0.01	0.03	
ADRDI	-0.28	(-0.62 - 0.07)	0.21	0.23	0.52	(0.49 - 0.55)	0.02	0.89	0.89	0.89	0.21	0.21	0.21	

(b) Results of the comparative analysis over three types of indicators.

Figure 3: Comparative performances of the prediction with the Cox regression model of the 5-year overall survival at the end of the first line of the Respiratory/Thoracic group at the HEGP hospital.



(a) Kaplan-Meier curves constructed on 1 – ADRDI (left), NP (middle), and OP_{Cox} (right) quartiles.

Cox regression models comparison
 $h(t) = h_0 * \exp(\theta_1 * \text{metric} + \theta_2 * \text{age} + \theta_3 * \text{sex})$

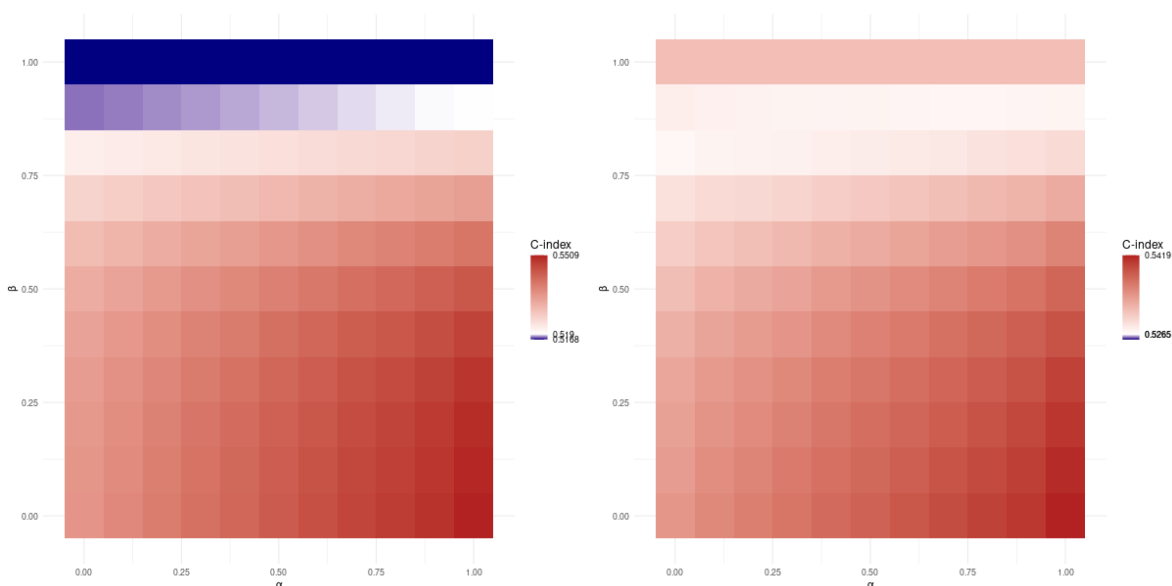
	Significance of the explanatory variable				Prediction score (C-index)			Discriminative power analysis between quartiles (LogRank test p-values)					
	θ_1	CI	sd	p-value	Value	CI	sd	1 st vs. 2 nd	1 st vs. 3 rd	2 nd vs. 3 rd	1 st vs. 4 th	2 nd vs. 4 th	3 rd vs. 4 th
OP _{Cox}	0.79	(0.22 - 1.34)	0.35	0.07	0.54	(0.49 - 0.60)	0.03	0.01	0.01	0.01	0.34	0.01	0.01
NP	1.15	(0.10 - 2.22)	0.67	0.16	0.53	(0.48 - 0.59)	0.03	0.09	0.01	0.02	0.40	0.02	0.01
ADRDI	-0.19	(-0.68 - 0.34)	0.32	0.38	0.53	(0.48 - 0.58)	0.03	0.02	0.98	0.02	0.03	0.98	0.02

(b) Results of the comparative analysis over three types of indicators.

Figure 4: Comparative performances of the prediction with the Cox regression model of the overall survival at the end of the first line of the Respiratory/Thoracic group at the UHB hospital.

137 2.5 Relative importance of ProtoDrift weights

138 We computed heat maps to provide for each group a view of the relative importance of the weights
 139 of ProtoDrift, and thus of the various types of adjustment (*e.g.*, dose, timing, cycle delay). Figure
 140 5 shows that for the Respiratory/Thoracic, first line group, both at HEGP and UHB, best survival
 141 prediction is reach for high value of α and low value of β , *i.e.*, when $\omega_t > \omega_d$ and $\omega_{intra} > \omega_{inter}$.
 142 In other terms, in-cycle time changes have more impact than in-cycle dose changes and changes in
 143 in-cycle timing and dosing have more impact than cycle delays (see Figure 7). We observe a similar
 144 trend for other groups, such as ENT, second line or Pancreas/Biliary Tract, first line (see <https://files.inria.fr/protodrift-surv/year-survival-22> and <https://files.inria.fr/protodrift-surv/year-survival-32>). However, in other groups, other balances are observed.
 147 For example, in Ovary, second line, and Colon, first line, we observe a stronger impact of
 148 dose changes with regards to time changes (see <https://files.inria.fr/protodrift-surv/year-survival-30> and <https://files.inria.fr/protodrift-surv/year-survival-16>).
 149



(a) Heat map profile of HEGP 1st line, R/T group

(b) Heat map profile of UHB 1st line, R/T group

Figure 5: Heat map representation of prediction gains with ProtoDrift (OP_{Cox}) *vs.* ADRDI depending on values of α (*i.e.*, $\frac{\omega_t}{\omega_t + \omega_d}$) and β (*i.e.*, $\frac{\omega_{inter}}{\omega_{inter} + \omega_{intra}}$), in patients with Respiratory/Thoracic (R/T) cancer groups in their first line of treatment, either at HEGP (left) or UHB (right). Figure 7 provides an interpretation guide to these heat maps.

150 3 Discussion

151 We introduced ProtoDrift, a novel metric for the fine-grained measure of chemotherapy adherence,
 152 and demonstrated its superiority to the state-of-the-art RDI, by showing how Protodrift, in particular
 153 when optimised, is more significantly associated with clinical outcomes.

154 This establishes our metric a new foundational tool to customise the design of chemotherapy regi-
 155 mens and the clinical adjustments of chemotherapy.

156 The comparative analysis of ProtoDrift weights reveals that ProtoDrift particularly outperforms
 157 ADRDI when the timing weight (ω_t) exceeds the dosage one (ω_d). This can be explained by the

158 fact that temporal adjustments are loosely considered in ADRDI that sums the dose changes for a
159 defined period of time, thus do not consider punctual timing adjustments.

160 Moreover, the relative importance of ProtoDrift weight provides elements of interpretability about
161 the type of adjustment that might impact clinical outcomes. For instance, Figure 5 illustrates that
162 in the first line treatment of Respiratory/Thoracic cancer, an overall delay in cycles or a change in
163 dosage may have minimal impact on survival compared to an in-cycle administration time shift.
164 Such distinctions could not be observed when using ADRDI.

165 ProtoDrift also brings new insights by its ability to better discriminate between patient groups.
166 Kaplan-Meier analyses, Figures 3a and 4a) enable to discuss the hypothesis that better adherence to
167 treatment correlates with improved survival. Indeed, at UHB, the least adherent quartile shows to be
168 significantly associated with higher survival rates. This observation echoes studies about chemother-
169 apy management in elderly patients, particularly those with non-small cell lung cancer (NSCLC),
170 where reduced dosages and delayed administrations might benefit survival.¹⁸ This highlights the
171 potential of ProtoDrift to further uncover nuanced treatment impacts, with high potential in advanc-
172 ing precision medicine in cancer therapy.

173 We analysed this discriminative power using quartiles based on OP, NP and 1-ADRDI. In contrast,
174 many RDI studies split their cohorts into two groups using an 80% threshold, a less stringent divi-
175 sion. Our quartile division, although generally robust, is not always suitable for discerning patient
176 clusters. This limitation is observed in Figure 11 where certain cohorts gain in C-index but loses in
177 discriminative power such as HEGP Bladder/Urothelial in first line (see <https://files.inria.fr/protodrift-surv/year-survival-8>).

179 It is worth noting that ProtoDrift can find applications beyond the field of oncology, and particularly
180 suits other treatments associated with cyclic protocols.¹⁹ On a group of patients with Auto-immune
181 and Inflammatory diseases, not included in our study, the comparison of ProtoDrift to RDI shows
182 gains on our three performance indicators (see <https://files.inria.fr/protodrift-surv/year-survival-4>).

184 ProtoDrift can be explored further. In particular, its interpretability capabilities could be extended
185 by considering the relative weights of the molecules of a regimen (*i.e.*, does a dose change with
186 molecule A will greatly impact the outcome than a dose change of molecule B?), or the mode of
187 administration (*i.e.*, does a bolus administration will greatly impact than slow infusion of the same
188 molecule?). However, one can expect that adding more parameters will complexify interpretations.
189 In assessing ProtoDrift, we avoided combining patient groups from the two hospitals or directly
190 applying optimised weights from one hospital to the other on purpose. This strategy was selected
191 to respect the unique characteristics and treatment deviations inherent to each hospital population.
192 Our approach focuses on understanding specific hospital contexts rather than creating a universally
193 applicable model. This distinction supports the use of ProtoDrift to explore variability in treatment
194 adherence and its impact, tailored to each clinical setting. This highlights that ProtoDrift does not
195 aim at being a predictive tool, but a means to assess and visualise the impact of different types of
196 adjustment on clinical outcomes.

197 The reproducibility of our observations with ProtoDrift could be further extended as they were lim-
198 ited to seven groups for NP (Figure 11) and one group for OP (Figures 3 and 4). In this work, we
199 optimised ProtoDrift for only one UHB location, primarily due to constraints on computational time
200 and data access. Particularly, the weight optimisation, which involves fitting and predicting regres-
201 sion models multiple times, is time-consuming. We aimed at additional validation and interoper-
202 ability with our effort to provide an open implementation of ProtoDrift that takes as input treatment

203 descriptions in an easy-to-reuse tabular format (see Code availability section for details).

204 4 Methods

205 4.1 Data sources and study design

206 We independently collected chemotherapy prescriptions and administrations HEGP and UHB hos-
207 pitals from 2003-07-01 to 2021-12-15 (about 18.5 years).²⁰

208 Both hospitals include in-stay and after-stay patient survival data that is the outcome used in this
209 study.²¹

210 We relied on ChemoOnto for reconstructing chemotherapy treatment course from anti-cancer medi-
211 cation records and theoretical regimens.^{22,23}

212 Groups of patients were defined by tumour location. In each hospital, only groups with at least 400
213 patients were considered. For each location, we also distinguished between chemotherapy adminis-
214 trated in either the first or second line of treatment.

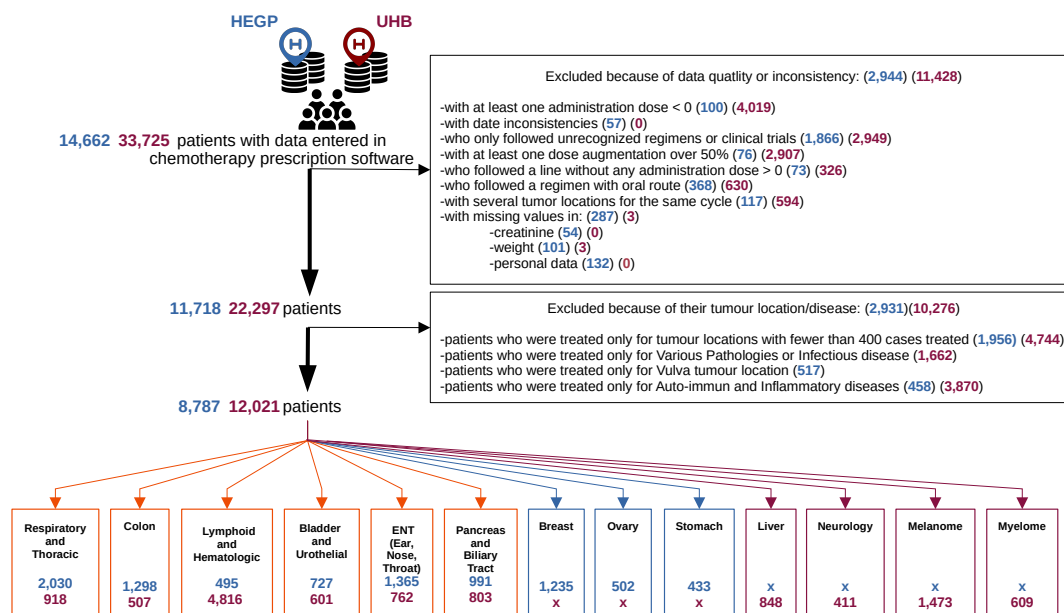


Figure 6: Study profile. After data cleaning, we considered tumour locations with more than 400 cases treated ($n > 400$). Six cancer locations are common to our two hospitals, three locations from HEGP only, and four from UHB only.

215 As illustrated by table 6, we excluded 2,944 patients at HEGP and 11,428 at UHB because of poor
216 data quality or inconsistency. 13 locations with more then 400 patients were kept, six found both at
217 HEGP and UHB, three at HEGP only, and four at UHB only. When considering treatment lines, the
218 study is composed of 18 groups from HEGP and 20 groups from UHB, described in tables 1 and 2.

219 Tumour location groups shown in Figure 6 are not disjoint because patients may have more than
220 one cancer location. For each location group, all patients have followed a first line of treatment, and

221 potentially, but not always, a second. Consequently, the size of the second line groups is smaller than
222 that of the first line groups, as can be observed in tables 1 and 2.
223 Details about patients selection are provided in Appendix B.1.

224 4.2 ProtoDrift model development

225 4.2.1 Definition of ProtoDrift

226 ProtoDrift is a multi-level weighted mean designed to quantify the deviation between an adminis-
227 tered chemotherapy treatment and the initially prescribed treatment protocol. Possible deviations
228 are quantified with dissimilarities, scaled from 0 to 1. Values close to 1 indicate high deviation.
229 The first step of ProtoDrift is to compute dissimilarities at the administration level, between actual
230 and theoretical cycle. For each administration, a dissimilarity δ_{adm} is computed as a weighted mean
231 of differences in dose (δ_d) and timing (δ_t) from the theoretical cycle. Formally,

$$\delta_{\text{adm}} = \frac{\omega_d \delta_d + \omega_t \delta_t}{\omega_d + \omega_t} \quad (4)$$

232 where ω_d and ω_t are the weights associated with dose and time changes. An alignment algorithm
233 pairs the planned and actual administrations to ensure that ProtoDrift consider them only once.
234 Details of the alignment algorithm are documented in Appendix Figure 8 and pseudo-code 1.
235 Administration-level dissimilarities are then averaged at the molecule level (δ_m), by considering all
236 the administrations of a same drug within a cycle. Next, an intra-cycle dissimilarity, noted δ_{intra} , is
237 calculated by aggregating molecule-level dissimilarities within a cycle. Besides, ProtoDrift computes
238 an inter-cycle dissimilarity, noted δ_{inter} that measures delays (or rare advances) in starting new cycles.
239 Then, intra- and inter-cycle dissimilarities are aggregated at the cycle level with a weighted mean as
240 follow:

$$\delta_{\text{cycle}} = \frac{\omega_{\text{intra}} \delta_{\text{intra}} + \omega_{\text{inter}} \delta_{\text{inter}}}{\omega_{\text{intra}} + \omega_{\text{inter}}} \quad (5)$$

241 where ω_{intra} and ω_{inter} are the respective weights for the intra- and inter-cycle dissimilarities. Finally,
242 cycle-level dissimilarities are summed at the line level to provide the final metric named ProtoDrift:

$$\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}}) = \frac{1}{l} \sum_{i=1}^l \delta_{\text{cycle}}^i \quad (6)$$

243 where l is the number of cycles of the treatment line \mathcal{L} , and $\mathcal{C}^{\text{theo}}$ the theoretical cycle as defined in
244 the protocol. Appendix Figure 9 summarises the various levels of dissimilarity and aggregation.
245 We measure ProtoDrift at the level of the treatment line (δ_{line}). Firstly because we want to account
246 for adjustments occurring within a treatment line. Secondly because studies with RDI generally
247 compute its value for a treatment line. Details on the computation of ProtoDrift are provided in
248 Appendix A.1.2.

249 4.2.2 Optimisation of ProtoDrift weights

250 ProtoDrift associates a weight with each of its composing dissimilarities, each one reflecting the rel-
251 ative importance of a type of deviation to a chemotherapy protocol. We particularly focused on
252 the weights that reflect dose adjustments, drug removal and timing shifts, either within or between

253 cycles (delays), *i.e.* ω_d , ω_t , ω_{intra} and ω_{inter} , associated with δ_d , δ_t , δ_{intra} and δ_{inter} dissimilarities, respec-
 254 tively.

255 We distinguish two versions of ProtoDrift: *Naive ProtoDrift (NP)* where each weight is set to 1, *i.e.*,
 256 each type of adjustment has a similar weight; and *Optimised ProtoDrift (OP)* where optimal weights
 257 are set on the basis of a grid search. This optimisation targets two goals:

- 258 • identifying the weight combination that offers the best survival predictions,
- 259 • helping interpreting what type of adjustment (*e.g.*, dose or time adjustment) has more impact
 260 on survival outcomes.

261 Optimal weight combinations can be searched for various groups, such as different cancer locations.
 262 The optimisation is performed on the 3- and 5-year overall survival, but it could alternatively be on
 263 progression free survival or toxicity occurrences. Here, we preferred overall survival as it is recorded
 264 routinely and with good quality. Moreover, RDI studies we compare with, usually takes the overall
 265 survival as their main outcome.

266 To simplify the exploration for optimal weights, we define two quantities α and β , which values are
 267 between 0 and 1, that summarise the four weights considered for optimisation (ω_d , ω_t , ω_{intra} , ω_{inter}):

$$\alpha = \frac{\omega_t}{(\omega_t + \omega_d)} \quad (7)$$

268 and

$$\beta = \frac{\omega_{\text{inter}}}{(\omega_{\text{inter}} + \omega_{\text{intra}})} \quad (8)$$

269 Those enable to rewrite the two following components of ProtoDrift:

$$\delta_{\text{adm}} = \alpha\delta_t + (1 - \alpha)\delta_d \quad (9)$$

270 and

$$\delta_{\text{cycle}} = \beta\delta_{\text{inter}} + (1 - \beta)\delta_{\text{intra}} \quad (10)$$

271 (See Appendix A.2 for the proof).

272 We grid search over α and β by a step of 0.1 computing at each step ProtoDrift (δ_{line}) and fit a logistic
 273 regression and a Cox regression model according to the two following equations:

$$\text{logit}(P(Y = 1)) = \theta_1\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha,\beta} + \theta_2\text{age} + \theta_3\text{sex} \quad (11)$$

$$h(t) = h_0 \exp(\theta_1\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha,\beta} + \theta_2\text{age} + \theta_3\text{sex}) \quad (12)$$

274 In the logistic regression (11), the binary response variable Y encodes the occurrence of the event
 275 before the survival time. In Cox regression (12), h is the hazard function. For genital cancer locations,
 276 the last term is removed from both formulas ($\theta_3\text{sex}$).

277 Predictions are evaluated using ROC-AUC for logistic regression and C-index for Cox regression to
 278 select the best α and β values. We note OP_{logit} and OP_{Cox} the versions of Protodrft optimised either

279 with the logistic or the Cox regression. We use bootstrap resampling with 500 samples to account for
 280 the variability in the sampled populations and assess the uncertainty of predictions.

281 The grid search computes a prediction score for every combinations of (α, β) pairs, what provides a
 282 view of their relative importance for the prediction of survival, and can be interpreted as:

- 283 • a high value of α (close to 1) signifies that $\omega_t > \omega_d$, that is to say in-cycle timing of administra-
 284 tions has more impact than dose changes;
- 285 • a high value of β (close to 1) signifies that $\omega_{inter} > \omega_{intra}$, that is to say the overall cycle delay
 286 has more impact than the in-cycle timing and dose changes.

287 For a particular group of patients, this relative importance can be visualised with heat maps of the
 288 survival prediction score plotted according to α and β values. Results can be interpreted following
 289 the guidelines provided in Figure 7. When $\beta = 1$, ProtoDrift is constant, and so is the prediction
 290 score. Indeed, in this case, only the overall cycle delay impacts (see proof in Appendix A.2).

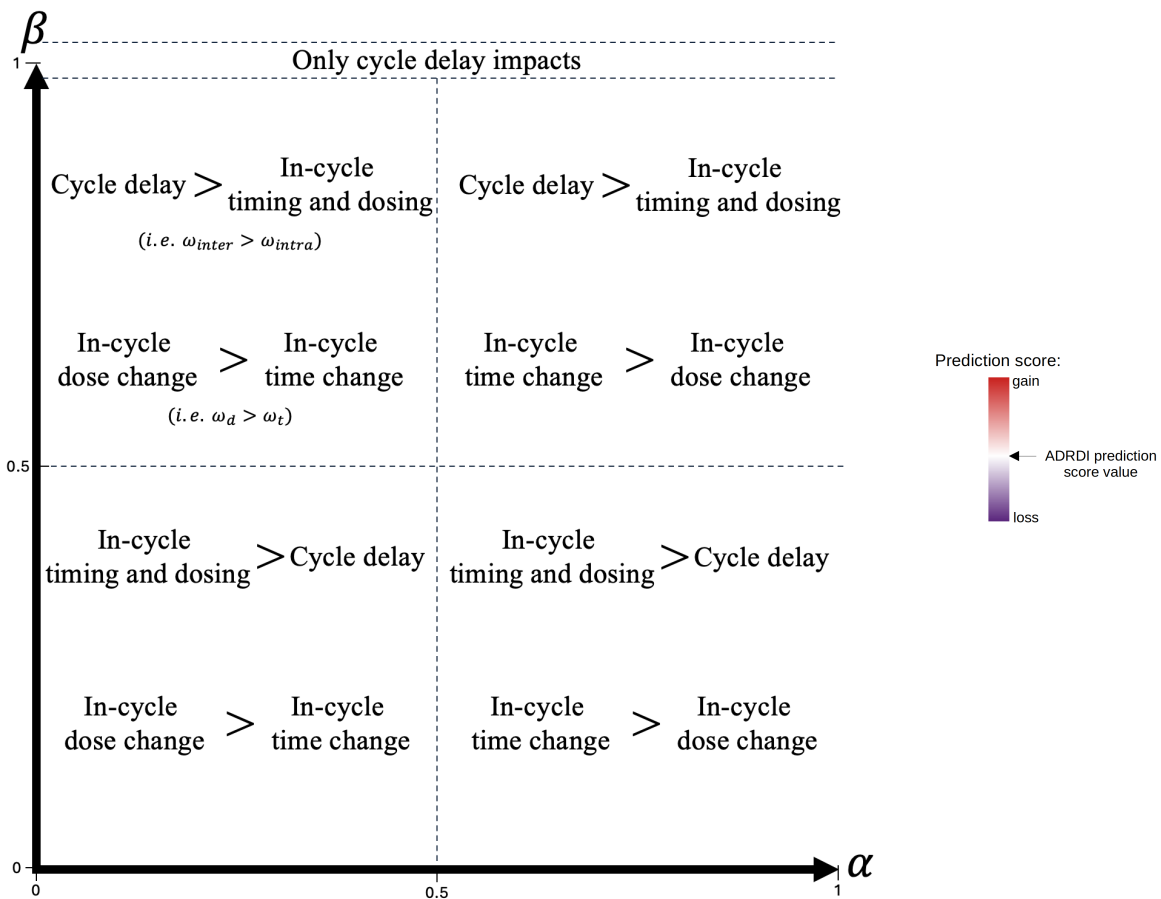


Figure 7: Interpretation guide for the relative importance of various ProtoDrift parameters on survival prediction.

291 4.3 Comparative analysis of ProtoDrift and Relative Dose Intensity

292 With the objective of demonstrating the benefit of ProtoDrift over the all drugs RDI (ADRDI), we
 293 compare their performance in predicting the overall survival with both logistic and Cox regression

294 models. To this aim, we use either NP, OP or ADRDI as the explanatory variable of our two predictive
295 models (11) and (12). The resulting models are detailed in Appendix A.2.

296 We assess the performance of the various approaches using three distinct indicators:

- 297 • The significance of the explanatory variable contribution to the regression model with the Wald
298 test p-value associated with each approach.
- 299 • Prediction score comparison: Prediction performances are measured with the ROC-AUC for
300 logistic regressions or C-index for Cox regressions. The difference of these metrics between
301 models with ADRDI and NP, or between ADRDI and OP, gives the gain in performance of
302 ADRDI *vs.* ProtoDrift.
- 303 • Discriminative power analysis: This evaluates the ability of each model to differentiate be-
304 tween four groups with distinct survival outcomes. First, we split patients into quartiles based
305 on their values of NP, OP and 1-ADRDI. Second, by analysing Kaplan-Meier survival curves
306 for these quartiles, we assess the effectiveness of the models in distinguishing varying survival
307 outcomes, validated through LogRank tests for statistical significance. We work with 1-ADRDI,
308 to facilitate the comparison with Protodrft, as ADRDI is high when a treatment is similar to
309 the planned protocol, while Protodrft is low.

310 To assess the reproducibility and validity of ProtoDrift, we conducted comparative analyses using
311 datasets from both HEGP and UHB. For the HEGP dataset, we performed comparisons between
312 ADRDI *vs.* NP and ADRDI *vs.* OP across all patient groups. In contrast, for the UHB dataset, while
313 the comparison between ADRDI *vs.* NP was conducted across all patient groups, the ADRDI *vs.* OP
314 comparison was carried out for the Respiratory/Thoracic first line group only.

315 5 Data availability

316 ADRDI-NP-OP comparative analysis of the 18 HEGP patient groups, with both Cox and logis-
317 tic regressions, and predicting both 3- and 5- year overall survival (72 analysis), are available at
318 <https://files.inria.fr/protodrft-surv/>. Patient data were collected during healthcare,
319 either at the Georges Pompidou Hospital in Paris, or at the University Hospital of Bordeaux, France.
320 Data were used under the IRB CSE-21-16 and CER-BDX-2024-80, respectively. These personal data
321 are not shared to preserve their confidentiality.

322

323 6 Code availability

324 The code to compute Naive ProtoDrift is available at [https://gitlab.inria.fr/arogier/](https://gitlab.inria.fr/arogier/protodrft)
325 [protodrft](https://gitlab.inria.fr/arogier/protodrft). The code to optimise its weights is available at <https://gitlab.inria.fr/arogier/protodrft>
326 The schema and the dictionary of the analysed data are those of ChemoOnto, available at [https://](https://gitlab.inria.fr/arogier/ChemoOntoTox)
327 gitlab.inria.fr/arogier/ChemoOntoTox.

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333 **Declaration of generative AI in the writing process**

334 During the preparation of this work, the authors used ChatGPT to improve language and readabil-
335 ity. After using this service, the authors reviewed and edited the content as needed and take full
336 responsibility for the content of the publication.

337 **7 Author contributions**

338 **AR:** Conceptualisation, Data curation, Formal analysis, Investigation, Methodology, Software, Visu-
339 alisation, Writing - original draft, Writing - Review & Editing. **EA, EP:** Interpretation, Investigation,
340 Discussion, Review & Editing. **CB, RG, VJ:** Data curation, Validation, Review & Editing. **BS, EZ:**
341 Data curation, Interpretation, Investigation, Review & Editing. **BR:** Conceptualisation, Methodology,
342 Validation, Resources, Writing - Review & Editing, Supervision, Project Administration, Funding ac-
343 quisition. **AC:** Conceptualisation, Methodology, Validation, Resources, Writing - Review & Editing,
344 Supervision, Project Administration, Funding acquisition.

345 **8 Competing Interests**

346 The authors declare that they have no known competing financial interests or personal relationships
347 that could have appeared to influence the work reported in this paper.

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404 Appendix

405 A Methods

406 A.1 ProtoDrift detailed methodology

407 A.1.1 Chemotherapy treatment concepts formalisation

- 408 • An i^{th} chemotherapy cycle followed is defined by a set of administrations $\mathcal{C}^i = \{a^1, \dots, a^n\}$.
- 409 Each cycle has a duration $\tau_{\mathcal{C}^i}$. We denote by \mathcal{C}^{theo} the theoretical cycle defined by the regimen
- 410 of duration $\tau_{\mathcal{C}^{theo}}$.
- 411 • A line \mathcal{L} is an ordered set of followed cycles: $\mathcal{L} = \{\mathcal{C}^1, \dots, \mathcal{C}^l\}$. A line has a duration $\tau_{\mathcal{L}}$.
- 412 • A protocol is a repetition of theoretical cycles.
- 413 • An anti-cancer drug m is a pair (*molecule, mode of administration*). For example, (cetuximab,
- 414 continuous infusion) or (cetuximab, bolus).
- 415 • A drug administration a is composed of three dimensions: $\langle a_m, a_t, a_d \rangle$:
- 416 – a_m is the anti-cancer drug m associated with the administration,
- 417 – a_t is the time between the start of the cycle and the administration. For example, 7 if the
- 418 administration must be done 7 days after the start of the cycle,
- 419 – a_d is the dose. For example, 300 if the administration must be done with a dose of 300 mg.
- 420 • \mathcal{C}_m^i is the subset of administrations in the cycle \mathcal{C}^i that have the same anti-cancer drug m (i.e.,
- 421 the same pair (*molecule, mode of administration*)).
- 422 • \mathcal{M} is the set of anti-cancer drugs in \mathcal{C}^i or \mathcal{C}^{theo} :

$$\mathcal{M} = \{m\} \cup \{m_{theo}\} \quad (13)$$

423 where $\{m\}$ (respectively $\{m_{theo}\}$) is the set of drugs in cycle \mathcal{C}^i (resp. \mathcal{C}^{theo}).

424 ADRDI notation

425 Here we adapt ADRDI definition (formula 3), with concept formalisation of section A.1.1.

426

427 For an anti-cancer drug m , a line \mathcal{L} , its duration in weeks $\tau_{\mathcal{L}}$, we have:

- 428 • The dose-intensity DI (1) is defined as:

$$DI(\mathcal{L}, m) = \frac{1}{\tau_{\mathcal{L}}} \sum_{i=1}^l \sum_{\forall a \in \mathcal{C}_m^i} a_d \quad (14)$$

- 429 • The theoretical dose-intensity:

$$DI(\mathcal{C}^{theo}, m) = \frac{1}{\tau_{\mathcal{C}^{theo}}} \sum_{\forall a \in \mathcal{C}_m^{theo}} a_d \quad (15)$$

- 430 • The relative dose-intensity of line \mathcal{L} :

$$\text{RDI}(\mathcal{L}^j, \mathcal{C}^{theo}, m) = \frac{\text{DI}(\mathcal{L}, m)}{\text{DI}(\mathcal{C}^{theo}, m)} \quad (16)$$

- 431 ADRDI across all drugs in a treatment line \mathcal{L} is defined as:

$$\text{ADRDI}(\mathcal{L}, \mathcal{C}^{theo}) = \frac{1}{|\mathcal{M}|} \sum_{i=1}^{|\mathcal{M}|} \text{RDI}(\mathcal{L}, \mathcal{C}^{theo}, i) \quad (17)$$

- 432 This ADRDI metric provides a normalised measure to compare the adherence of actual treatment to
 433 the prescribed regimen, with values ranging between 0 and 1. A higher ADRDI value indicates closer
 434 adherence to the prescribed treatment regimen, contrasting with the line-protocol dissimilarity: δ_{line}
 435 where a higher value signifies greater deviation.

436 A.1.2 The different dissimilarity components of ProtoDrift and their formulation

- 437 At different time scales of chemotherapy treatment, we define dissimilarities traducing deviations
 438 with the planned protocol. These dissimilarities are defined between 0 and 1: when the dissimilarity
 439 is close to 0, it means that the patient is following the protocol. In the case where the dissimilarity
 440 equals 1, the protocol is not followed at all.

442 Administration dissimilarities

- 443 At the level of anti-cancer drug administration, differences can occur in terms of the relative time
 444 since the start of the cycle and/or in terms of dosage.

- 445
 446 Dose dissimilarity is defined as follows:

$$\delta_d(a, a') = \frac{\text{abs}(a_d - a'_d)}{\max(a_d, a'_d)} \quad (18)$$

- 447 where a_d is the drug dose.

- 448
 449 The notation `abs` stands for absolute value to avoid any confusion with the notation $|S|$, which rep-
 450 represents the cardinality of a set. According to this definition, $\delta_d(a, a')$ is a real number between 0 and
 451 1. When both doses are equal, the dissimilarity is zero. As the administered dose diverges from the
 452 theoretical dose, the dissimilarity increases, reaching 1 when the dose is either omitted or added.
 453 This aligns with our definition of dissimilarity.

- 454
 455 Administration day dissimilarity $\delta_t(a, a')$ is defined as follows:

$$\delta_t(a, a') = \begin{cases} \text{abs}(a_t - a'_t) / \tau_{\mathcal{C}^{theo}} & \text{if } a_t \leq \tau_{\mathcal{C}^{theo}} \\ \text{abs}(a_t - a'_t) / \tau_{\mathcal{C}^i} & \text{if } a_t > \tau_{\mathcal{C}^{theo}} \\ 1 & \text{if } a = \emptyset \text{ or } a' = \emptyset \end{cases} \quad (19)$$

- 456 where $\tau_{\mathcal{C}^i}$ and $\tau_{\mathcal{C}^{theo}}$ are respectively the durations of the cycles of administrations a and a' .

457

458 The administration day dissimilarity cannot be normalised in the same way as dose dissimilarity.
 459 It cannot be normalised by the maximum between the theoretical administration day and the fol-
 460 lowed administration day. Indeed, such normalisation would result in higher dissimilarity when
 461 administration delays occur at the beginning of the cycle rather than at the end. Thus, when the
 462 administration day (a_t) is less than the theoretical cycle duration ($\tau_{\mathcal{C}^{theo}}$), the dissimilarity is nor-
 463 malised by the theoretical cycle duration. When the administration day exceeds the theoretical cycle
 464 duration, it is normalised by the followed cycle duration ($\tau_{\mathcal{C}^i}$). In this way, the administration day
 465 dissimilarity is between 0 and 1.

466

467 The dissimilarity δ_{adm} between two administrations, or between an administration and the absence
 468 of administration (if a or $a' = \emptyset$), is defined as a weighted sum of the time and dose dissimilarities.

$$\delta_{\text{adm}}(a, a') = \begin{cases} \text{undefined} & \text{if } a_m \neq a'_m \\ \frac{\omega_t \delta_t(a, a') + \omega_d \delta_d(a, a')}{\omega_t + \omega_d} & \text{if } a_m = a'_m \\ 1 & \text{if } a = \emptyset \text{ or } a' = \emptyset \end{cases} \quad (20)$$

469 where ω_t and ω_d respectively parameterise the weights associated with time dissimilarity δ_t and dose
 470 dissimilarity δ_d . The weights are defined in the interval $[0, 1]$ and cannot both be zero.

471

472 Drug dissimilarity within a cycle

473 For a given anti-cancer drug m , we define drug dissimilarity as the sum of administration dissimilar-
 474 ities for that drug within a cycle. However, the parameters of drug administrations can vary within a
 475 cycle. For the same drug a_m , there might be different time (a_t) and dose (a_d) parameters. Therefore,
 476 it is necessary to match the theoretical and actual administrations.

477 For example, in a theoretical cycle, a drug m might be scheduled for three different doses on three dif-
 478 ferent days. We define an alignment algorithm to pair the closest matching administrations between
 479 the theoretical and actual cycles.

480 We define \mathcal{A}_m as the aligned set of theoretical/actual administration pairs by matching the closest
 481 administrations between the theoretical and followed cycles:

$$\mathcal{A}_m = \{(a, a')_1, \dots, (a, a')_n\}.$$

482 The cardinality of \mathcal{A}_m is the maximum number of administrations from either the theoretical or actual
 483 cycle: $|\mathcal{A}_m| = \max(|\mathcal{C}^i|, |\mathcal{C}^{theo}|)$. If the number of administrations differs between the two cycles, it
 484 means an administration is missing (most often from the actual cycle). In that case, the pair $(a, a')_i$
 485 will be represented as $(a, \emptyset)_i$ or $(\emptyset, a')_i$.

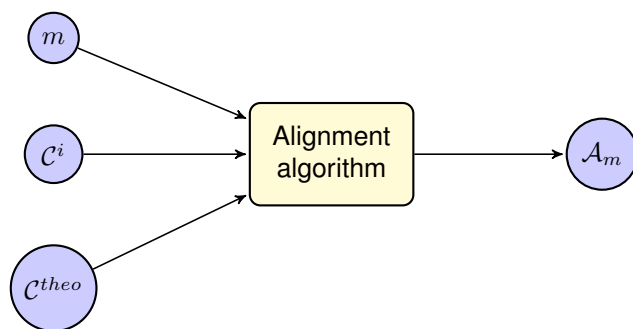


Figure 8: Schematic view of the input and output of the ProtoDrift alignment algorithm, with C^{theo} and C^i a theoretical and an actually administrated cycle, m a pair (molecule, mode of administration) and \mathcal{A}_m the set of aligned pairs of administrations for m .

486 The pseudo-code of the algorithm is presented below.

Algorithm 1 Alignment algorithm

```

1: Input:  $C^i, C^{theo}, m$                                 ▷ Two cycles and a molecule
2:  $\mathcal{A}_m \leftarrow \emptyset$                                 ▷ An empty alignment
3:  $C_m^i, C_m^{theo} \leftarrow \text{select}(C^i, C^{theo}, m)$     ▷ Reduce to a particular molecule
4: if  $|C_m^i| \leq |C_m^{theo}|$  then                        ▷ Set  $\mathcal{C}$  as the smallest cycle
5:    $\mathcal{C} \leftarrow C_m^i; \mathcal{C}' \leftarrow C_m^{theo}$         ▷ Set  $\mathcal{C}'$  as the largest cycle
6: else
7:    $\mathcal{C} \leftarrow C_m^{theo}; \mathcal{C}' \leftarrow C_m^i$ 
8: end if
9: for  $a \in \mathcal{C}$  do                                       ▷ For each administration of the shortest cycle
10:   $\mathcal{P} \leftarrow \emptyset$ 
11:   $\delta_{min} \leftarrow 1$ 
12:  for  $a' \in \mathcal{C}'$  do
13:    if  $\delta_{adm}(a, a') < \delta_{min}$  then
14:       $\mathcal{P} \leftarrow \{(a, a')\}$ 
15:       $\delta_{min} \leftarrow \delta_{adm}(a, a')$ 
16:    end if
17:  end for
18:   $\mathcal{A}_m \leftarrow \mathcal{A}_m \cup \mathcal{P}$                             ▷ Keep the pair with the min dissimilarity
19: end for
20: for  $a' \in \mathcal{C}'$  do                                       ▷ Manage unmatched  $a'$  left in  $\mathcal{C}'$ 
21:  if  $\text{notin}(a', \mathcal{A}_m)$  then
22:     $\mathcal{A}_m \leftarrow \mathcal{A}_m \cup \{(\emptyset, a')\}$ 
23:  end if
24: end for
25: Output:  $\mathcal{A}_m$ 

```

487 We define the dissimilarity between the theoretical and actual cycles for a drug m (a pair of molecule
488 and administration mode) as the average of the administration dissimilarities for that drug:

$$\delta_m(C^i, C^{theo}) = \sum_{(a, a') \in \mathcal{A}_m} \frac{\delta(a, a')}{\max(|C_m^i|, |C_m^{theo}|)}. \quad (21)$$

489 Intra and inter cycle dissimilarities

490 To calculate the intra-cycle dissimilarity, we sum the dissimilarities of the different drugs of the cycle.

491 For each drug m (molecule, mode), there can be a drug dissimilarity δ_m within the cycle.

492

493 The intra-cycle dissimilarity δ_{intra} is defined as:

$$\delta_{\text{intra}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) = \frac{\sum_{m \in \mathcal{M}} \omega_m \delta_m(\mathcal{C}^i, \mathcal{C}^{\text{theo}})}{\sum_{m \in \mathcal{M}} \omega_m} \quad (22)$$

494 In this article, the weights assigned to each drug are equal, meaning each drug is given the same

495 importance. In this case, the intra-cycle dissimilarity is written as:

$$\delta_{\text{intra}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) = \sum_{m \in \mathcal{M}} \frac{1}{|\mathcal{M}|} \delta_m(\mathcal{C}^i, \mathcal{C}^{\text{theo}}). \quad (23)$$

496 We now introduce inter-cycle dissimilarity, which measures the time gap between two cycles, also

497 called the "inter-cure." Previously, we considered the timing of drug administrations in relation to

498 the start of each cycle. Now, we will account for differences caused by the time gap between cycles.

499 To explain this dissimilarity more concretely, let's consider an example. After completing four chemother-

500 apy cycles in December, it is decided to delay the start of the fifth cycle until after the Christmas

501 holidays, allowing the patient to spend time with family. As a result, the fifth cycle begins later than

502 its planned start date.

503 A simple way to define inter-cycle dissimilarity is to measure the difference between the actual start

504 date of cycle i and its theoretical start date. However, this method has a drawback: if cycle 5 is

505 delayed, it will cause delays in all the following cycles as well.

506 To avoid this issue, we define the dissimilarity for cycle i so that it does not depend on delays in

507 earlier cycles. Instead, the delay for cycle i is based only on the longer inter-cure period between

508 cycle $i - 1$ and cycle i .

509

510 The inter-cycle dissimilarity is defined as:

$$\delta_{\text{inter}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) = \begin{cases} 0 & \text{if } i = 1 \\ \frac{\text{abs}(\tau_{\mathcal{C}^{i-1}} - \tau_{\mathcal{C}^{\text{theo}}})}{\max(\tau_{\mathcal{C}^{i-1}}, \tau_{\mathcal{C}^{\text{theo}}})} & \text{if } i > 1 \end{cases} \quad (24)$$

511 where $\tau_{\mathcal{C}^{i-1}}$ and $\tau_{\mathcal{C}^{\text{theo}}}$ are the durations of cycle $i - 1$ and the theoretical cycle, respectively.

512 The inter-cycle dissimilarity reflects the delay of cycle i due to the longer inter-cure duration of cycle

513 $i - 1$ compared to the theoretical inter-cure. In this way, the delay in cycle i does not affect the

514 subsequent cycles ($j > i$).

515 From cycle to line dissimilarities

516 The dissimilarity between two cycles is a normalised weighted sum of the two intra and inter cycle

517 dimensions:

$$\delta_{\text{cycle}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) = \frac{\omega_{\text{intra}} \delta_{\text{intra}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) + \omega_{\text{inter}} \delta_{\text{inter}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}})}{\omega_{\text{intra}} + \omega_{\text{inter}}} \quad (25)$$

518 Finally, the line dissimilarity, δ_{line} , is defined as the cumulative dissimilarity at the last cycle of a line
 519 of treatment, as follow:

$$\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}}) = \frac{1}{l} \sum_{i=1}^l \delta_{\text{cycle}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) \quad (26)$$

520 where l is the total number of cycles in line \mathcal{L} (or the last cycle number of the line).

521 A.1.3 Dissimilarity tree

522 ProtoDrift's methodology can be visualised as a hierarchical tree, showcasing the relationship be-
 523 tween various levels of dissimilarities. This tree structure captures the essence of physicians' deci-
 524 sions at different treatment stages and time frames, providing a comprehensive view of the treatment
 525 deviations

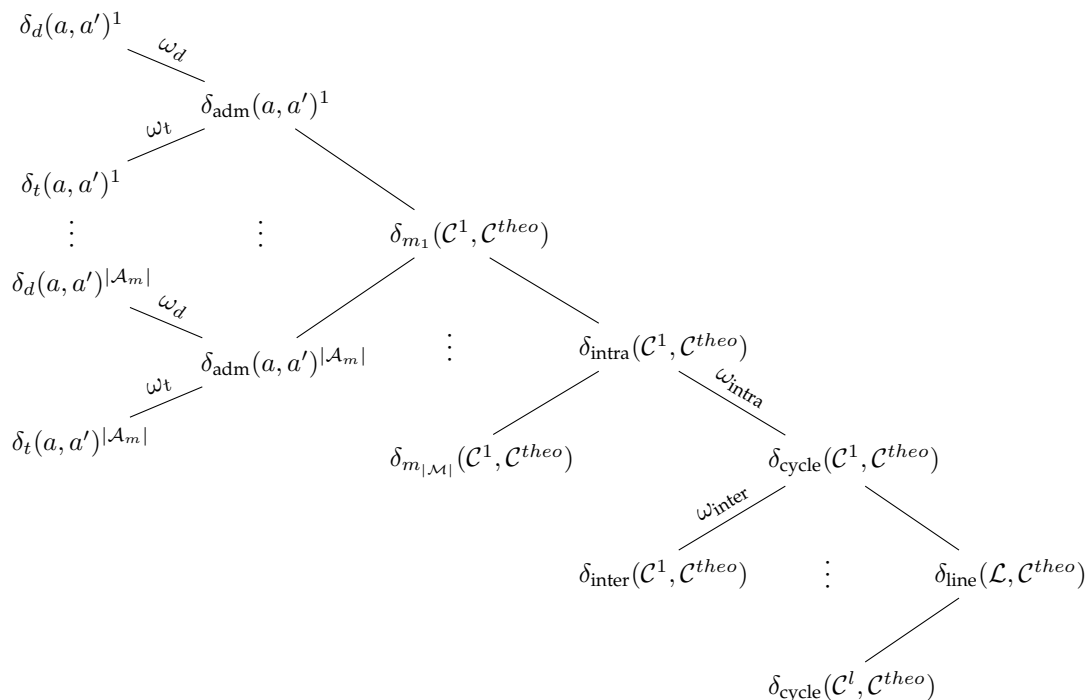


Figure 9: The weighted dissimilarities of ProtoDrift, at different levels, from dose and timing dissimilarities of single administrations, at the extreme left, passing by molecule level dissimilarities, intra- and inter-cycle dissimilarities, to finally aggregate at the cycle and line levels, at the extreme right. Dissimilarities measures the gap between a theoretical protocol defined by a theoretical cycle $\mathcal{C}^{\text{theo}}$ and an actual line of treatment \mathcal{L} composed of l cycles followed by a patient. (a, a') are pairs of administrations, one actual and one planned, compared to compute dose and time shifts. These pairs are computed by the alignment algorithm described figure 8. $|\mathcal{A}_m|$ is the maximum number of administrations of either the actual or theoretical cycle for the molecule m . $|\mathcal{M}|$ is to the number of distinct anti-cancer molecules in the cycles.

526 A.2 ProtoDrift weights optimisation

527 Dissimilarity reformulations

528 We provide here the proof of the reformulations of δ_{adm} and δ_{cycle} as stated in 9 and 10.

529

530 Given the definition of α , we can express ω_d as a function of ω_t and α :

$$\omega_d = \frac{\omega_t(1 - \alpha)}{\alpha}$$

531 which allows us to write δ_{adm} as

$$\begin{aligned} \delta_{\text{adm}}(a, a') &= \left(\omega_t \cdot \delta_t(a, a') + \frac{\omega_t(1 - \alpha)\delta_d(a, a')}{\alpha} \right) \frac{1}{\omega_t + \omega_d} \\ &= \alpha\delta_t(a, a') + \frac{\omega_t}{\alpha(\omega_t + \omega_d)}(1 - \alpha)\delta_d(a, a') \\ &= \alpha\delta_t(a, a') + (1 - \alpha)\delta_d(a, a') \end{aligned}$$

532 which depends only on α . The same reasoning can be applied to express δ_{cycle} using β .

533 $\delta_{\text{line}}(\alpha, \beta = 1)$ is constant

534 For all values of α , $\delta_{\text{line}}(\alpha, \beta = 1)$ is a constant. Since the models only vary with the explanatory
535 variable $\delta_{\text{line}}(\alpha, \beta)$, and $\delta_{\text{line}}(\alpha, \beta = 1)$ is constant, the prediction scores based on this value are also
536 constant.

$$\begin{aligned} \beta = 1 &\Leftrightarrow \frac{\omega_{\text{inter}}}{\omega_{\text{inter}} + \omega_{\text{intra}}} = 1 \\ &\Leftrightarrow \omega_{\text{intra}} = 0 \\ &\Leftrightarrow \delta_{\text{cycle}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) = \delta_{\text{inter}} \\ &\Leftrightarrow \delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}}) = \frac{1}{l} \sum_{i=1}^l \delta_{\text{inter}}(\mathcal{C}^i, \mathcal{C}^{\text{theo}}) \\ &\Leftrightarrow \forall \alpha, \delta_{\text{line}}(\alpha, \beta = 1) \text{ is constant.} \end{aligned}$$

537

538 Details on the predictive models

539 The effectiveness of ProtoDrift and its optimised versions against the standard RDI is evaluated using
540 the regression models defined in 11 and 12, and replacing the explanatory variable by ADRDI.

541 Note that ADRDI quantity is taken at the end of a treatment line, to be comparable with δ_{line} dissim-
542 ilarity.

543 The three model modalities are summarised in tables A.2 and A.2.

Explanatory variable	Model formulation
ADRDI	$\text{logit}(P(Y = 1)) = \theta_0 + \theta_1 \text{ADRDI} + \theta_2 \text{age} + \theta_3 \text{sex}$
$\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha=\frac{1}{2}, \beta=\frac{1}{2}}$	$\text{logit}(P(Y = 1)) = \theta_0 + \theta_1 \delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha=\frac{1}{2}, \beta=\frac{1}{2}} + \theta_2 \text{age} + \theta_3 \text{sex}$
$\text{argmax}_{\alpha, \beta} \text{AUC}(\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha, \beta})$	$\text{logit}(P(Y = 1)) = \theta_0 + \theta_1 \text{argmax}_{\alpha, \beta} \text{AUC}(\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha, \beta}) + \theta_2 \text{age} + \theta_3 \text{sex}$

Table 3: Logistic regression model formulations

Explanatory variable	Model formulation
ADRDI	$h(t) = h_0(t) \times \exp(\theta_1 \text{ADRDI} + \theta_2 \text{age} + \theta_3 \text{sex})$
$\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha=\frac{1}{2}, \beta=\frac{1}{2}}$	$h(t) = h_0(t) \times \exp(\theta_1 \delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha=\frac{1}{2}, \beta=\frac{1}{2}} + \theta_2 \text{age} + \theta_3 \text{sex})$
$\text{argmax}_{\alpha, \beta} \text{C-index}(\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha, \beta})$	$h(t) = h_0(t) \times \exp(\theta_1 \text{argmax}_{\alpha, \beta} \text{C-index}(\delta_{\text{line}}(\mathcal{L}, \mathcal{C}^{\text{theo}})_{\alpha, \beta}) + \theta_2 \text{age} + \theta_3 \text{sex})$

Table 4: Cox regression model formulations

544 B Results

545 B.1 Study profile

546 From the patients available in the chemotherapy prescription and administration software (14,662 at
547 HEGP, 33,725 at UHB) we first excluded those for whom it was impossible to compute ProtoDrift or
548 perform a survival analysis due to data quality issues or inconsistencies (2,944 at HEGP, 11,428 at
549 UHB).

550 Specifically, we removed patients with missing values that prevented us from calculating a nor-
551 malised administration dose (155 at HEGP, 3 at UHB). Thus, patients on carboplatin regimens were
552 excluded if their creatinine values were missing, as the carboplatin dose is calculated using this data
553 (54 at HEGP, 0 at UHB). We also excluded patients on regimens involving drugs administered in
554 mg/kg if weight data was missing (101 at HEGP, 3 at UHB).

555 Additionally, patients with inconsistencies in their administration dates (*i.e.* doses recorded outside
556 the reported treatment period or after the date of death) were removed (57 at HEGP, 0 at UHB).

557 We found a number of administrated protocols for which we were unable to find the correspond-
558 ing theoretical protocol. Patients associated only with these unrecognised protocols were excluded
559 (1,866 at HEGP, 2,949 at UHB).

560 We also removed patients whose recorded doses were all null (73 at HEGP, 326 at UHB).

561 We removed patients who followed a regimen with oral administrations, based on the recommenda-
562 tion from pharmacists who noted that oral administrations were not reliably entered in the software
563 (368 at HEGP, 630 at UHB).

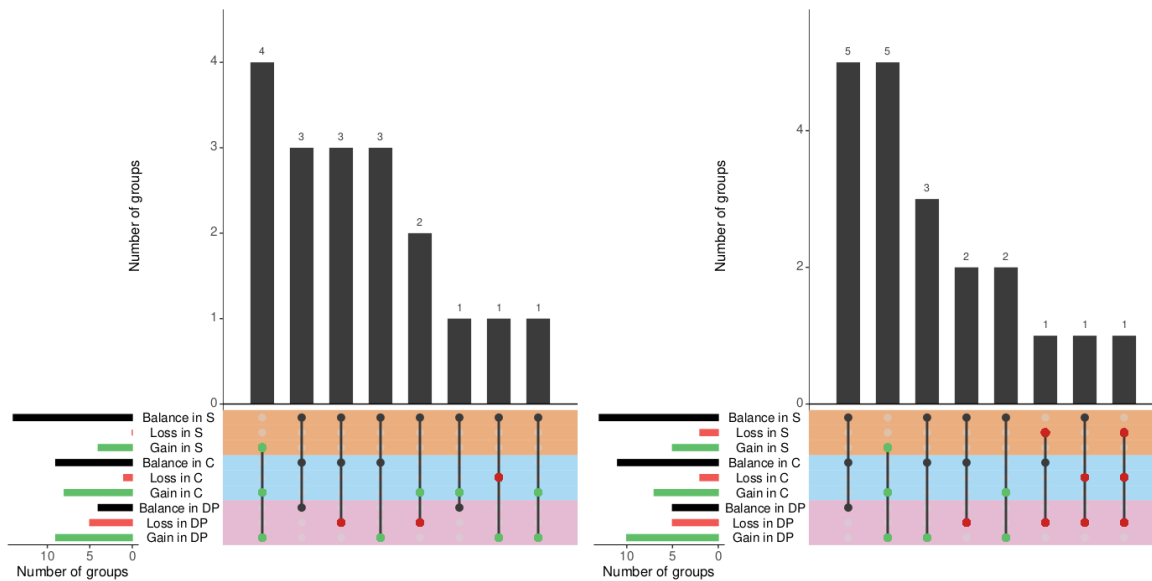
564 Patients with cycles administered to two distinct locations were also removed (117 at HEGP, 594 at
565 UHB).

566 Finally, patients with missing gender or birth date, were excluded as these data are needed to per-
567 form survival analysis (132 at HEGP, 0 at UHB).

568

569 Secondly, we excluded patients treated for tumours with fewer than 400 cases (1,956 at HEGP, 4,744
 570 at UHB). At HEGP, patients treated for vulva tumour (517 cases) were removed due to uncertainties
 571 regarding the specific conditions referenced in these entries. Additionally, we excluded patients
 572 not treated for cancer-related pathologies; this included 1,662 patients at UHB treated for various
 573 pathologies and infectious diseases, and patients treated for autoimmune and inflammatory diseases
 574 (458 at HEGP and 3,870 at UHB).

575 B.2 Naive ProtoDrift results



(a) Gain, balance or loss per HEGP patient group.

(b) Gain, balance or loss per UHB patient group.

Legend		
Comparison in performance indicator	Units/Range	Bar color
Significance of the explanatory variable (S)	1 if Cox fit significant for NP and not ADRDI, -1 if Cox fit significant for ADRDI and not for NP, 0 otherwise	Orange
Prediction score (C-index) (C)	Relative difference of NP vs. ADRDI values in percentage (0 if between -0.9 and 0.9 %)	Blue
Discriminative power analysis between quartiles (DP)	Relative difference of NP vs. ADRDI significant LogRank test number. Ranges from -6 to 6.	Pink

● Gain

● Balance

● Loss

(c) Description of our three performance indicators.

Figure 10: Overall advantage of using Naive ProtoDrift (NP) *vs.* ADRDI, across the 18 patient groups of HEGP (a) and the 20 of UHB (b). Vertical bars quantify the number of groups that either gain, loss or have balanced results in using NP instead of ADRDI with regards to three performance indicators, described in the colour-coded matrix (c). Green indicate gains, black indicates balanced indicators, and red losses. We present here performances obtained on 5-year overall survival.

576 For each group, the three Cox indicators, namely Cox regression significance, C-index and LogRank
 577 test significance were computed for both NP and ADRDI. Results are summarised in Appendix fig-
 578 ures 10 that counts groups where we observe either a gain, loss or balanced result in predicting 5-year
 579 overall survival using NP instead of ADRDI.

580 We observe that, in general, NP outperforms ADRDI. Specifically, 12 out of 18 groups of the HEGP
 581 (67%) and 15 out of 20 groups of the UHB (75%) either have comparative or better results with NP.
 582 9 out of 18 groups at HEGP (50%) and 10 out of 20 groups at UHB (50%) have better results for at

583 least one indicator, and better or similar results for the two others. Appendix figure 11a provides the
584 details of those gains per group and per hospital. Over the two hospitals, we observe that it is bene-
585 ficial to use NP over ADRDI, with at least one better indicator and no loss for Respiratory/Thoracic,
586 Colon, Lymphoid/Haematologic, Pancreas/Biliary Tract, Ovary and Melanoma groups at first line;
587 and for Colon, Bladder/Urothelial, ENT, Ovary, Stomach, Neurology and Melanoma groups at sec-
588 ond line.

589 Notably, four groups at HEGP (22%) and five at UHB (25%) show gains across all the three dimen-
590 sions (HEGP: Respiratory/Thoracic, Colon and Ovary at first line, ENT at second line; UHB: Colon,
591 ENT, Melanoma first line, Colon and Melanoma second line).

592 Inversely, ADRDI is better than NP (at least one loss and no gain) in seven groups (18%), which
593 are HEGP ENT and UHB Liver, Bladder/Urothelial, Neurology and Myeloma at first line; HEGP
594 Pancreas/Biliary Tract and UHB Myeloma at second line.

595 These results suggests that ProtoDrift, even without optimisation, offers a more nuanced capture of
596 treatment adherence compared to ADRDI.

597 Complete results of the comparative analysis between NP and ADRDI, including performance met-
598 rics from Cox and logistic regression models predicting 5-year overall survival across both hospitals,
599 are detailed in Appendix B.3.

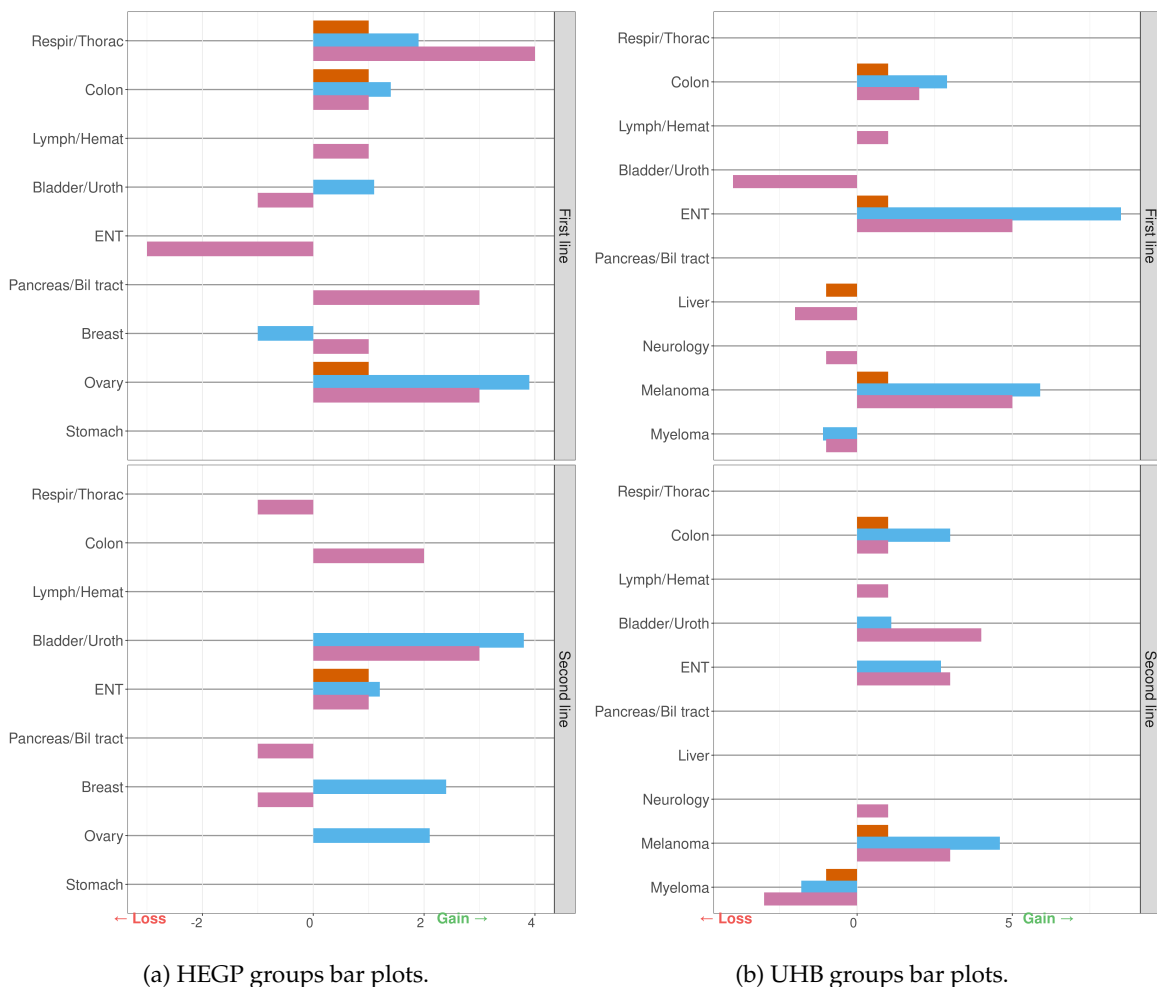


Figure 11: Detailed advantages of using NP in comparison with ADRDI, per cancer location and first or second line of treatment across the 38 groups of HEGP (a) and UHB (b). Each color bar refers to one of the three indicators presented Figure 10 (c) for a group. Bars to the right indicate gains and to the left indicate losses for the three indicators. Note that each indicator has a different unit. No bar indicates a balanced indicator for the group.

600 B.3 Comparative analysis detail results

601 This annex contains detailed results from our comparative analysis of ProtoDrift against RDI, con-
 602 ducted across two hospitals and focusing on 5-year survival predictions. The results are organised
 603 into three sections, corresponding to Cox and logistic regressions across both hospitals.

604 Each section starts with a table summarising the three performance indicators: significance of regres-
 605 sion outcomes, prediction accuracy scores, and the number of significant survival time differences
 606 between quartile pairs. The tables use color coding: orange for regression significance, blue for pre-
 607 diction scores, and pink for discriminative power, with significant results (p-values less than 0.05)
 608 highlighted in bold.

609 The second table in each section provides details on the discriminative power analysis, listing the
 610 number of significant LogRank test pairs and the survival time differences. These differences are
 611 calculated using the median survival times or, for long survival time, the area under the Kaplan-
 612 Meier curves calculated through the Restricted Mean Survival Time (RMST).

613 Results for 3-year survival predictions are available upon request. These tables ensure transparency

614 in presenting our findings.

615 **B.3.1 Cox regression - 5 years overall survival**

616 **HEGP**

method	Line	Cox regression fit results		Cox regression prediction results		Survival time differences	
		θ_1	p-value	C-index	Number of significant LogRank tests between quartile pairs		
Colon							
OP	1	1.297	0.029	0.521			3
NP	1	1.682	0.044	0.518			1
ADRDI	1	-0.263	0.304	0.504			0
OP	2	0.44	0.305	0.493			0
NP	2	0.102	0.447	0.489			2
ADRDI	2	0.199	0.408	0.491			0
Stomach							
OP	1	1.157	0.159	0.533			0
NP	1	0.697	0.387	0.521			0
ADRDI	1	0.144	0.44	0.518			0
OP	2	1.243	0.268	0.511			0
NP	2	1.558	0.31	0.506			0
ADRDI	2	-0.126	0.425	0.5			0
Lymph/Hemat							
OP	1	1.351	0.101	0.588			3
NP	1	1.647	0.15	0.586			2
ADRDI	1	-0.515	0.256	0.581			1
OP	2	-1.358	0.234	0.522			1
NP	2	-1.323	0.297	0.521			0
ADRDI	2	0.477	0.36	0.52			0
ENT							
OP	1	0.384	0.412	0.519			0
NP	1	0.203	0.422	0.518			0
ADRDI	1	-0.526	0.129	0.527			3
OP	2	1.099	0.007	0.538			3
NP	2	1.746	0.02	0.53			3
ADRDI	2	-0.659	0.106	0.518			2
Ovary							
OP	1	1.716	0.019	0.535			4
NP	1	2.759	0.038	0.524			3
ADRDI	1	-0.441	0.357	0.485			0
OP	2	1.634	0.057	0.544			4
NP	2	2.192	0.121	0.525			2
ADRDI	2	-0.73	0.276	0.504			2
Pancreas/Bil tract							
OP	1	0.931	0.051	0.561			0
NP	1	0.84	0.212	0.548			3
ADRDI	1	-0.166	0.408	0.541			0
OP	2	-1.7	0.077	0.554			3
NP	2	0.748	0.32	0.529			0
ADRDI	2	-0.31	0.346	0.527			1
Respir/Thorac							
OP	1	1.101	0	0.551			6
NP	1	1.442	0.006	0.538			4
ADRDI	1	-0.283	0.234	0.519			0
OP	2	0.713	0.072	0.527			2
NP	2	0.947	0.149	0.523			1
ADRDI	2	-0.255	0.348	0.515			2
Breast							
OP	1	5.032	0	0.655			6
NP	1	4.581	0	0.653			6
ADRDI	1	-2.567	0	0.663			5
OP	2	3.942	0	0.595			5
NP	2	3.92	0	0.594			4
ADRDI	2	-1.806	0.003	0.57			5
Bladder/Uroth							
OP	1	1.222	0.01	0.552			4
NP	1	1.167	0.173	0.53			2
ADRDI	1	-0.17	0.407	0.519			3
OP	2	1.982	0.047	0.553			4
NP	2	2.881	0.078	0.536			5
ADRDI	2	-0.375	0.371	0.498			2

Results of three performance indicators for HEGP patient groups

Survival time difference and LogRank test significance details by quartile pair

Metric	Line	1 st vs 2 nd		1 st vs 3 rd		1 st vs 4 th		2 nd vs 3 rd		2 nd vs 4 th		3 rd vs 4 th	
		p-value	Method	p-value	Method	p-value	Method	p-value	Method	p-value	Method	p-value	Method
Colon													
NP	1	0.1181	Median	0.5834	Median	0.1181	Median	0.0695	Median	0.004	Median	0.2651	Median
OP	1	0.6368	Median	0.6269	Median	0.0083	Median	0.8492	Median	0.0032	Median	0.0028	Median
ADRFI	1	0.1721	Median	0.1901	Median	0.8767	Median	0.8422	Median	0.1721	Median	0.1802	Median
NP	2	0.2733	Median	0.0029	Median	0.9537	Median	0.0954	Median	0.2733	Median	0.0029	Median
OP	2	0.6949	Median	0.1152	Median	0.561	Median	0.2435	Median	0.6949	Median	0.3284	Median
ADRFI	2	0.3958	Median	0.4622	Median	0.1465	Median	0.1465	Median	0.4622	Median	0.0569	Median
Stomach													
NP	1	0.6309	Median	0.7229	Median	0.6309	Median	0.7229	Median	0.8941	Median	0.7229	Median
OP	1	0.9848	Median	0.9848	Median	0.5318	Median	0.9848	Median	0.5318	Median	0.57	Median
ADRFI	1	0.1965	Median	0.1478	Median	0.9626	Median	0.8522	Median	0.1965	Median	0.1478	Median
NP	2	0.4729	Median	0.1478	Median	0.9114	Median	0.9114	Median	0.4729	Median	0.4729	Median
OP	2	0.3323	Median	0.4248	Median	0.9586	Median	0.8345	Median	0.3323	Median	0.4248	Median
ADRFI	2	0.9731	Median	0.5604	Median	0.3516	Median	0.5604	Median	0.3516	Median	0.1823	Median
Lymph/Hemat													
NP	1	0.1839	AUC	9e-04	Median	0.0123	Median	0.0676	Median	0.2426	Median	0.4046	Median
OP	1	0.0283	AUC	5e-04	Median	3e-04	Median	0.2209	Median	0.1839	Median	0.8067	Median
ADRFI	1	0.0944	Median	0.8218	Median	0.3655	Median	0.0718	Median	0.0102	Median	0.4636	Median
NP	2	0.9072	Median	0.4845	Median	0.6355	AUC	0.4845	Median	0.6355	AUC	0.2993	Median
OP	2	0.0754	Median	0.2886	Median	0.6344	AUC	0.4046	Median	0.0376	Median	0.1572	Median
ADRFI	2	0.7909	Median	0.7909	Median	0.7909	Median	0.7909	Median	0.8069	AUC	0.7909	Median
ENT													
NP	1	0.7667	Median	0.7035	Median	0.7035	Median	0.7035	Median	0.7667	Median	0.7667	Median
OP	1	0.7002	Median	0.7002	Median	0.7636	Median	0.7002	Median	0.7002	Median	0.7002	Median
ADRFI	1	0.5433	Median	0.0856	Median	0.0013	Median	0.02	Median	1e-04	Median	0.0856	Median
NP	2	0.4042	Median	0.9545	Median	2e-04	Median	0.4042	Median	0	Median	4e-04	Median
OP	2	0.1043	Median	0.8464	Median	0	Median	0.1603	Median	0.0015	Median	0	Median
ADRFI	2	0.4989	Median	0.2855	Median	0.0295	Median	0.0977	Median	0.005	Median	0.2855	Median

Detailed discriminative power results for HEGP patient groups (1/3)

Survival time difference and LogRank test significance details by quartile pair																													
Metric	Line	1 st vs 2 nd			1 st vs 3 rd			1 st vs 4 th			2 nd vs 3 rd			2 nd vs 4 th			3 rd vs 4 th												
		p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method							
Ovary																													
NP	1	0.3983	-435	Median	0.019	-878	Median	0.0035	-935	Median	0.1162	-443	Median	0.0239	-500	Median	0.4854	-57	Median	0.9503	-16	AUC	0.9503	34	Median				
OP	1	0.9503	-16	AUC	0.002	-969	Median	0.002	-935	Median	0.002	-969	Median	0.002	-935	Median	0.9503	34	Median	0.3905	286	Median	0.3905	-416	Median	0.7133	26	Median	
ADRD	1	0.6046	286	Median	0.4446	482	Median	0.6909	66	Median	0.6046	196	Median	0.5058	-220	Median	0.3905	-416	Median	0.1117	-665	Median	0.1117	-484	Median	0.8839	-56	Median	
NP	2	0.1117	-665	Median	7e-04	-1176	Median	0.0022	-1150	Median	0.0581	-510	Median	0.1117	-484	Median	0.7133	26	Median	0.0309	-796	Median	0.0309	-796	Median	0.8839	-56	Median	
OP	2	0.0309	-796	Median	0	-1160	Median	1e-04	-1215	Median	0.0325	-364	Median	0.0534	-419	Median	0.8839	-56	Median	0.5967	416	Median	0.5967	-285	Median	0.0475	-490	Median	
ADRD	2	0.5967	416	Median	0.9214	130	Median	0.0585	-360	Median	0.5967	-285	Median	0.0149	-776	Median	0.0475	-490	Median										
Pancreas/Bil tract																													
NP	1	0.0012	-202	Median	0.019	-194	Median	0.014	-151	Median	0.3891	9	Median	0.3891	52	Median	0.9128	42	Median	0.0577	-193	Median	0.0577	-209	Median	0.6546	-14	Median	
OP	1	0.0577	-193	Median	0.1645	-196	Median	0.0577	-209	Median	0.6658	-2	Median	0.8511	-16	Median	0.6546	-14	Median	0.8533	98	Median	0.8533	86	Median	0.8533	73	Median	
ADRD	1	0.8533	98	Median	0.8533	14	Median	0.8533	86	Median	0.8533	-84	Median	0.8533	-12	Median	0.8533	73	Median	0.6828	-34	Median	0.6828	-19	Median	0.6828	34	Median	
NP	2	0.6828	-34	Median	0.6828	-53	Median	0.6828	-20	Median	0.6828	-19	Median	0.6828	14	Median	0.6828	34	Median	0.0232	114	Median	0.0232	114	Median	0.6549	66	Median	
OP	2	0.0232	114	Median	0.0101	206	Median	0.0028	272	Median	0.9024	92	Median	0.6549	158	Median	0.6549	66	Median	0.5576	5	Median	0.5576	5	Median	0.0072	-131	Median	
ADRD	2	0.5576	5	Median	0.4281	152	Median	0.0963	21	Median	0.1689	147	Median	0.287	16	Median	0.0072	-131	Median										
Respir/Thorac																													
NP	1	0.8934	-69	Median	0.0491	-162	Median	0	-227	Median	0.06	-93	Median	0	-158	Median	0.0334	-65	Median	0.0011	121	Median	0.0421	-147	Median	0.034	-62	Median	
OP	1	0.0011	121	Median	0.8881	-21	Median	0.8881	-21	Median	0.8881	25	Median	0.209	-53	Median	0.209	-78	Median	0.8881	-21	Median	0.8881	-21	Median	0.209	-78	Median	
ADRD	1	0.8881	-21	Median	0.862	-56	Median	0.2497	-104	Median	0.2497	-52	Median	0.209	-53	Median	0.209	-78	Median	0.2497	-4	Median	0.2497	-52	Median	0.2497	-47	Median	
NP	2	0.2497	-4	Median	0.5706	-10	Median	0.0615	-122	Median	0.2113	-124	Median	0.0219	-100	Median	0.2497	-47	Median	0.0615	114	Median	0.0615	-122	Median	0.027	-112	Median	
OP	2	0.0615	114	Median	0.1038	70	Median	0.7253	27	Median	0.3886	-110	Median	2e-04	-236	Median	0.2497	-47	Median	0.1038	70	Median	0.1038	27	Median	0.027	-112	Median	
ADRD	2	0.0191	180	Median	0.0222	-177	Median	0.0017	-1124	Median	0.3886	-110	Median	0.0191	-153	Median	0.144	-42	Median	0.0222	-177	Median	0.0222	-177	Median	0.144	-42	Median	
Breast																													
NP	1	1e-04	120	AUC	0.0222	-177	AUC	0	-1054	Median	0	-296	AUC	0	-1054	Median	0	-1054	Median	1e-04	120	AUC	0.0222	-177	AUC	0	-1054	Median	
OP	1	0.032	58	AUC	0.0043	-181	AUC	0	-1047	Median	0	-239	AUC	0	-1047	Median	0	-1047	Median	0.032	58	AUC	0.0043	-181	AUC	0	-1047	Median	
ADRD	1	0.0086	166	AUC	0.3596	0	AUC	0	-1102	Median	3e-04	-166	AUC	0	-1102	Median	0	-1102	Median	0.0086	166	AUC	0.3596	0	AUC	0	-1102	Median	
NP	2	0.2222	73	AUC	0.0663	-364	Median	0	-1394	Median	0.0023	-364	Median	0	-1394	Median	0	-1394	Median	0.2222	73	AUC	0.0663	-364	Median	0	-1394	Median	
OP	2	0.0705	134	AUC	0.0322	-689	Median	0	-1378	Median	1e-04	-689	Median	0	-1378	Median	5e-04	-689	Median	0.0705	134	AUC	0.0322	-689	Median	5e-04	-689	Median	
ADRD	2	0.0035	177	Median	0.6057	46	Median	0.0017	-1124	Median	0.0125	-131	Median	0	-1301	Median	4e-04	-1170	Median	0.0035	177	Median	0.6057	46	Median	4e-04	-1170	Median	

Detailed discriminative power results for HEGP patient groups (2/3)

Survival time difference and LogRank test significance details by quartile pair																			
Metric	Line	1 st vs 2 nd			1 st vs 3 rd			1 st vs 4 th			2 nd vs 3 rd			2 nd vs 4 th			3 rd vs 4 th		
		p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method
Bladder/Uroth																			
NP	1	0.1119	-300	Median	0.8734	162	Median	0.0101	-523	Median	0.1325	462	Median	0.2259	-223	Median	0.0101	-685	Median
OP	1	0.0571	843	Median	0.0452	-353	Median	4e-04	-570	Median	2e-04	-1196	Median	0	-1413	Median	0.1414	-217	Median
ADPDI	1	0.707	-64	Median	0.0061	-492	Median	0.707	138	Median	0.0077	-428	Median	0.9286	202	Median	0.0077	630	Median
NP	2	0.0363	-370	Median	0.0363	-344	Median	1e-04	-576	Median	0.9938	26	Median	0.0363	-206	Median	0.0363	-232	Median
OP	2	0.9468	-34	Median	0.0026	-418	Median	0.001	-492	Median	0.0022	-383	Median	9e-04	-457	Median	0.4839	-74	Median
ADPDI	2	0.8227	-124	Median	0.0432	-142	Median	0.4786	-218	Median	0.0474	-19	Median	0.4786	-94	Median	0.2391	-75	Median

Detailed discriminative power results for HEGP patient groups (3/3)

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method	Line	Cox regression fit results		Cox regression prediction results	Survival time differences
		θ_1	p-value	C-index	Number of significant LogRank tests between quartile pairs
Colon					
NP	1	-2.698	0.015	0.569	2
ADRDI	1	0.538	0.222	0.54	0
NP	2	-3.575	0.005	0.626	4
ADRDI	2	1.169	0.064	0.596	3
Melanoma					
NP	1	3.257	0	0.565	5
ADRDI	1	-0.254	0.391	0.506	0
NP	2	4.067	0.001	0.559	3
ADRDI	2	-0.455	0.355	0.513	0
Liver					
NP	1	-1.754	0.053	0.534	1
ADRDI	1	0.715	0.043	0.533	3
NP	2	-1.721	0.226	0.526	0
ADRDI	2	0.862	0.187	0.531	0
Myeloma					
NP	1	-3.468	0.002	0.595	3
ADRDI	1	1.902	0.001	0.606	4
NP	2	-2.233	0.149	0.524	0
ADRDI	2	1.553	0.039	0.542	3
Lymph/Hemat					
NP	1	0.998	0.003	0.621	5
ADRDI	1	-0.334	0.033	0.617	4
NP	2	0.797	0.116	0.578	4
ADRDI	2	-0.222	0.277	0.574	3
Neurology					
NP	1	-1.935	0.231	0.53	0
ADRDI	1	0.864	0.139	0.536	1
NP	2	-3.066	0.151	0.49	1
ADRDI	2	1.6	0.153	0.491	0
ENT					
NP	1	-7.376	0	0.582	5
ADRDI	1	-0.382	0.361	0.497	0
NP	2	-3.292	0.124	0.575	3
ADRDI	2	0.31	0.42	0.548	0
Pancreas/Bil tract					
NP	1	0.79	0.276	0.519	0
ADRDI	1	-0.154	0.416	0.515	0
NP	2	-1.733	0.237	0.499	0
ADRDI	2	0.6	0.287	0.494	0
Respir/Thorac					
OP	1	0.789	0.072	0.542	5
NP	1	1.152	0.155	0.534	4
ADRDI	1	-0.191	0.375	0.527	4
OP	2	-0.023	0.44	0.501	0
NP	2	-0.023	0.44	0.501	0
ADRDI	2	0.164	0.423	0.504	0
Bladder/Uroth					
NP	1	-0.383	0.431	0.501	0
ADRDI	1	-0.311	0.365	0.509	4
NP	2	-3.508	0.207	0.471	4
ADRDI	2	1.016	0.373	0.46	0

Table 10: Results of three performance indicators for UHB patient groups

Survival time difference and LogRank test significance details by quartile pair																			
Metric	Line	1 st vs 2 nd			1 st vs 3 rd			2 nd vs 3 rd			2 nd vs 4 th			3 rd vs 4 th					
		p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method			
Colon																			
NP	1	0.0835	102	Median	6e-04	789	Median	6e-04	782	Median	0.1104	687	Median	0.0835	680	Median	0.5907	-7	Median
ADPDI	1	0.6329	143	Median	0.5416	498	Median	0.5416	247	Median	0.5416	355	Median	0.6329	104	Median	0.6329	-251	Median
NP	2	0.0046	138	Median	1e-04	300	Median	0	898	Median	0.2621	162	Median	0.0398	760	Median	0.4107	598	Median
ADPDI	2	0.646	104	Median	0.0351	259	Median	0.0122	669	Median	0.0525	155	Median	0.0122	565	Median	0.646	410	Median
Melanoma																			
NP	1	0.0163	101	AUC	0	-1450	Median	0	-1450	Median	0	-1450	Median	0	-1450	Median	0.1917	1	Median
ADPDI	1	0.9	-606	Median	0.3589	166	Median	0.3589	80	Median	0.3589	772	Median	0.3589	686	Median	0.9238	-86	Median
NP	2	0.8242	59	AUC	0.8242	39	AUC	0	-1439	Median	0.9769	-21	AUC	0	-1439	Median	0	-1439	Median
ADPDI	2	0.5836	-305	Median	0.2628	141	AUC	0.5836	62	AUC	0.1516	305	Median	0.3866	305	Median	0.3866	-78	AUC
Liver																			
NP	1	0.1665	608	Median	0.1666	601	Median	0.0073	901	Median	0.87	-8	Median	0.1665	292	Median	0.1665	300	Median
ADPDI	1	0.6244	-40	Median	0.2024	-366	Median	0.0453	546	Median	0.403	-325	Median	0.0244	587	Median	0.0012	912	Median
NP	2	0.6015	200	Median	0.6015	851	Median	0.5722	1086	Median	0.9927	651	Median	0.5722	886	Median	0.5722	236	Median
ADPDI	2	0.9895	-80	Median	0.0941	1020	Median	0.6604	708	Median	0.0941	1100	Median	0.6604	788	Median	0.3641	-312	Median
Myeloma																			
NP	1	0.4701	-2	AUC	0.4701	-17	AUC	0	258	AUC	0.9232	-15	AUC	2e-04	260	AUC	2e-04	274	AUC
ADPDI	1	0.0085	248	AUC	0.0896	110	AUC	0	356	AUC	0.3834	-138	AUC	0.0084	108	AUC	0.0012	246	AUC
NP	2	0.2373	146	AUC	0.1207	194	AUC	0.1207	180	AUC	0.7649	49	AUC	0.7649	34	AUC	0.95	-14	AUC
ADPDI	2	0.0979	173	AUC	0.1598	151	AUC	1e-04	356	AUC	0.7095	-22	AUC	0.0232	183	AUC	0.011	205	AUC
Lymph/Hemat																			
NP	1	1e-04	-103	AUC	0	-223	AUC	0	-252	AUC	1e-04	-121	AUC	0	-150	AUC	0.2042	-29	AUC
ADPDI	1	0.366	-15	AUC	0	-204	AUC	0	-170	AUC	0	-189	AUC	0	-155	AUC	0.2685	34	AUC
NP	2	0.0843	55	AUC	0.3199	-27	AUC	6e-04	-144	AUC	0.0092	-82	AUC	0	-199	AUC	0.0092	-117	AUC
ADPDI	2	0.7466	-1	AUC	0.5795	-20	AUC	0.0026	-133	AUC	0.6827	-19	AUC	0.0035	-131	AUC	0.0136	-112	AUC
Neurology																			
NP	1	0.4404	-7	AUC	0.4404	59	AUC	0.2207	84	AUC	0.2207	66	AUC	0.0683	91	AUC	0.4404	25	AUC
ADPDI	1	0.2148	38	AUC	0.017	104	AUC	0.1946	87	AUC	0.2148	66	AUC	0.7985	49	AUC	0.2612	-17	AUC
NP	2	0.3458	49	AUC	0.4322	28	AUC	0.0108	126	AUC	0.7722	-20	AUC	0.0666	78	AUC	0.0535	98	AUC
ADPDI	2	0.7853	-39	AUC	0.2822	43	AUC	0.0532	86	AUC	0.2417	82	AUC	0.0532	126	AUC	0.2961	44	AUC

Detailed discriminative power results for UHB patient groups (1/2)

Survival time difference and LogRank test significance details by quartile pair

Metric	Line	1 st vs 2 nd				1 st vs 3 rd				1 st vs 4 th				2 nd vs 3 rd				2 nd vs 4 th				3 rd vs 4 th									
		p-value	(-)	Method	(-)	p-value	(-)	Method	(-)	p-value	(-)	Method	(-)	p-value	(-)	Method	(-)	p-value	(-)	Method	(-)	p-value	(-)	Method	(-)	p-value	(-)	Method			
ENT																															
NP	1	0	1443	Median	0	1443	Median	0	1443	Median	0	334	AUC	0.005	196	AUC	0.2009	-138	AUC	0.8001	254	Median	0.8001	254	Median	0.8001	254	Median	0.8001	254	Median
ADRFI	1	0.8001	-23	AUC	0.1125	-254	Median	0.1882	-176	AUC	0.1125	-254	Median	0.1854	-153	AUC	0.8001	254	Median	0.8001	254	Median	0.8001	254	Median	0.8001	254	Median	0.8001	254	Median
NP	2	0.2274	138	Median	0.0347	980	Median	0.001	1484	Median	0.2274	842	Median	0.0144	1346	Median	0.1934	504	Median	0.1934	504	Median	0.1934	504	Median	0.1934	504	Median	0.1934	504	Median
ADRFI	2	0.3918	1013	Median	0.5009	-26	Median	0.551	299	Median	0.0876	-1039	Median	0.551	-714	Median	0.2908	325	Median	0.2908	325	Median	0.2908	325	Median	0.2908	325	Median	0.2908	325	Median
Pancreas/Bil tract																															
NP	1	0.9656	15	Median	0.3544	36	Median	0.3544	5	Median	0.3544	21	Median	0.3544	-20	Median	0.1046	-41	Median	0.1046	-41	Median	0.1046	-41	Median	0.1046	-41	Median	0.1046	-41	Median
ADRFI	1	0.0662	148	Median	0.0662	115	Median	0.9505	95	Median	0.9697	-34	Median	0.0662	-54	Median	0.0662	-20	Median	0.0662	-20	Median	0.0662	-20	Median	0.0662	-20	Median	0.0662	-20	Median
NP	2	0.1838	160	Median	0.3803	106	Median	0.0705	158	Median	0.4522	-54	Median	0.3803	-2	Median	0.2045	52	Median	0.2045	52	Median	0.2045	52	Median	0.2045	52	Median	0.2045	52	Median
ADRFI	2	0.5642	138	Median	0.4382	132	Median	0.4382	69	Median	0.7664	-6	Median	0.7664	-69	Median	0.7664	-63	Median	0.7664	-63	Median	0.7664	-63	Median	0.7664	-63	Median	0.7664	-63	Median
Respir/Thorac																															
NP	1	0.0848	-472	Median	1e-04	-670	Median	0.4012	846	Median	0.0242	-198	Median	0.0242	1318	Median	0	1516	Median	0	1516	Median	0	1516	Median	0	1516	Median	0	1516	Median
OP	1	0.0144	-697	Median	0	-726	Median	0.3368	792	Median	0.0063	-28	Median	0.0063	1488	Median	0	1517	Median	0	1517	Median	0	1517	Median	0	1517	Median	0	1517	Median
ADRFI	1	0.0218	667	Median	0.982	200	Median	0.0316	1100	Median	0.0218	-468	Median	0.982	432	Median	0.0218	900	Median	0.0218	900	Median	0.0218	900	Median	0.0218	900	Median	0.0218	900	Median
NP	2	0.8153	-199	Median	0.8554	138	Median	0.9394	60	Median	0.8554	338	Median	0.8153	258	Median	0.8554	-79	Median	0.8554	-79	Median	0.8554	-79	Median	0.8554	-79	Median	0.8554	-79	Median
OP	2	0.8153	-199	Median	0.8554	138	Median	0.9394	60	Median	0.8554	338	Median	0.8153	258	Median	0.8554	-79	Median	0.8554	-79	Median	0.8554	-79	Median	0.8554	-79	Median	0.8554	-79	Median
ADRFI	2	0.4824	66	Median	0.8894	128	Median	0.2451	406	Median	0.4824	62	Median	0.4824	340	Median	0.2451	278	Median	0.2451	278	Median	0.2451	278	Median	0.2451	278	Median	0.2451	278	Median
Bladder/Uroth																															
NP	1	0.6336	-96	AUC	0.6336	-50	AUC	0.8848	21	AUC	0.9268	46	AUC	0.6336	117	AUC	0.6336	71	AUC	0.6336	71	AUC	0.6336	71	AUC	0.6336	71	AUC	0.6336	71	AUC
ADRFI	1	0.5754	26	AUC	5e-04	-335	AUC	7e-04	-296	AUC	1e-04	-361	AUC	1e-04	-322	AUC	0.8399	40	AUC	0.8399	40	AUC	0.8399	40	AUC	0.8399	40	AUC	0.8399	40	AUC
NP	2	0.0443	461	AUC	0.6918	45	AUC	0.0318	548	AUC	0.0482	-416	AUC	0.6918	87	AUC	0.0318	503	AUC	0.0318	503	AUC	0.0318	503	AUC	0.0318	503	AUC	0.0318	503	AUC
ADRFI	2	0.5006	-159	AUC	0.5006	-249	AUC	0.9255	66	AUC	0.9244	-90	AUC	0.5006	225	AUC	0.5006	315	AUC	0.5006	315	AUC	0.5006	315	AUC	0.5006	315	AUC	0.5006	315	AUC

Detailed discriminative power results for UHB patient groups (2/2)

618 **B.3.2 Logistic regression - 5 years overall survival**

619 **HEGP**

method	Line	Logistic regression fit results		Logistic regression prediction results		Survival time differences
		θ_1	p-value	ROC-AUC	Number of significant LogRank tests between quartile pairs	
Autoimm/Inflam						
OP	1	-2.553	0.037	0.792		4
NP	1	-3.568	0.047	0.79		3
BADRDI	1	0.186	0.459	0.776		1
OP	2	-2.322	0.331	0.799		0
NP	2	-1.995	0.339	0.795		0
BADRDI	2	1.263	0.301	0.799		0
Colon						
OP	1	-1.452	0.243	0.56		1
NP	1	-1.303	0.241	0.559		1
BADRDI	1	0.271	0.384	0.553		0
OP	2	0.629	0.371	0.524		3
NP	2	0.209	0.426	0.513		2
BADRDI	2	-0.338	0.403	0.518		0
Stomach						
OP	1	-0.922	0.343	0.531		0
NP	1	-0.658	0.434	0.52		0
BADRDI	1	0.361	0.407	0.523		0
OP	2	-1.376	0.434	0.57		0
NP	2	-1.217	0.372	0.563		0
BADRDI	2	-0.028	0.398	0.564		0
Lymph/Hemat						
OP	1	-1.923	0.051	0.712		2
NP	1	-3.142	0.059	0.707		2
BADRDI	1	0.806	0.237	0.7		1
OP	2	0.604	0.371	0.672		0
NP	2	0.237	0.445	0.669		0
BADRDI	2	-0.085	0.432	0.668		0
ENT						
OP	1	0.352	0.348	0.561		0
NP	1	0.62	0.363	0.56		0
BADRDI	1	0.834	0.143	0.573		3
OP	2	-1.641	0.025	0.567		3
NP	2	-2.68	0.049	0.561		3
BADRDI	2	1.056	0.134	0.55		2
Ovary						
OP	1	-3.687	0.03	0.594		4
NP	1	-4.179	0.032	0.592		3
BADRDI	1	0.898	0.311	0.517		0
OP	2	-2.56	0.108	0.583		4
NP	2	-3.45	0.158	0.565		2
BADRDI	2	1.766	0.189	0.551		2
Pancreas/Bil tract						
OP	1	-3.642	0.092	0.596		1
NP	1	-2.141	0.173	0.576		3
BADRDI	1	1.215	0.119	0.588		0
OP	2	-1.617	0.176	0.538		2
NP	2	-2.02	0.29	0.514		0
BADRDI	2	1.317	0.182	0.539		1
Respir/Thorac						
OP	1	-2.255	0.037	0.547		4
NP	1	-1.555	0.126	0.534		4
BADRDI	1	0.567	0.233	0.526		0
OP	2	-1.736	0.284	0.519		1
NP	2	-1.204	0.331	0.51		1
BADRDI	2	0.331	0.431	0.5		2
Breast						
OP	1	-7.779	0	0.731		6
NP	1	-6.789	0	0.727		6
BADRDI	1	4.199	0	0.751		5
OP	2	-6.717	0.003	0.674		5
NP	2	-5.553	0.002	0.669		4
BADRDI	2	2.449	0.006	0.641		5
Bladder/Uroth						
OP	1	-1.681	0.036	0.599		4
NP	1	-1.588	0.234	0.559		2
BADRDI	1	0.611	0.271	0.555		3
OP	2	-3.931	0.087	0.622		3
NP	2	-6.168	0.073	0.607		5
BADRDI	2	1.158	0.332	0.498		2

Results of three performance indicators for HEPG patient groups using logistic regression

Survival time difference and LogRank test significance details by quartile pair																			
Metric	Line	1 st vs 2 nd			1 st vs 3 rd			1 st vs 4 th			2 nd vs 3 rd			2 nd vs 4 th			3 rd vs 4 th		
		p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method
Colon																			
NP	1	0.1181	266	Median	0.5834	-148	Median	0.1181	-300	Median	0.0695	-414	Median	0.004	-567	Median	0.2651	-152	Median
OP	1	0.3493	236	Median	0.6998	-104	Median	0.1246	-302	Median	0.2423	-341	Median	0.0165	-538	Median	0.1928	-197	Median
AD/DRDI	1	0.1721	209	Median	0.1901	136	Median	0.8767	-24	Median	0.8422	-72	Median	0.1721	-234	Median	0.1802	-161	Median
NP	2	0.2733	-212	Median	0.0029	-292	Median	0.9537	22	Median	0.0954	-80	Median	0.2733	234	Median	0.0029	314	Median
OP	2	0.8584	-23	Median	0.0476	-213	Median	0.7687	67	Median	0.0476	-190	Median	0.783	90	Median	0.031	280	Median
AD/DRDI	2	0.3958	28	Median	0.4622	-16	Median	0.1465	168	Median	0.1465	-44	Median	0.4622	140	Median	0.0569	184	Median
Stomach																			
NP	1	0.6309	-210	Median	0.7229	-18	Median	0.6309	-206	Median	0.7229	192	Median	0.8941	4	Median	0.7229	-188	Median
OP	1	0.9848	15	Median	0.9848	-8	Median	0.5318	-256	Median	0.9848	-24	Median	0.5318	-271	Median	0.57	-248	Median
AD/DRDI	1	0.1965	-165	Median	0.1478	-116	Median	0.9626	91	Median	0.8522	49	Median	0.1965	256	Median	0.1478	207	Median
NP	2	0.4729	-148	Median	0.4729	-59	Median	0.9114	-26	Median	0.9114	89	Median	0.4729	122	Median	0.4729	32	Median
OP	2	0.9112	-23	Median	0.9112	64	Median	0.9112	98	Median	0.9112	86	Median	0.9112	122	Median	0.9112	35	Median
AD/DRDI	2	0.9731	32	Median	0.5604	-2	Median	0.3516	211	Median	0.5604	-34	Median	0.3516	179	Median	0.1823	212	Median
Lymph/Hemat																			
NP	1	0.1839	-168	AUC	9e-04	-922	Median	0.0123	-816	Median	0.0676	-922	Median	0.2426	-816	Median	0.4046	106	Median
OP	1	0.0579	-173	AUC	0.0016	-686	Median	2e-04	-1080	Median	0.192	-686	Median	0.0579	-1080	Median	0.4729	-394	Median
AD/DRDI	1	0.0944	14	Median	0.8218	-558	Median	0.3655	-819	Median	0.0718	-572	Median	0.0102	-833	Median	0.4636	-261	Median
NP	2	0.9072	-38	Median	0.4845	-917	Median	0.6355	67	AUC	0.4845	-917	Median	0.6355	106	AUC	0.2993	917	Median
OP	2	0.5215	140	Median	0.4588	-764	Median	0.3405	268	Median	0.8443	-904	Median	0.0961	128	Median	0.0961	1032	Median
AD/DRDI	2	0.7909	163	Median	0.7909	-736	Median	0.7909	163	Median	0.7909	-899	Median	0.8069	84	AUC	0.7909	899	Median
ENT																			
NP	1	0.7667	-167	Median	0.7035	-389	Median	0.7035	-310	Median	0.7035	-222	Median	0.7667	-144	Median	0.7667	78	Median
OP	1	0.7613	-83	Median	0.7613	-297	Median	0.7613	-207	Median	0.7613	-214	Median	0.7613	-124	Median	0.7613	90	Median
AD/DRDI	1	0.5433	213	Median	0.0856	-236	Median	0.0013	-506	Median	0.02	-448	Median	1e-04	-718	Median	0.0856	-270	Median
NP	2	0.4042	19	Median	0.9545	-168	Median	2e-04	-320	Median	0.4042	-188	Median	0	-340	Median	4e-04	-152	Median
OP	2	0.1043	-138	Median	0.8464	30	Median	0	-344	Median	0.1603	168	Median	0.0015	-206	Median	0	-374	Median
AD/DRDI	2	0.4989	161	Median	0.2855	-178	Median	0.0295	-146	Median	0.0977	-339	Median	0.005	-307	Median	0.2855	32	Median

Detailed discriminative power results for HEGP patient groups using logistic regression (1 / 3)

Survival time difference and LogRank test significance details by quartile pair

Metric	Line	1 st vs 2 nd		1 st vs 3 rd		1 st vs 4 th		2 nd vs 3 rd		2 nd vs 4 th		3 rd vs 4 th	
		p-value	(-) Method	p-value	(-) Method	p-value	(-) Method	p-value	(-) Method	p-value	(-) Method	p-value	(-) Method
Ovary													
NP	1	0.3983	-435 Median	0.019	-878 Median	0.0035	-935 Median	0.1162	-443 Median	0.0239	-500 Median	0.4854	-57 Median
OP	1	0.7987	-21 AUC	0.0129	-886 Median	0.003	-974 Median	0.0173	-886 Median	0.0033	-974 Median	0.5757	-88 Median
ADRD	1	0.6046	286 Median	0.4446	482 Median	0.6909	66 Median	0.6046	196 Median	0.5058	-220 Median	0.3905	-416 Median
NP	2	0.1117	-665 Median	7e-04	-1176 Median	0.0022	-1150 Median	0.0581	-510 Median	0.1117	-484 Median	0.7133	26 Median
OP	2	0.0859	-665 Median	1e-04	-1160 Median	1e-04	-1206 Median	0.029	-494 Median	0.029	-542 Median	0.9203	-47 Median
ADRD	2	0.5967	416 Median	0.9214	130 Median	0.0585	-360 Median	0.5967	-285 Median	0.0149	-776 Median	0.0475	-490 Median
Pancreas/Bil tract													
NP	1	0.0012	-202 Median	0.019	-194 Median	0.014	-151 Median	0.3891	9 Median	0.3891	52 Median	0.9128	42 Median
OP	1	0.2505	-3 Median	0.0267	-26 Median	0.2505	98 Median	0.2505	-23 Median	0.8712	101 Median	0.1073	124 Median
ADRD	1	0.8533	98 Median	0.8533	14 Median	0.8533	86 Median	0.8533	-84 Median	0.8533	-12 Median	0.8533	73 Median
NP	2	0.6828	-34 Median	0.6828	-53 Median	0.6828	-20 Median	0.6828	-19 Median	0.6828	14 Median	0.6828	34 Median
OP	2	0.1247	-129 Median	0.6842	-58 Median	0.0027	-184 Median	0.286	71 Median	0.1247	-55 Median	0.0096	-126 Median
ADRD	2	0.5576	5 Median	0.4281	152 Median	0.0963	21 Median	0.1689	147 Median	0.287	16 Median	0.0072	-131 Median
Respir/Thorac													
NP	1	0.8934	-69 Median	0.0491	-162 Median	0	-227 Median	0.06	-93 Median	0	-158 Median	0.0334	-65 Median
OP	1	0.8385	-53 Median	0.001	-203 Median	0	-245 Median	0.001	-150 Median	0	-192 Median	0.2844	-42 Median
ADRD	1	0.8881	-21 Median	0.8881	4 Median	0.209	-74 Median	0.8881	25 Median	0.209	-53 Median	0.209	-78 Median
NP	2	0.2497	-4 Median	0.862	-56 Median	0.2497	-104 Median	0.2497	-52 Median	0.0219	-100 Median	0.2497	-47 Median
OP	2	0.5273	55 Median	0.5822	-28 Median	0.1488	-88 Median	0.2942	-82 Median	0.0341	-143 Median	0.2942	-60 Median
ADRD	2	0.0191	180 Median	0.1038	70 Median	0.7253	27 Median	0.3886	-110 Median	0.0191	-153 Median	0.144	-42 Median
Breast													
NP	1	1e-04	120 AUC	0.0222	-177 AUC	0	-1054 Median	0	-296 AUC	0	-1054 Median	0	-1054 Median
OP	1	0.032	58 AUC	0.0043	-181 AUC	0	-1047 Median	0	-239 AUC	0	-1047 Median	0	-1047 Median
ADRD	1	0.0086	166 AUC	0.3596	0 AUC	0	-1102 Median	3e-04	-166 AUC	0	-1102 Median	0	-1102 Median
NP	2	0.2222	73 AUC	0.0663	-364 Median	0	-1394 Median	0.0023	-364 Median	0	-1394 Median	0	-1030 Median
OP	2	0.3939	48 AUC	0.0049	-856 Median	0	-1323 Median	3e-04	-856 Median	0	-1323 Median	0.0022	-467 Median
ADRD	2	0.0035	177 Median	0.6057	46 Median	0.0017	-1124 Median	0.0125	-131 Median	0	-1301 Median	4e-04	-1170 Median

Detailed discriminative power results for HEGP patient groups using logistic regression (2/3)

Survival time difference and LogRank test significance details by quartile pair

Metric	Line	1 st vs 2 nd			1 st vs 3 rd			1 st vs 4 th			2 nd vs 3 rd			2 nd vs 4 th			3 rd vs 4 th		
		p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method	p-value	(-)	Method
Bladder/Uroth																			
NP	1	0.1119	-300	Median	0.8734	162	Median	0.1325	462	Median	0.2259	-223	Median	0.0101	-685	Median	0.0716	-251	Median
OP	1	0.0177	987	Median	0.1043	-276	Median	2e-04	-1213	Median	0	-1464	Median	0.0077	630	Median	0.0077	630	Median
ADPDI	1	0.707	-64	Median	0.0061	-492	Median	0.0077	-428	Median	0.9286	202	Median	0.0363	-232	Median	0.0363	-232	Median
NP	2	0.0363	-370	Median	0.0363	-344	Median	0.9938	26	Median	0.0363	-206	Median	0.0012	-291	Median	0.0034	-233	Median
OP	2	0.1836	-312	Median	0.0579	-370	Median	0.5296	-58	Median	0.4786	-94	Median	0.2391	-75	Median	0.2391	-75	Median
ADPDI	2	0.8227	-124	Median	0.0432	-142	Median	0.0474	-19	Median	0.4786	-94	Median	0.2391	-75	Median	0.2391	-75	Median

Detailed discriminative power results for HEGP patient groups using logistic regression (3/3)