

Table S1. PFS population survival kinetics assessment for NSCLC postoperative adjuvant platinum regimens vs controls

Study arm	1-phase decay models				2-phase decay models									
	Overall half-life ^a	95% CI ^{a,b}		R ²	Relapsing subpopulation						Potentially cured subpopulation			R ²
		Low	High		% of total	95% CI ^b		Half-life ^a	95% CI ^{a,b}		Half-life ^a	95% CI ^{a,b}		
						Low	High		Low	High		Low	High	
ANITA control [12]	35.0	31.0	39.3	0.79	60	55	66	10.0	8.8	11.5	207.9	137.0	503.3	0.99
ANITA chemo [12]	47.2	44.5	50.0	0.82	41	38	44	9.9	8.9	11.0	114.2	103.1	129.6	0.99
IALT control [13]	40.1	37.8	42.4	0.82	57	54	60	12.9	12.2	13.8	212.7	170.9	290.0	0.99
IALT chemo [13]	46.2	44.1	48.5	0.99	42	40	45	11.7	10.9	12.5	120.8	111.2	133.4	0.99
CALGB control [14]	59.9	57.4	62.5	0.82	94	?	96	55.4	?	?	1x10 ¹⁴	?	?	0.91
CALGB chemo [14]	74.9	71.9	78.2	0.89	60	56	62	29.5	27.5	30.7	4x10 ¹⁵	?	?	0.99
BR10 control [15]	64.8	58.3	72.1	0.27	50	49	51	10.9	10.4	?	4x10 ¹⁵	?	?	0.99
BR10 chemo [15]	100.0	95.3	105	0.84	40	31	48	23.0	18.0	28.0	671.6	314.2	?	0.99

a. months

b. 95% CI: 95% confidence intervals

?: could not be defined

Table S2: PFS population survival kinetics assessment of chemoradiation for locally advanced NSCLC

Study	Arm ^a	1-phase decay models				2-phase decay models									
		Overall half-life ^b	95% CIs ^{b,c}		R ²	Relapsing subpopulation						Potentially cured subpopulation			R ²
			Low	High		% of total	95% CIs ^c		Half-life ^b	95% CIs ^{b,c}		Half-life ^b	95% CIs ^{b,c}		
							Low	High		Low	High		Low	High	
Ahn [18]	cis + doce	9.3	8.8	9.7	0.98	95	84	97	8.2	7.4	8.7	7.3x10 ¹³	32.6	?	0.99
Ahn [18]	cis + doce + consol	10.1	9.5	10.7	0.97	91	87	93	8.0	7.5	?	499.0	90.3	?	0.99
Atagi elderly [19]	daily carb	9.6	9.1	10.1	0.95	91	88	93	7.8	7.4	8.2	180.3	104.2	649.7	0.99
Bradley [20]	74 Gy carb + pacl	11.4	10.9	12.0	0.94	89	86	90	8.5	8.1	?	5.4x10 ¹⁵	?	?	0.97
Bradley [20]	60 Gy carb + pacl	15.5	14.8	16.1	0.92	85	82	?	10.2	9.7	?	5.6x10 ¹⁵	?	?	0.97
Butts [21]	plat chemo	11.8	10.9	12.8	0.88	79	75	82	6.5	6.1	6.9	197.7	100.2	?	0.99
Butts [21]	plat chemo + temcemotide	13.9	13.0	14.7	0.89	79	75	81	7.8	7.2	?	740.5	137.6	?	0.99
Carter [22]	carb + pacl + maintenance	9.1	8.6	9.7	0.88	90	86	93	7.2	6.7	7.9	4.2x10 ¹⁵	?	?	0.91
Carter [22]	carb + pacl	15.0	14.3	15.9	0.88	85	82	88	10.4	9.4	11.3	1.5x10 ¹³	74.8	?	0.92
Chang [23]	proton + carb + pacl	18.0	16.7	19.3	0.90	77	66	86	10.6	9.1	12.1	111.1	60.0	5239	0.97

Choy [24]	cis + pem + consol	16.0	15.3	16.6	0.94	93	?	?	14.5	?	?	5.7x10 ¹⁵	?	?	0.94
Faivre-Finn [25]	plat chemo	10.0	8.9	11.2	0.75	74	71	77	4.1	3.8	4.4	97.2	69.6	165.8	0.99
Faivre-Finn [25]	plat chemo + durvalumab	23.6	22.1	25.2	0.66	43	41	45	4.0	3.7	4.3	61.4	57.2	66.4	0.99
Fenwick [26]	cis + vino	25.9	25.0	26.9	0.94	67	44	79	13.5	9.9	?	158.3	54.5	?	0.97
Flentje [27]	cis + vino + maintenance	8.1	7.6	8.7	0.93	89	87	90	6.1	5.8	?	4.9x10 ¹⁵	?	?	0.98
Flentje [27]	cis + vino	7.2	6.5	7.9	0.90	78	74	82	4.3	4.0	4.6	68.0	47.3	123.3	0.99
Fournel [28]	chemo induction + concur	12.0	11.3	12.8	0.93	89	86	91	9.1	8.6	?	4.6x10 ¹⁵	?	?	0.97
Fournel [28]	chemo concur + consol	13.6	12.0	15.3	0.77	81	78	83	7.4	6.9	?	4.0x10 ¹⁵	?	?	0.94
Garrido [29]	chemo induction + concur	13.1	12.7	13.5	0.97	85	70	88	9.5	8.3	?	5.8x10 ¹⁵	?	?	0.98
Glinski [52]	Cis + vino	40.3	38.1	42.6	0.86	48	41	57	11.1	9.5	13.1	258.7	144.6	?	0.99
Govindan [30]	carb + pem + cetuximab	13.7	13.2	14.1	0.96	90	78	93	10.9	9.7	11.7	9.4x10 ¹³	45.0	?	0.97
Hoang [31]	carb + pacl + thalidomide	8.4	8.1	8.7	0.97	95	87	99	7.6	7.1	8.2	6.1x10 ¹⁵	?	?	0.98
Hoang [31]	carb + pacl	8.5	8.2	8.8	0.97	90	84	92	6.8	6.3	7.2	5.7x10 ¹⁵	?	?	0.99
Horin-ouchi [32]	chemo concur + consol	16.9	15.3	18.5	0.89	87	85	88	11.4	10.8	?	4.3x10 ¹⁵	?	?	0.98
Imamura [33]	hyperfrac + boost +chemo	25.6	23.3	28.1	0.85	65	55	74	10.2	8.5	12.1	148.8	85.1	1227	0.97
Isla [34]	cis + etop	11.8	11.2	12.4	0.95	85	62	89	8.2	6.5	?	185.0	28.4	?	0.97
Isla [34]	cis + vino	13.8	13.3	14.4	0.95	85	83	86	9.5	9.0	9.9	5.8x10 ¹¹	66.4	?	0.98
Kawaguchi [35]	chemo concur + consol	12.8	12.2	13.4	0.94	88	84	91	9.7	9.0	?	3.8x10 ¹⁵	?	?	0.96
Kerner [36]	chemo induction + concur	24.1	22.2	26.2	0.85	80	75	82	13.6	12.5	?	3.7x10 ¹⁵	?	?	0.96
Landau [93]	Cis + vino	23.5	22.6	24.3	0.95	9	?	?	12.4	?	?	25.0	?	?	0.95
Lawrence [37]	hyperfrac + chemo + amifostine	12.1	11.4	12.8	0.94	88	82	90	9.1	8.3	?	5.9x10 ¹⁵	?	?	0.97
Lawrence [37]	hyperfrac + chemo	12.6	12.1	13.1	0.97	91	82	93	10.0	9.0	?	5.9x10 ¹⁵	?	?	0.99
Lerouge [38]	chemo induction + concur	19.7	18.8	20.6	0.91	75	70	78	10.7	9.9	?	3.7x10 ¹⁵	?	?	0.98
Liang [39]	cis + pacl	11.6	10.9	12.4	0.92	90	87	92	9.3	8.7	?	3.4x10 ¹⁵	?	?	0.95
Liang [39]	cis + etop	16.6	15.6	17.6	0.93	86	83	88	11.8	11.1	12.6	5.6x10 ¹⁵	?	?	0.97
Lu [40]	chemo + AE-941	18.2	16.3	20.3	0.67	67	64	70	5.9	5.6	6.3	205.5	138.6	416.7	0.99
Lu [40]	chemo induction + concur	21.6	19.7	23.6	0.72	67	63	71	7.5	6.9	8.2	379.6	166.5	?	0.98
Niho [41]	cis + pem	16.1	15.3	17.0	0.94	87	84	91	11.8	10.6	13.2	5.1x10 ¹¹	39.5	?	0.96
Niho [41]	cis + S-1	21.2	18.9	23.8	0.63	70	67	72	8.0	7.3	?	3.6x10 ¹⁵	?	?	0.95

Park [42]	chemo- EGFR unknown	14.1	13.0	15.2	0.82	76	75	78	7.1	6.8	?	5.6x10 ¹⁵	?	?	0.97
Park [42]	chemo- EGFR WT	15.6	14.8	16.4	0.91	83	72	85	9.9	8.6	10.6	3.2x10 ¹⁵	?	?	0.97
Price [43]	Gemcit	16.9	15.3	18.7	0.94	27	21	36	5.5	4.1	7.4	35.2	32.0	39.8	0.96
Provencio [44]	chemo induction + concur	13.2	12.8	13.6	0.97	94	90	99	11.7	10.6	?	7.7x10 ¹²	20.7	?	0.97
Sasaki [45]	cis + vino	13.6	12.9	14.3	0.93	89	83	94	10.9	9.8	?	3.2x10 ¹⁵	?	?	0.94
Sasaki [45]	cis + S-1	16.4	15.8	17.1	0.90	79	78	?	9.3	9.1	?	4.6x10 ¹⁰	137.0	?	0.96
Senan [46]	cis + etop	12.0	11.3	12.7	0.96	92	88	94	9.7	9.1	?	5.0x10 ¹⁵	?	?	0.98
Senan [46]	cis + pem	14.1	13.3	14.9	0.95	89	85	91	10.3	9.6	?	5.0x10 ¹⁵	?	?	0.98
Shimokawa [47]	cis + S-1	14.3	13.7	14.8	0.94	88	81	91	10.9	10.1	11.8	4.6x10 ¹⁵	?	?	0.96
Shimokawa [47]	Cis + doce	21.0	20.6	21.3	0.99	4	0.2	?	5.2	1.3	?	21.8	20.9	73.3	0.99
Tsuchiya-Kawano [88]	Carb + nab-pacl	14.6	14.1	15.2	0.95	No 2-phase model fit									
van Baardwijk [48]	chemo induction + concur	19.7	18.9	20.7	0.93	80	73	83	15.7	11.5	13.8	4.7x10 ¹⁵	?	?	0.96
Vera [49]	chemo induction + concur	16.5	16.0	16.9	0.96	89	77	93	13.3	12.3	?	1.9x10 ¹³	52.2	?	0.97
Wada [50]	60 Gy + chemo	10.6	9.7	11.7	0.83	84	82	86	7.3	6.8	?	4.3x10 ¹⁵	?	?	0.95
Wada [50]	hyperfrac + chemo	21.5	19.7	23.4	0.81	76	72	78	10.5	9.7	11.2	4.4x10 ¹⁵	?	?	0.97
Yamamoto [51]	carb + irinotecan	8.9	8.2	9.6	0.88	89	88	89	6.3	6.0	6.5	1.2x10 ¹¹	179.8	?	0.98
Yamamoto [51]	cis + vindesine + mito	10.2	9.4	10.9	0.89	88	86	89	7.1	6.7	?	5.4x10 ¹⁵	?	?	0.97
Yamamoto [51]	carb + pacl	11.0	10.4	11.7	0.91	88	87	90	7.9	7.5	?	3.3x10 ¹⁵	?	?	0.98

a. cis: cisplatin; doce: docetaxel; consol: consolidation chemotherapy; carb: carboplatin; pacl: paclitaxel; plat: platinum; chemo: chemotherapy; pem: pemetrexed; vino: vinorelbine; concur: concurrent chemotherapy; hyperfrac: hyperfractionated radiotherapy; etop: etoposide; EGFR WT: EGFR wild type; mito: myomycin-C

b. months

c. CIs: confidence intervals

?: could not be defined

Study	Arm ^a	1-phase decay models		2-phase decay models												
				Relapsing subpopulation						Potentially cured subpopulation				R ²		
		Overall half-life ^b	95% CIs ^{b,c}		R ²	% of total	95% CIs ^c		Half-life ^b	95% CIs ^{b,c}		Half-life ^b	95% CIs ^{b,c}			
			Low	High			Low	High		Low	High		Low	High		
Arriagada [54]	XRT 45-55Gy	16.3	15.3	17.3	0.91	88	77	93	12.4	10.9	?	4.4x10 ¹⁵	?	?	0.93	
Arriagada [54]	XRT 65Gy	15.0	14.1	16.0	0.92	no 2-phase model fit										

Arriagada [53]	Alternating chemo/XRT	15.2	14.4	16.0	0.95	88	86	89	11.0	10.6	?	4.3x10 ¹⁵	?	?	0.99
Beith [55]	maintenance	17.4	15.0	20.2	0.76	82	80	84	10.1	9.7	10.6	666	380.0	2845.0	0.99
Beith [55]	no maintenance	9.0	8.0	10.1	0.9	75	72	78	5.4	5.0	5.8	86.1	72.3	105.7	0.99
Blackstock [56]	concurrent XRT	10.7	9.9	11.7	0.94	82	75	88	7.4	6.6	8.3	105.8	63.3	330.7	0.98
Blackstock [56]	split course XRT	12.2	11.5	12.9	0.97	93	91	96	10.5	9.7	11.4	1.3x10 ¹²	33.3	?	0.97
Bogart [57]	concurrent XRT	15.1	14.7	15.6	0.96	91	60	98	12.9	10.9	?	3.9x10 ¹⁵	?	?	0.96
Bonner [58]	once daily XRT	17.8	17.3	18.4	0.96	88	83	?	14.2	?	?	6.2x10 ¹¹	19.7	?	0.96
Bonner [58]	twice daily XRT	16.8	16.3	17.4	0.95	no 2-phase model fit, but 2-phase decay on log-linear plot									
Edelman [59]	concurrent XRT	11.6	11.0	12.2	0.92	90	84	93	9.0	8.3	?	4.8x10 ¹⁵	?	?	0.94
Ettlinger [60]	hyperfractionated XRT	16.8	15.8	17.9	0.91	84	80	87	11.2	10.4	?	4.2x10 ¹⁵	?	?	0.96
Glisson [61]	hyperfractionated XRT	25.5	25.0	26.1	0.98	no 2-phase model fit									
Goodman [62]	CAV+etop	17.3	16.5	18.1	0.96	95	?	?	15.6	14.0	?	9.0x10 ¹³	?	?	0.96
Goodman [62]	cis-etop/CAV alternating	16.4	15.7	17.1	0.96	93	72	97	14.3	12.4	?	3.8x10 ¹⁵	?	?	0.97
Gregor [63]	sequential XRT	12.7	12.1	13.4	0.94	92	87	95	10.6	9.7	?	3.7x10 ¹⁵	?	?	0.95
Gregor [63]	alternating chemo/XRT	10.2	9.8	10.7	0.95	96	93	97	9.2	8.7	?	4.5x10 ¹⁵	?	?	0.96
Gronberg [64]	hyperfractionated 45Gy	17.7	16.2	19.3	0.84	77	69	80	9.7	8.5	?	5.2x10 ¹⁵	?	?	0.94
Gronberg [64]	hyperfractionated 60Gy	25.4	24.1	26.9	0.91	75	58	78	13.9	11.3	?	5.1x10 ¹⁵	?	?	0.97
Halvorsen [65]	comorbid	11.2	10.0	12.4	0.9	87	84	91	8.0	7.1	9.0	2.3x10 ¹³	52.3	?	0.94
Halvorsen [65]	no comorbid	17.3	16.0	18.7	0.92	86	69	89	12.4	10.3	14.4	3.8x10 ¹⁵	?	?	0.94
Horn [66]	concurrent XRT	16.3	15.4	17.2	0.92	no 2-phase model fit									
Hugli [67]	hyperfractionated XRT	17.9	16.2	19.8	0.75	75	71	76	7.8	7.1	8.4	3.3x10 ¹⁵	?	?	0.96
Jett [68]	CAV	8.4	7.8	9.0	0.92	93	90	95	7.3	6.7	?	5.3x10 ¹⁵	?	?	0.94
Jett [68]	CAV+etop	11.5	10.6	12.5	0.9	88	83	89	8.6	7.9	9.0	7.3x10 ¹⁴	169.1	?	0.98
Kelley [69]	concurrent XRT	13.3	12.6	14.0	0.95	89	86	94	10.3	9.3	11.6	1.3x10 ¹²	40.7	?	0.96
Komaki [70]	hyperfractionated XRT	11.5	10.9	12.2	0.95	94	77	99	10.3	9.1	?	4.2x10 ¹⁵	?	?	0.95
Kubota [71]	cis-etop	21.2	18.9	23.6	0.82	70	54	84	9.8	7.4	12.7	105.1	52.0	?	0.94
Kubota [71]	cis-etop/ cis-irinotecan	23.6	20.4	27.0	0.67	76	66	78	9.9	8.2	?	3.7x10 ¹⁵	?	?	0.93
Laack [73]	concurrent XRT	7.7	7.3	8.1	0.96	no 2-phase model fit									
Le [72]	Tirapazamine /XRT	13.5	12.9	14.2	0.95	92	42	97	11.2	7.8	?	4.9x10 ¹⁵	?	?	0.96
Mano-Haran [74]	no PET scan	23.3	21.2	25.6	0.79	78	73	81	12.3	11.1	13.7	4.4x10 ¹⁵	?	?	0.93
Mano-Haran [74]	PET scan	28.3	26.0	30.8	0.81	74	68	76	13.0	11.8	?	5.0x10 ¹⁵	?	?	0.96
Maurer [75]	no warfarin	14.6	13.8	15.4	0.95	91	87	93	11.4	10.7	12.0	4.1x10 ¹⁵	?	?	0.98
Maurer [75]	warfarin	23.0	21.6	24.5	0.88	70	64	77	10.8	9.6	12.0	138.5	88.8	380.7	0.99

McClay [76]	No tamoxifen	16.5	15.5	17.5	0.92	88	86	90	11.8	11.1	12.5	2.0x10 ¹³	113.4	?	0.97
McClay [76]	Tamoxifen	13.8	13.1	14.6	0.93	90	75	95	11.2	9.5	?	184.7	41.0	?	0.95
Miller [77]	concurrent XRT	15.0	14.1	16.0	0.86	79	77	81	8.4	7.8	?	5.1x10 ¹⁵	?	?	0.96
Murray [78]	early XRT	18.9	17.7	20.2	0.9	88	82	96	14.9	12.9	17.7	2.2x10 ¹³	40.5	?	0.91
Murray [78]	late XRT	14.6	13.7	15.7	0.91	91	73	97	12.3	10.6	?	3.3x10 ¹⁵	?	?	0.92
Perry [79]	early XRT	11.2	10.9	11.6	0.99	no 2-phase model fit, but 2-phase decay on log-linear plot									
Perry [79]	late XRT	13.1	12.6	13.7	0.98	97	90	99	12.4	11.4	?	542.4	44.3	?	0.98
Perry [79]	no XRT	8.2	7.9	8.6	0.97	no 2-phase model fit, but 2-phase decay on log-linear plot									
Qiu [80]	hyperfractionated XRT	16.8	15.7	17.9	0.93	89	75	94	12.9	11.2	?	3.4x10 ¹⁵	?	?	0.94
Qiu [80]	once daily XRT	26.5	24.7	28.6	0.84	70	62	75	13.3	11.4	15.4	3.7x10 ¹⁵	?	?	0.92
Salama [81]	concurrent XRT	16.1	14.2	18.2	0.83	80	75	83	8.5	7.7	?	361.3	131.5	?	0.98
Schild [82]	daily XRT	16.7	15.9	17.5	0.93	84	80	86	11.2	10.5	?	6.0x10 ¹⁵	?	?	0.97
Schild [82]	twice daily XRT	17.6	16.7	18.6	0.91	81	79	84	10.9	10.1	11.8	1.7x10 ¹³	200.2	?	0.96
Spiro [83]	early XRT	12.6	11.0	14.4	0.81	85	83	86	7.9	7.4	?	3.3x10 ¹³	?	?	0.97
Spiro [83]	late XRT	16.2	14.5	18.1	0.87	84	79	85	9.7	8.9	?	4.6x10 ¹⁵	?	?	0.98
Takada [84]	concurrent XRT	16.7	15.2	18.2	0.87	83	79	85	10.4	9.6	?	6.1x10 ¹⁵	?	?	0.96
Takada [84]	late XRT	11.1	10.2	12.1	0.9	90	84	92	8.8	8.0	9.5	3.7x10 ¹⁵	?	?	0.94
Thomas [85]	SW-9229	10.8	10.2	11.3	0.95	95	?	?	9.8	?	11.2	4.1x10 ¹⁵	?	?	0.95
Thomas [86]	SW-8269	18.2	16.1	20.5	0.92	59	54	64	7.5	6.7	8.3	59.5	52.5	68.6	0.99
Xia [87]	XRT	30.0	27.1	31.1	0.87	67	56	71	12.9	10.9	14.6	3.7x10 ¹⁵	?	?	0.96

a. all groups received chemotherapy; XRT: radiation; Gy: Grays; CAV: cyclophosphamide + doxorubicin + vincristine; etop: etoposide; cis: cisplatin; comorbid: comorbidities

b. months

c. 95% confidence intervals

d. could not be fit to an EDNLRA

? could not be determined

Tutorial S1 on Population Survival Kinetics Methodology:

Population survival kinetics analyses can be useful in supplementing standard statistical analyses of clinical trials data. These analyses assume that progression-free survival (PFS) and overall survival (OS) curves generally approximate first-order kinetics. On log-linear plots, deviations of these curves from a straight line can offer biological insights into population behavior and factors that might influence this, and they can be useful in generating and testing hypotheses. Population survival kinetics analyses use exponential decay nonlinear regression analysis to calculate progression-free survival (PFS) and overall survival (OS) half-lives (time to progression or death of half the remaining patients), and these half-lives can be useful in performing further calculations.

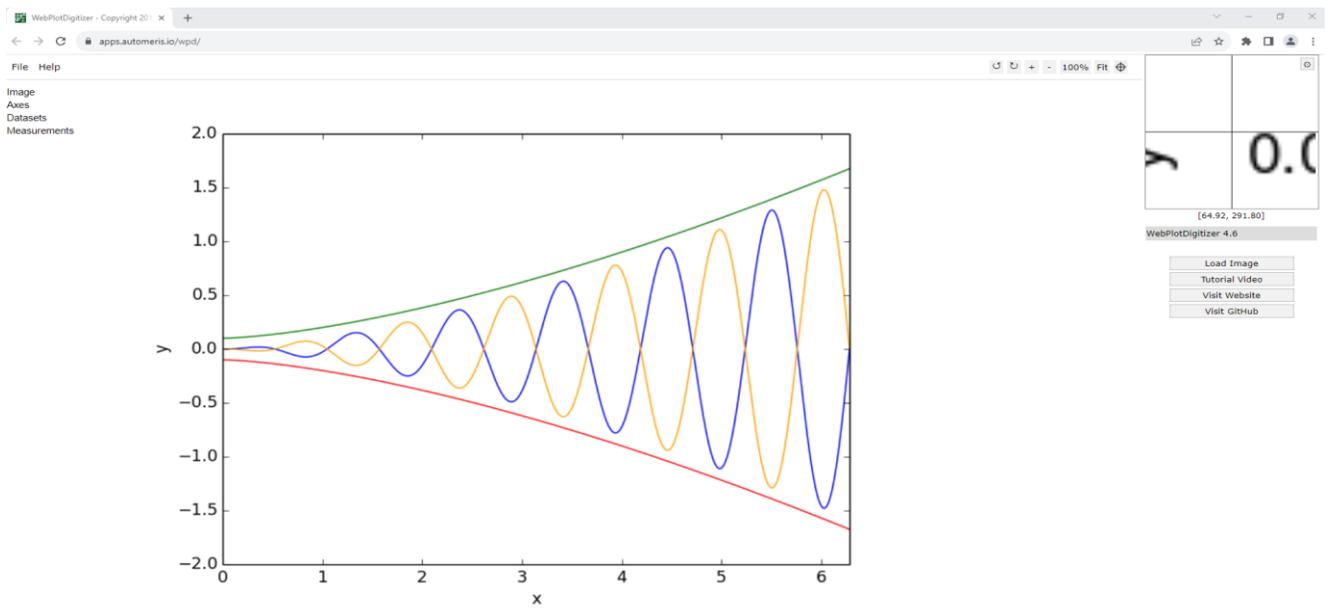
Exponential decay nonlinear regression analyses can also assess whether PFS and OS curve data can be fit by 2-phase exponential decay models. If the curve can be fit by 2-phase decay models, this suggests that there are two distinct subpopulations with differing rates of tumor progression or death. The models can estimate the relative size of the two subpopulations and can estimate the PFS or OS half-lives for the rapidly progressing and slowly progressing subpopulations. For curves fitting 2-phase decay models, log-linear plots typically demonstrate a curve inflection point to the right.

As is generally the case with assessment of clinical research data, confidence in the interpretation of population survival kinetics results may vary with number of patients on the trial(s), length and maturity of patient follow up, model R^2 values, width of 95% confidence intervals, and consistency of observations across different trials of a therapy. If patient follow-up is relatively short, then 95% confidence intervals for parameter upper and lower boundaries may be very wide or undefinable, while they may be narrow with longer follow-up.

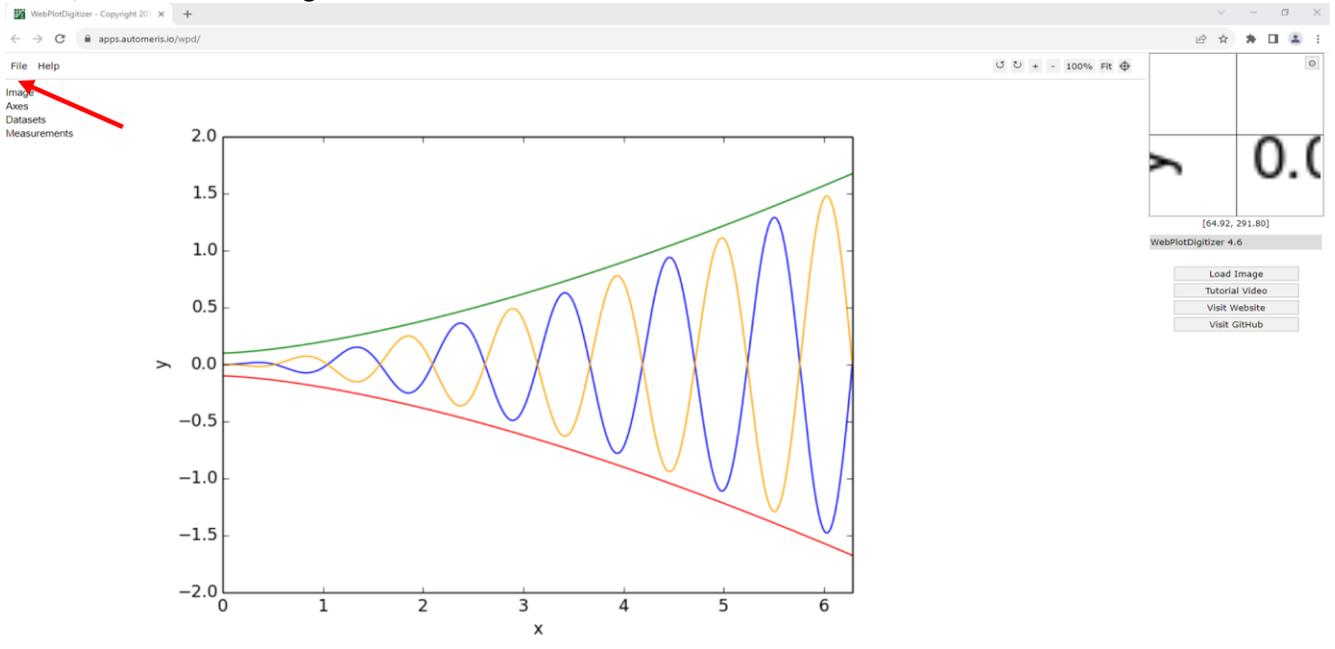
As a starting point for interested investigators, clinicians, and trainees, we have provided details on proposed population survival kinetics methodologies below. We have not compared our approaches to other potential approaches that might also be considered. For this illustration, we are using PFS data from patient populations with a potentially cured subpopulation, but the same approaches also apply for overall survival and for patients with incurable metastatic disease. We will start by illustrating how to digitize a published curve, and will follow with a discussion of exponential decay nonlinear regression analysis of the digitized data.

How to digitize a published survival curve:

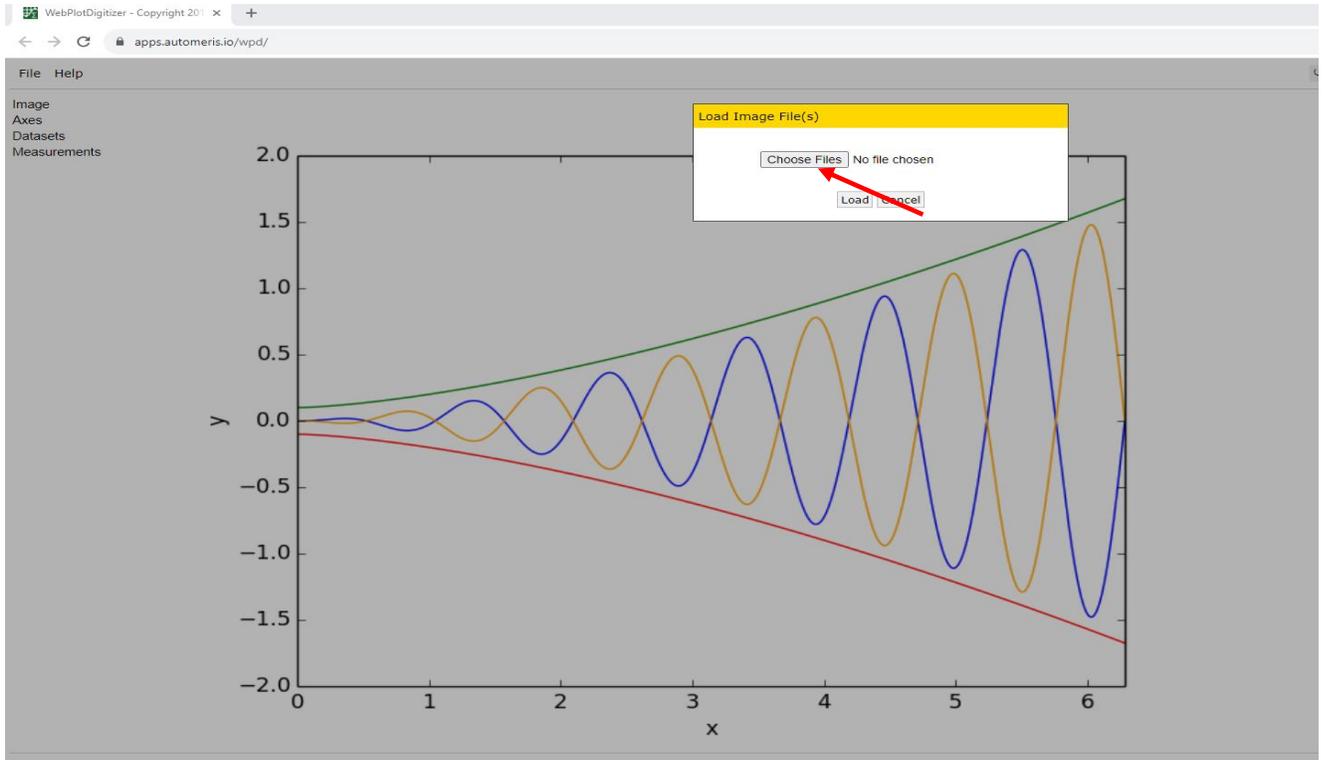
1. Access the online data digitizing program <https://apps.automeris.io/wpd/> (Copyright 2010-2022 Ankit Rohatgi) (or similar program) to digitize curves.
2. Save a screenshot of a survival curve of interest as a PNG file. Other file types may not work with this data digitizing program.
3. When opened, the online program appears as follows:



4. To load the curve of interest, click on “File” on the top left. A drop-down menu will appear. From this drop-down menu, click on “Load images”:



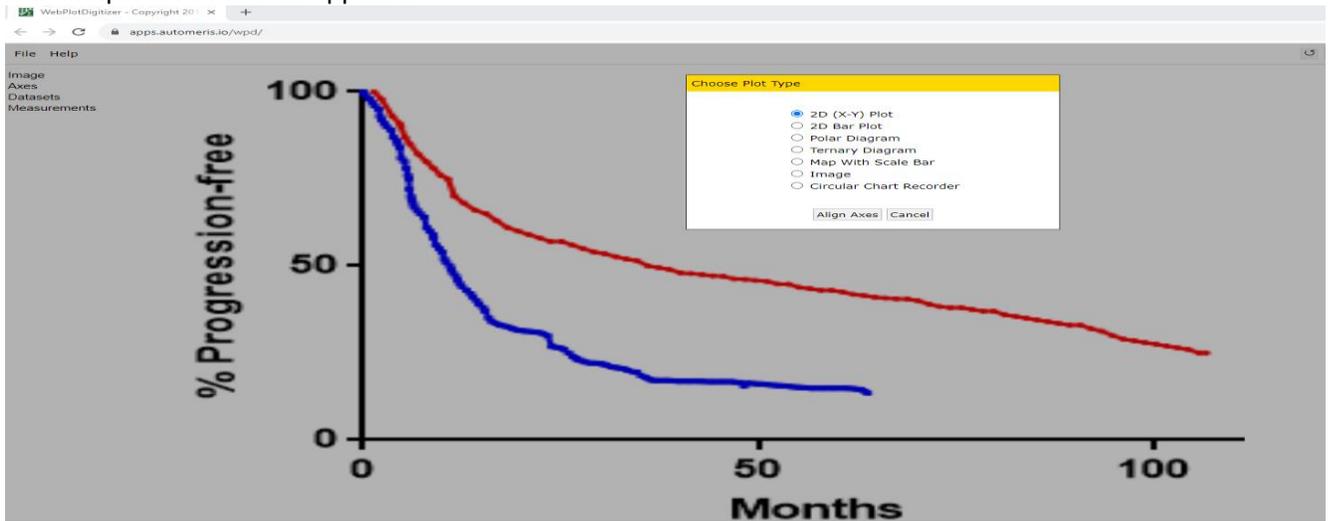
5. Click on Choose File:



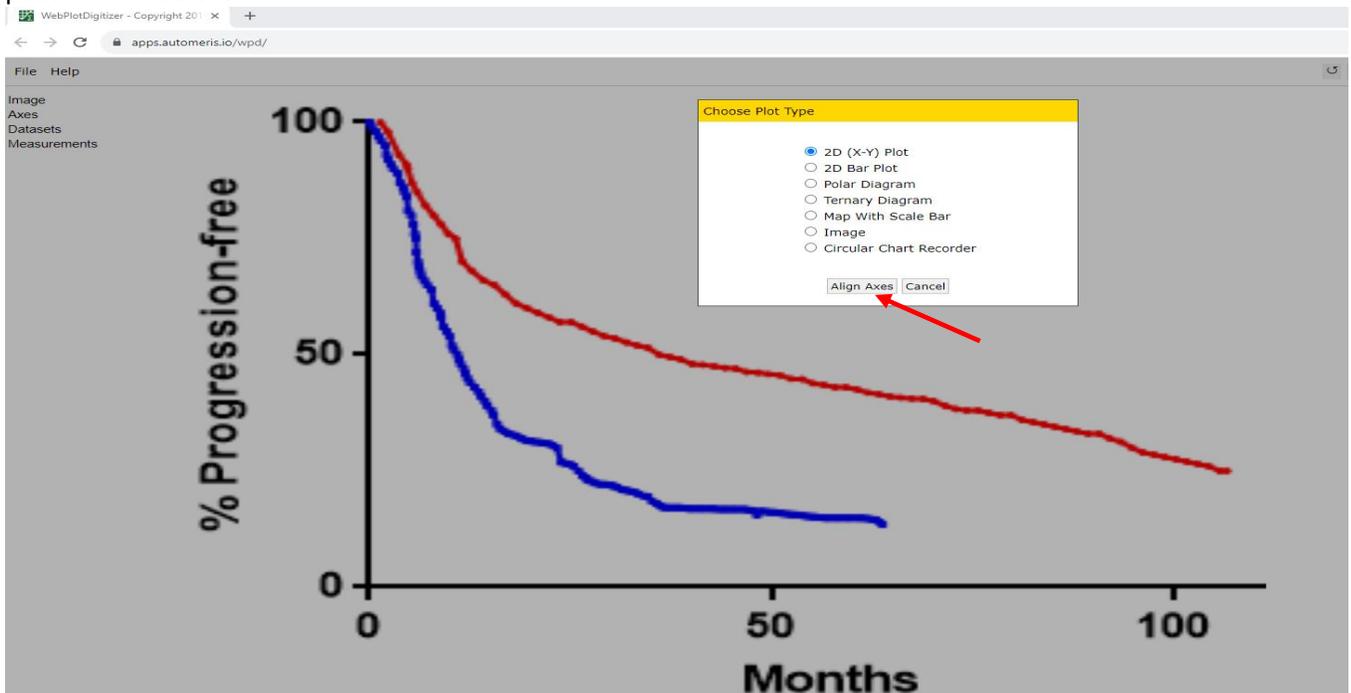
6. Go to files where PNG images are stored and click on the relevant PNG file:

Name	Status	Date modified	Type	Size
old	✓	2023-09-19 5:48 PM	File folder	
Appendix-Population survival kinetics of ...	↻	2023-09-20 9:43 AM	Microsoft Word D...	561 KB
Curable tumors population kinetics- with...	↻	2023-09-19 5:48 PM	Microsoft Word D...	273 KB
sample curves	✓	2023-09-19 7:02 PM	PNG File	12 KB
Table 1	✓	2023-09-10 11:08 AM	Microsoft Word D...	19 KB

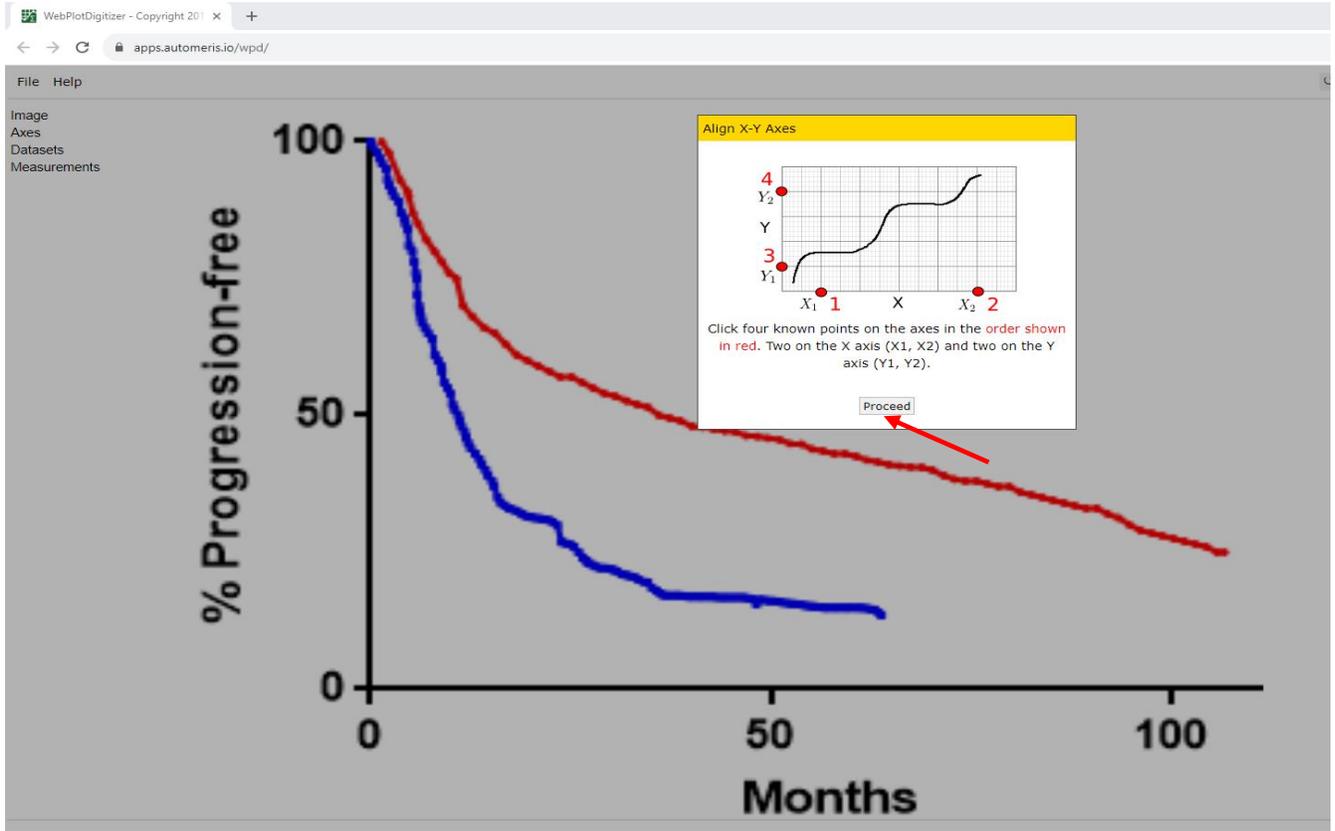
7. Our sample PNG file then appears:



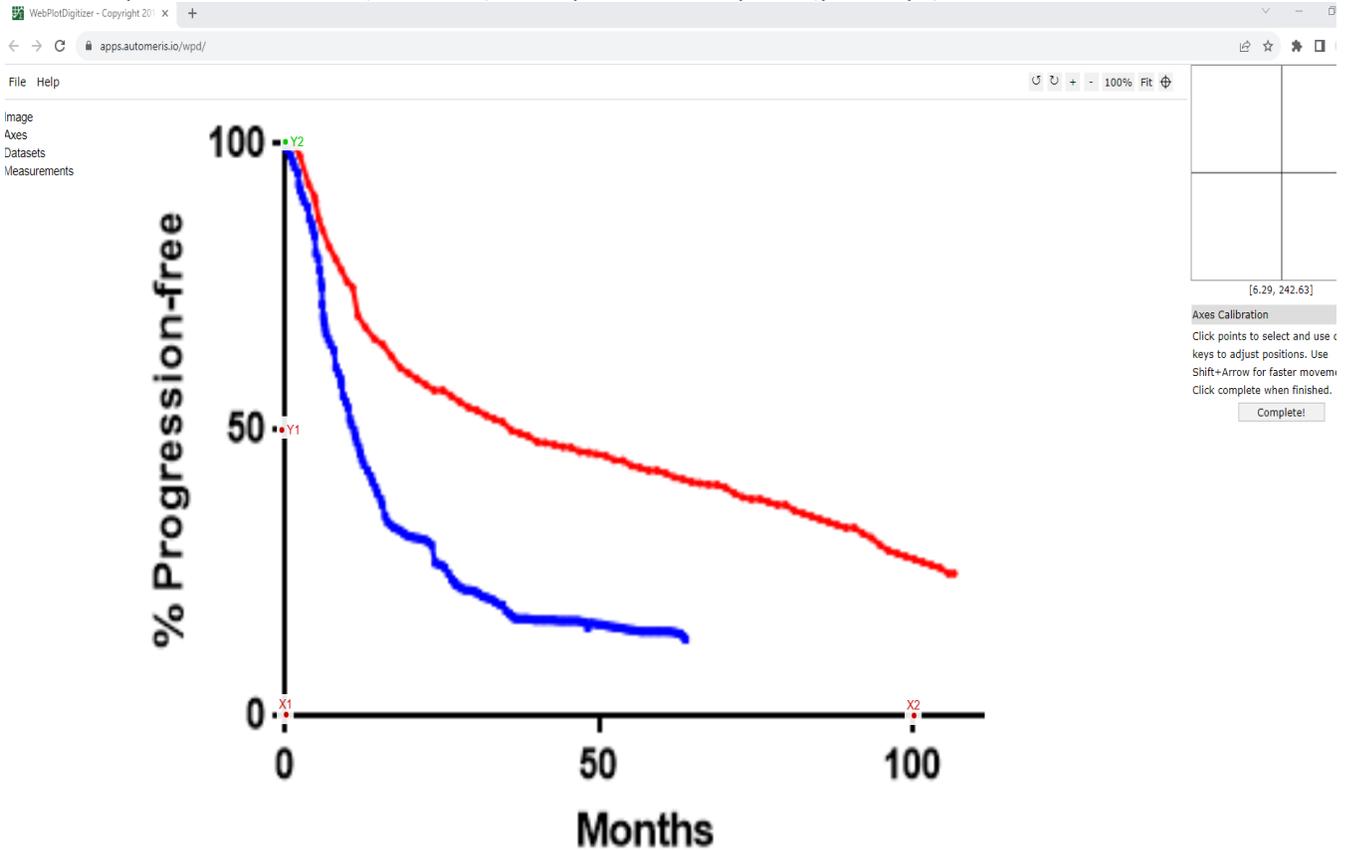
8. Click on "Align Axes". This will set the scale that permits the program to define the proper co-ordinates for each point on the curve.



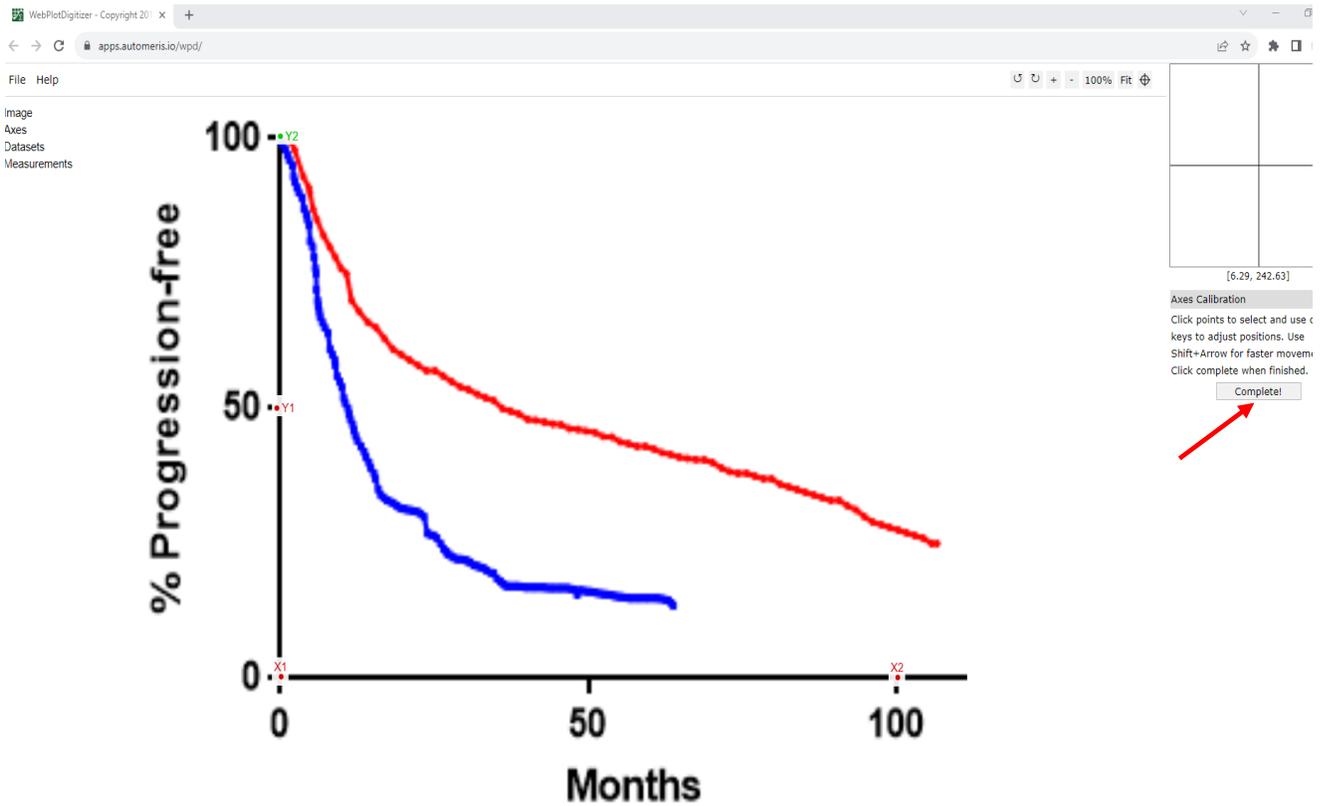
9. Click on "Proceed"



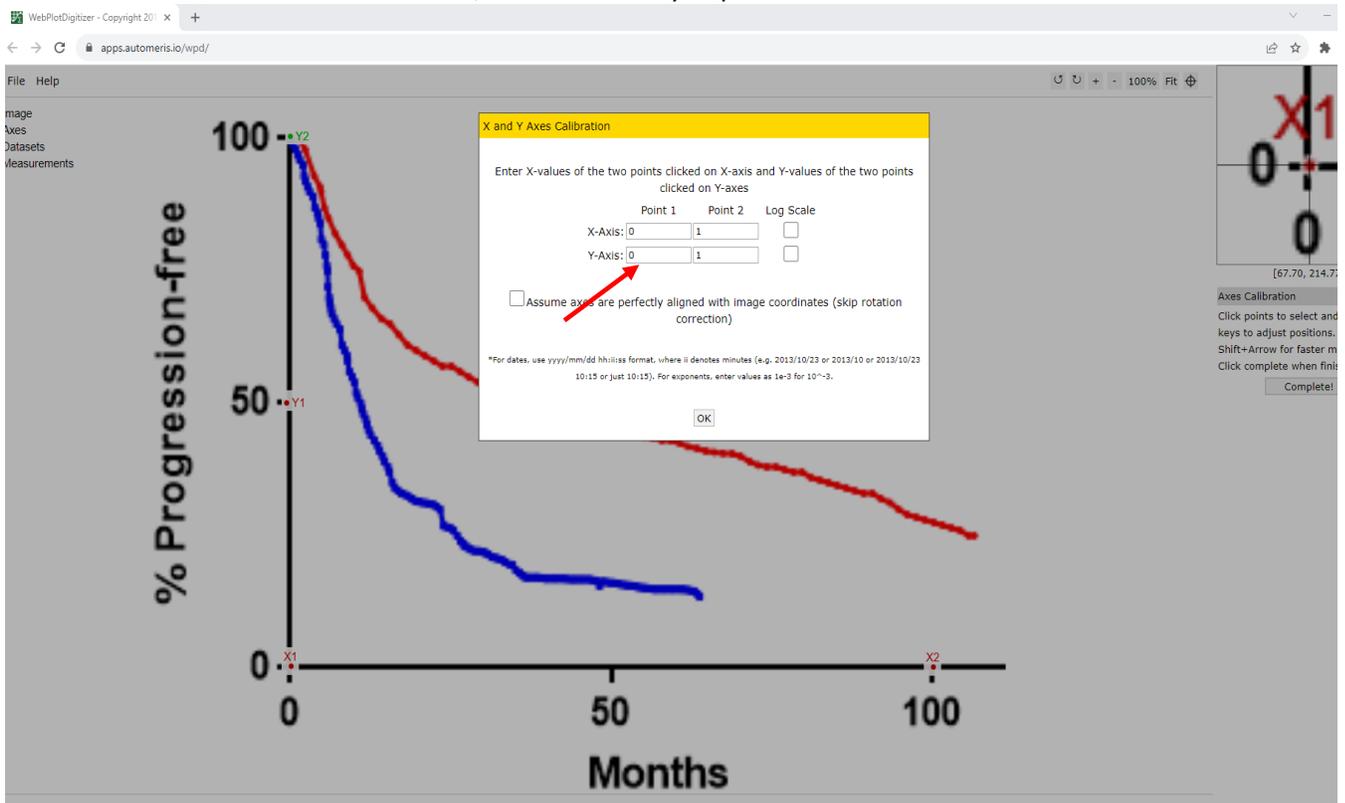
10. Click on 2 points on the x-axis (x1 and x2) and 2 points on the y-axis (y1 and y2):



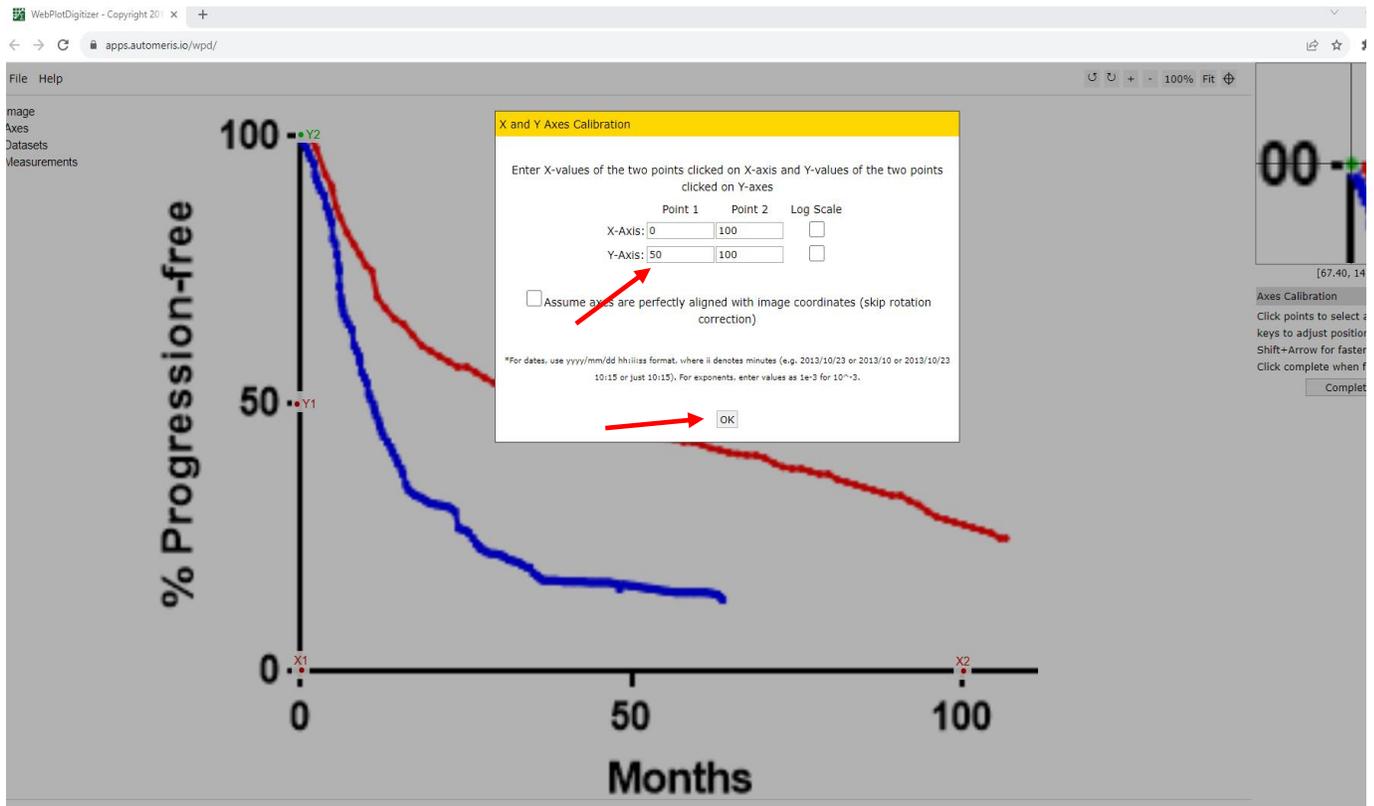
11. Click on "complete":



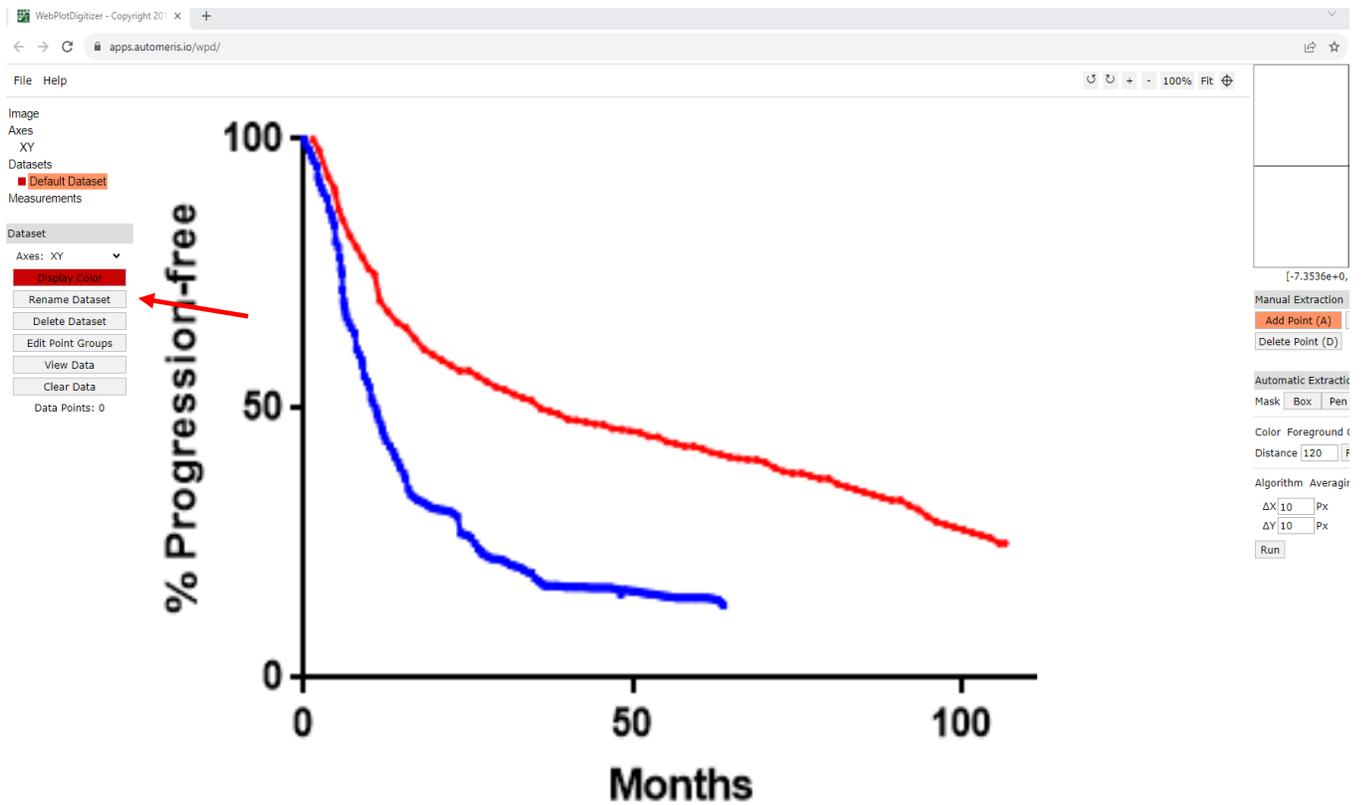
12. Fill in the values for Point 1 and Point 2, based on what you picked:



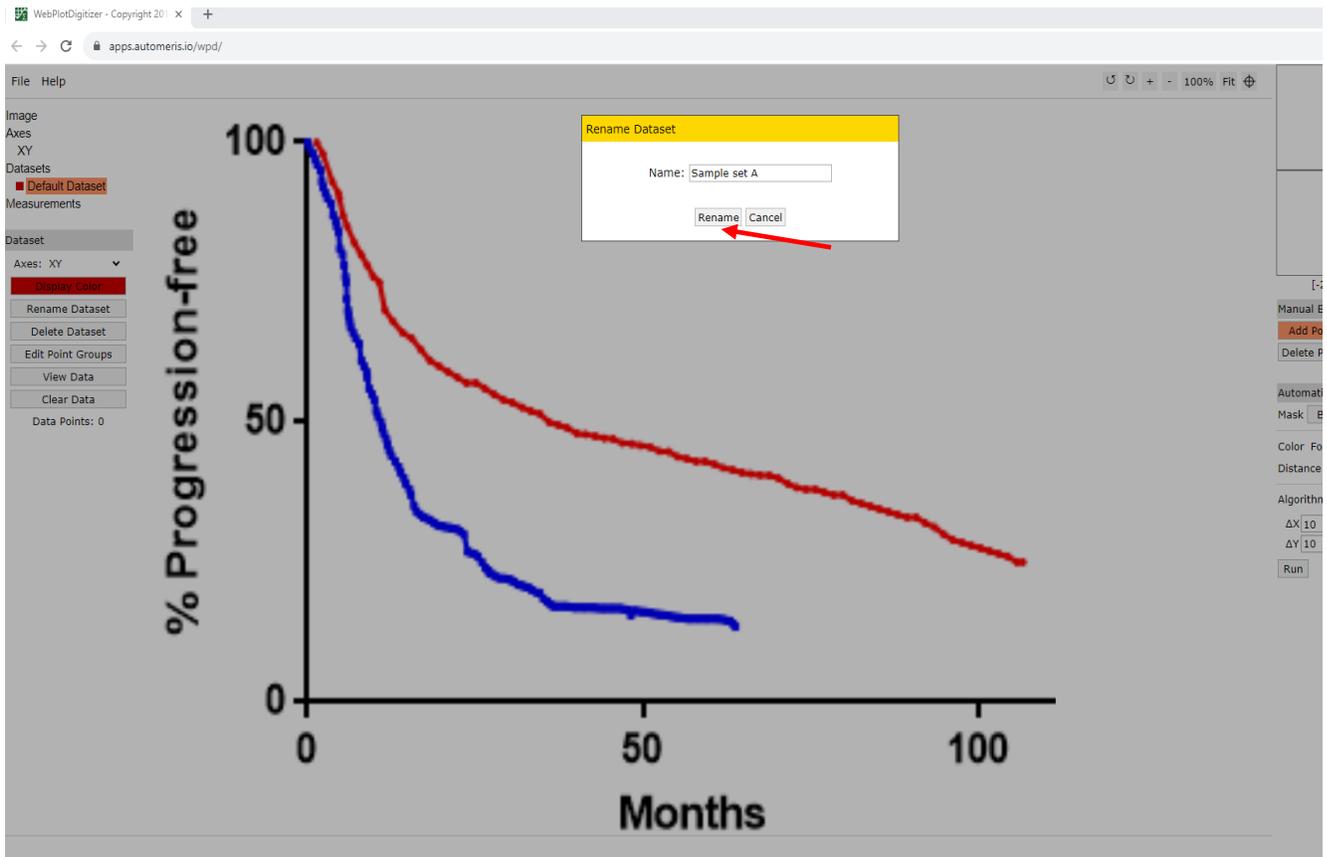
13. After the correct values have been inserted, click OK:



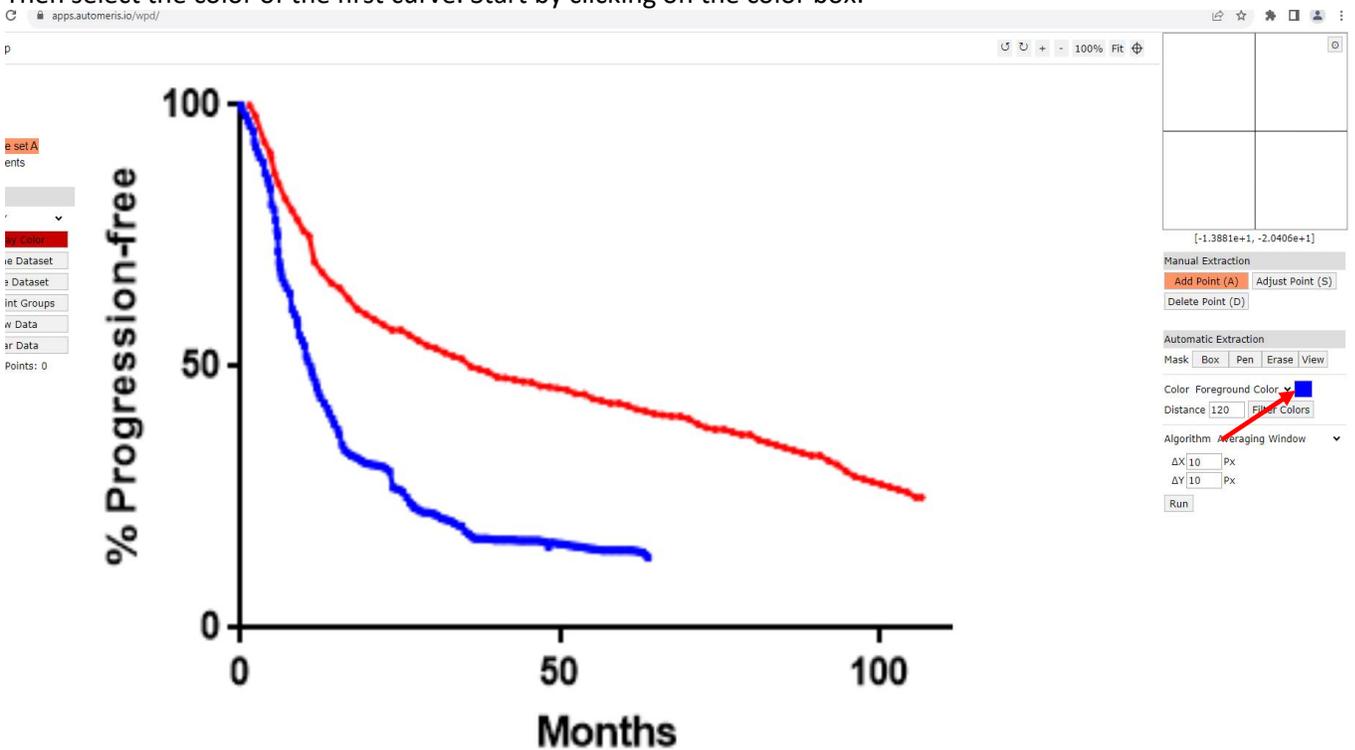
14. Rename the dataset, based on which curve you will analyze next.



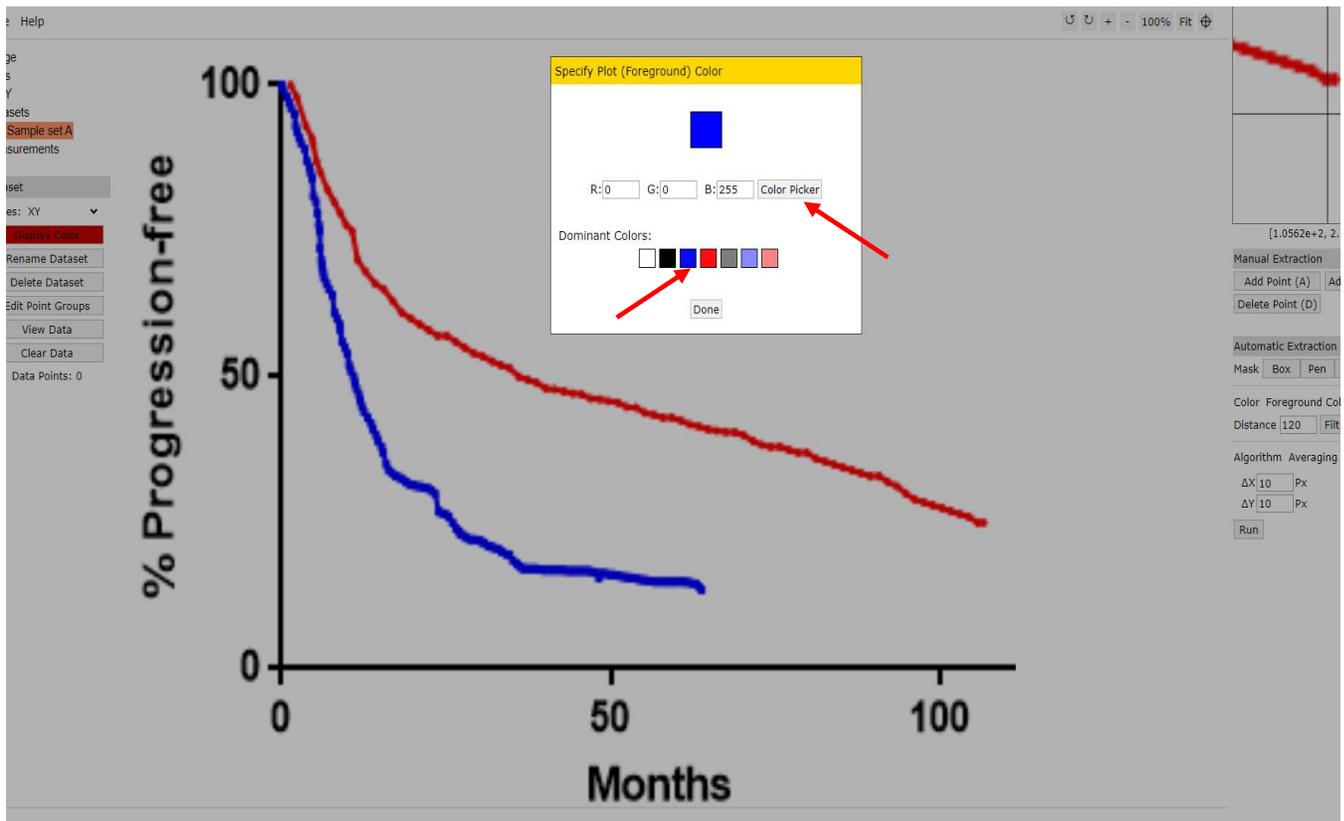
15. We will call the blue curve "Sample set A". Insert that name in the box, then hit "Rename":



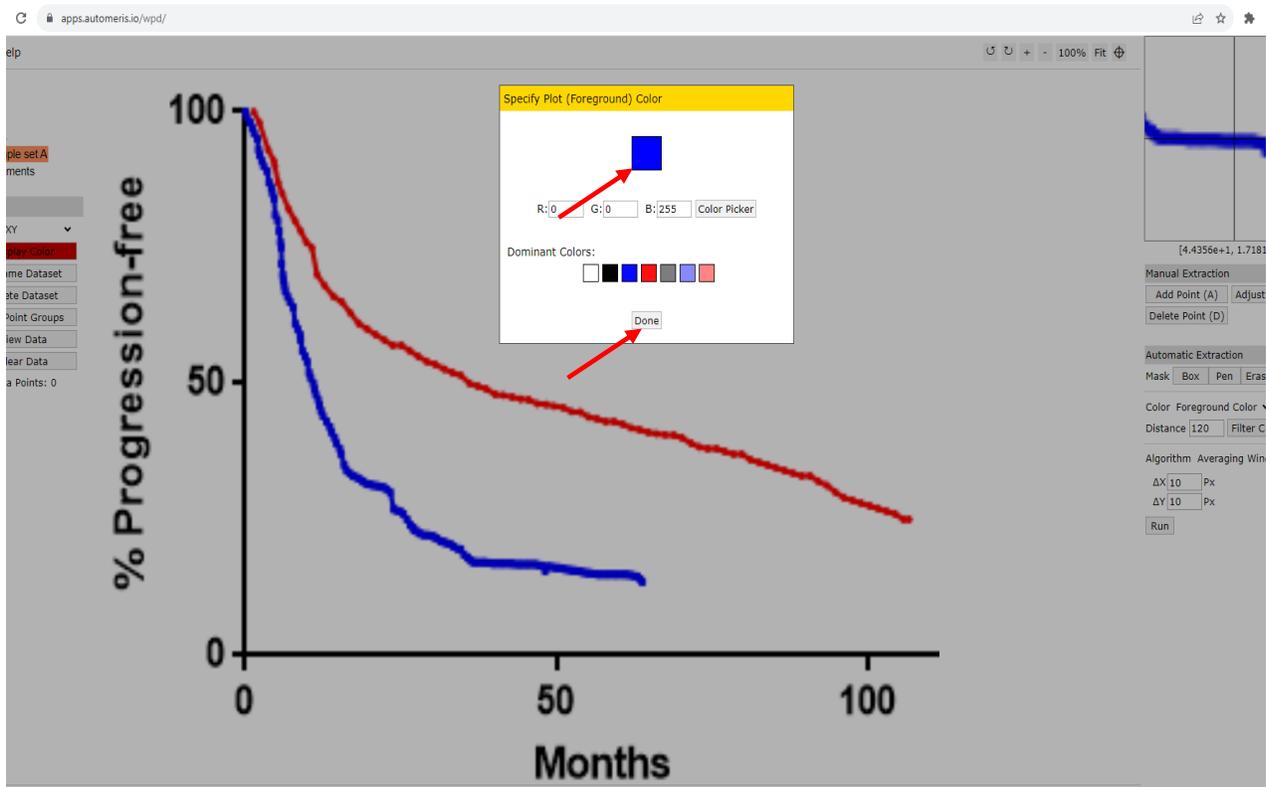
16. Then select the color of the first curve. Start by clicking on the color box:



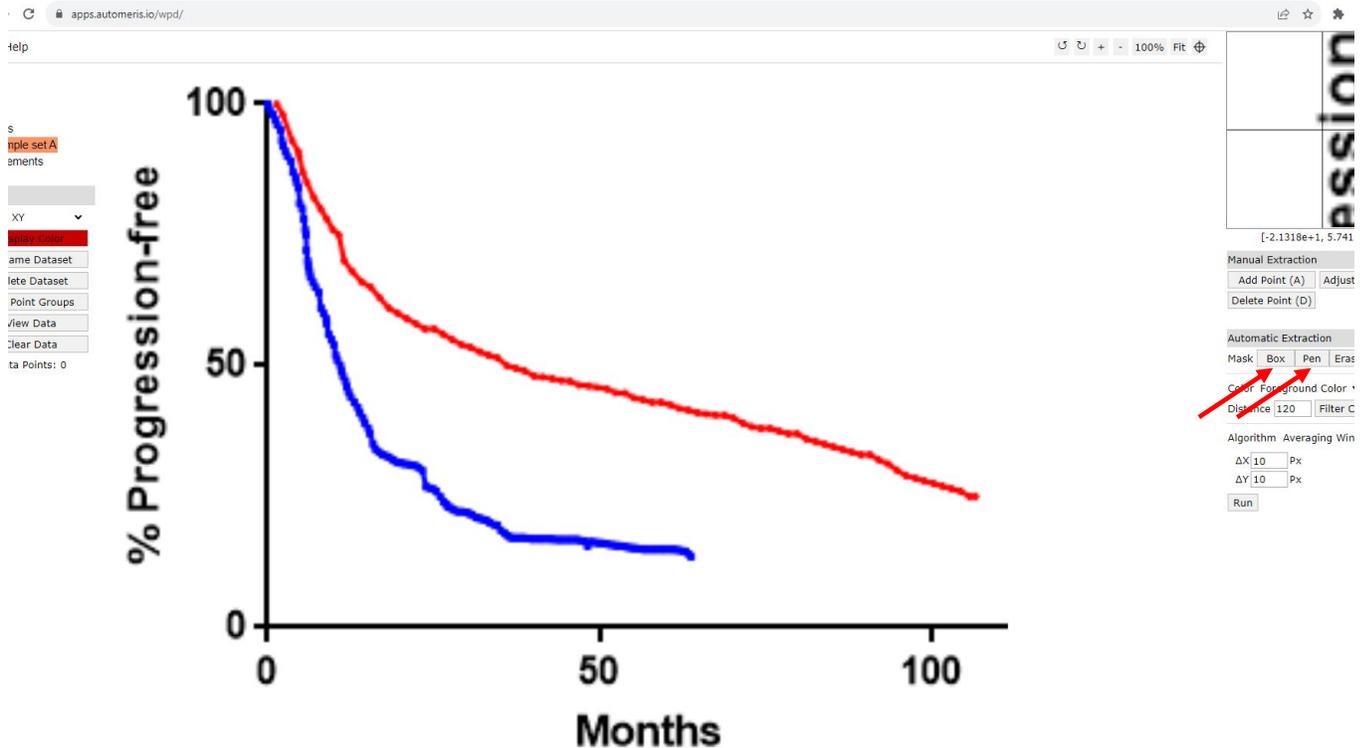
17. Then click on either the correct color as identified by the program (in this case, the blue option, which is also the program's default color), or else click on "Color Picker" to specifically target the color of one curve if you are not happy with the options offered by the program:



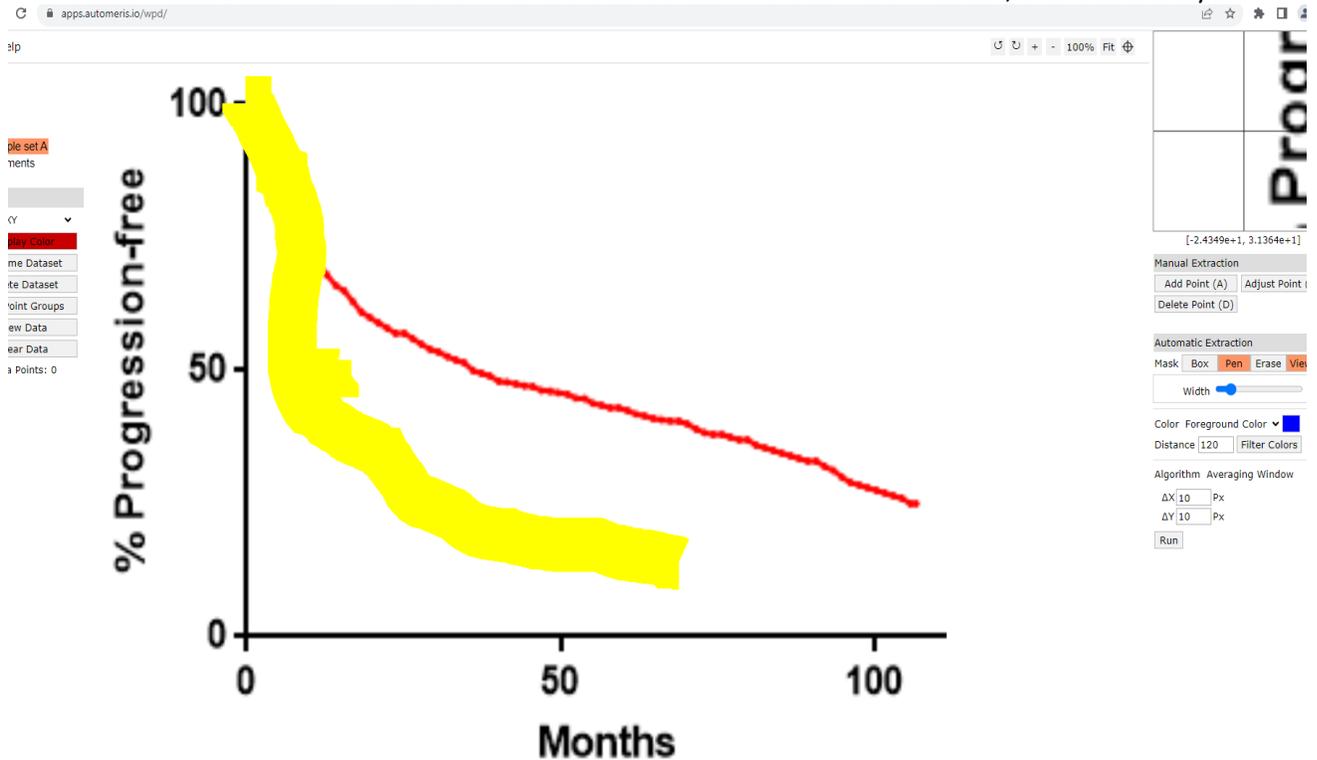
18. If you select “Color Picker”, put the cursor directly over the curve of interest (in this case, the blue curve) and hit enter. The color of interest will then appear in the upper box (although it was already there in this particular example since it is the program default color). Then hit “Done”.



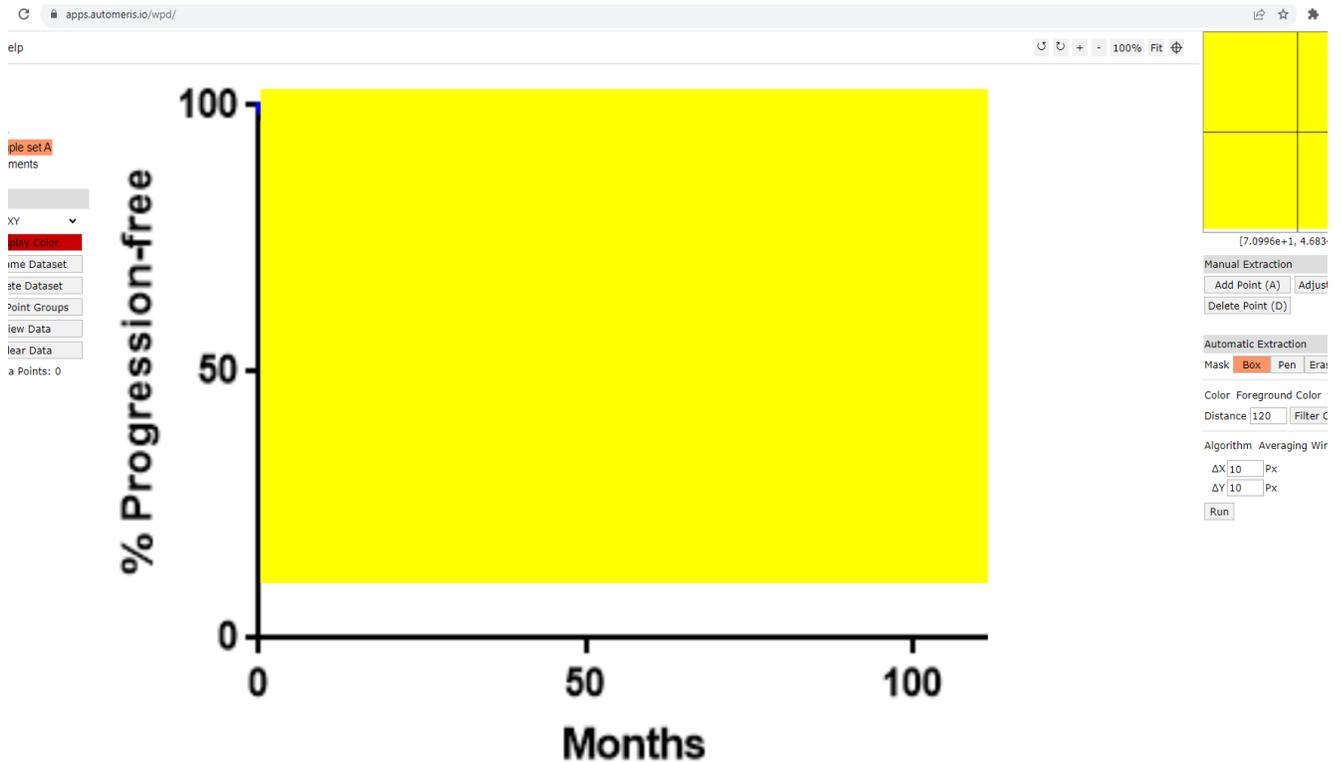
19. Then click on either “Pen” (which is most useful if different curves have similar colors) or “Box” (which can be used if there are no other factors on the graph that are similar to the color that you picked).



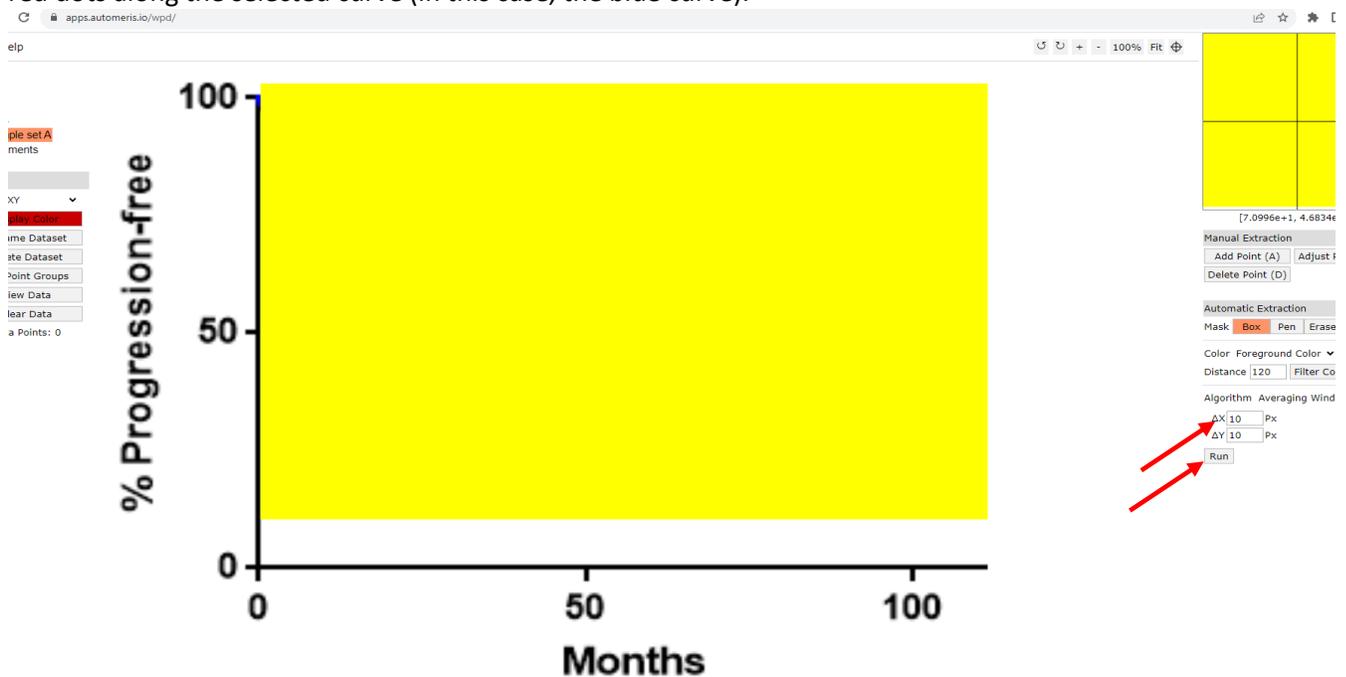
20. In this case we selected "Pen". You then move the cursor down the curve of interest, and it colors it yellow.



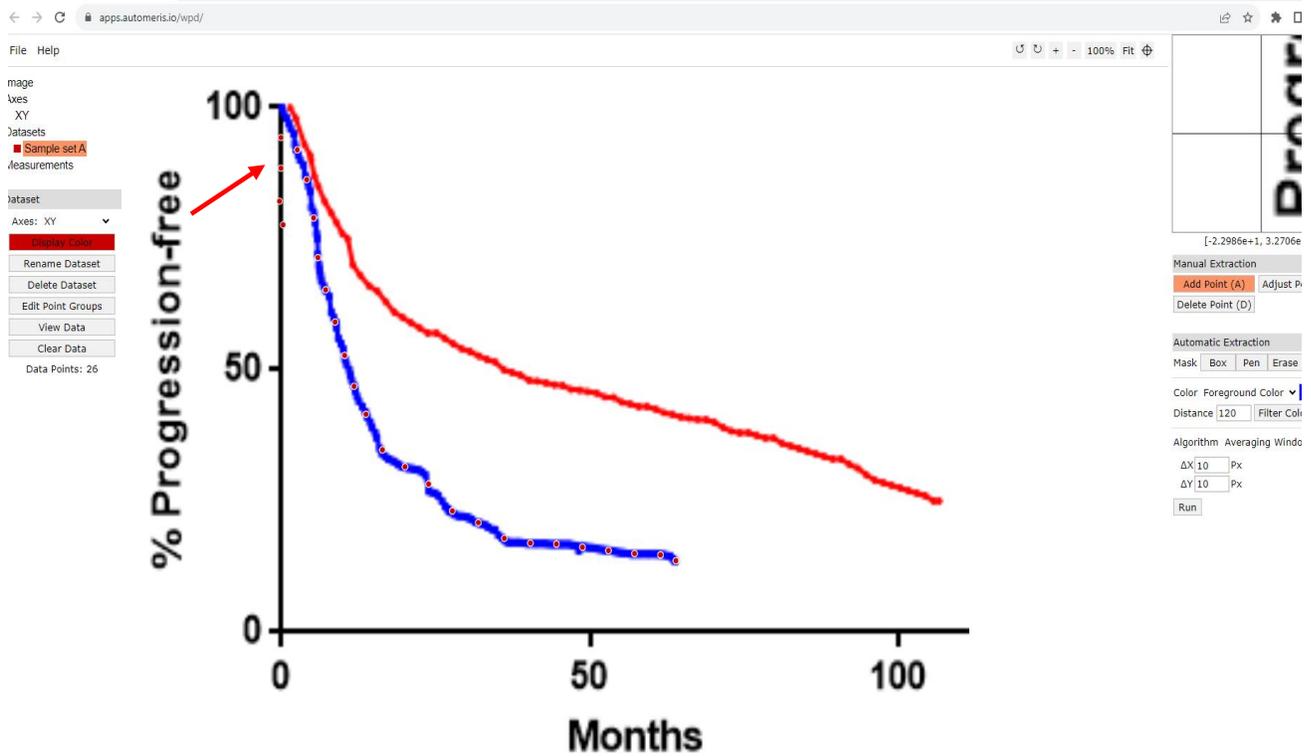
21. If we instead select "Box", we can move the cursor over the entire area of interest, and it will select it all. This approach is a bit more efficient but can result in erroneous entries if there are other structures similar in color to the curve of interest.



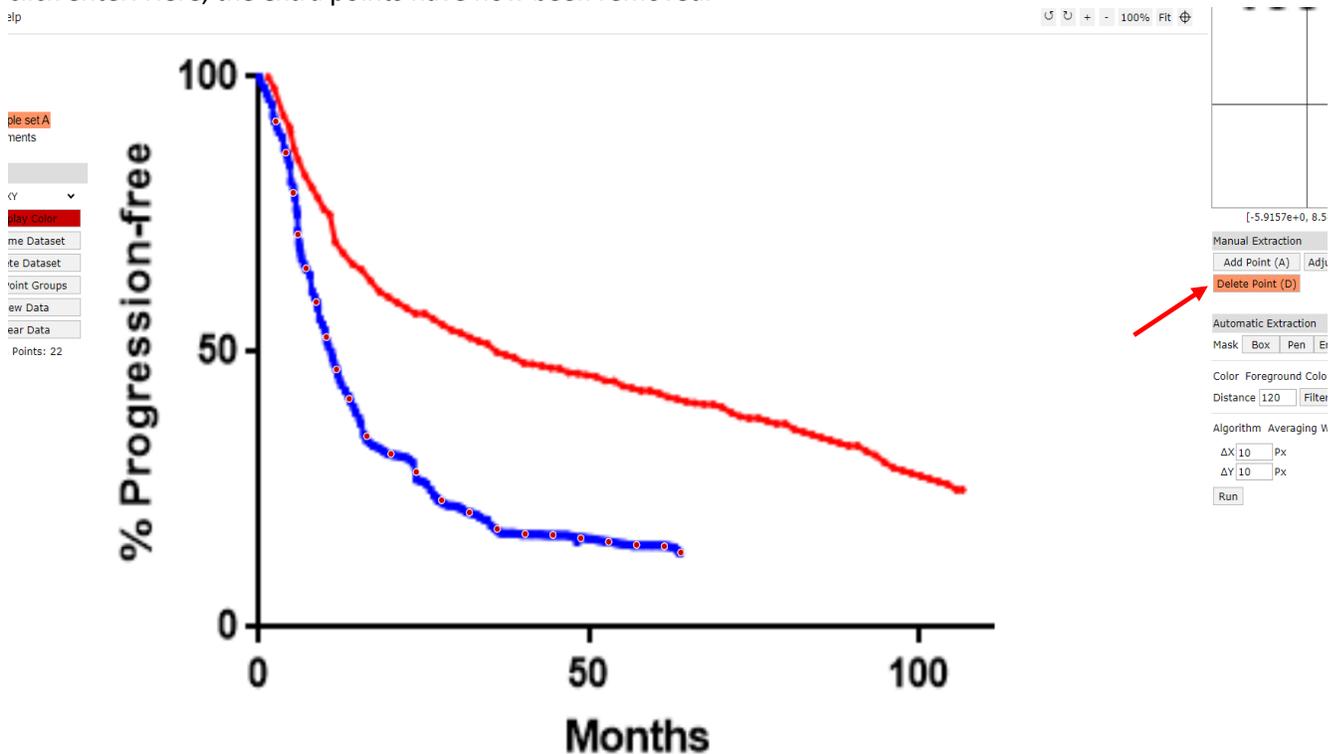
22. We could then elect to adjust the pixel size. The default setting is 10. Setting it smaller means data points will be closer together and setting it larger means they will be further apart. Then hit “Run” and the program will put red dots along the selected curve (in this case, the blue curve).



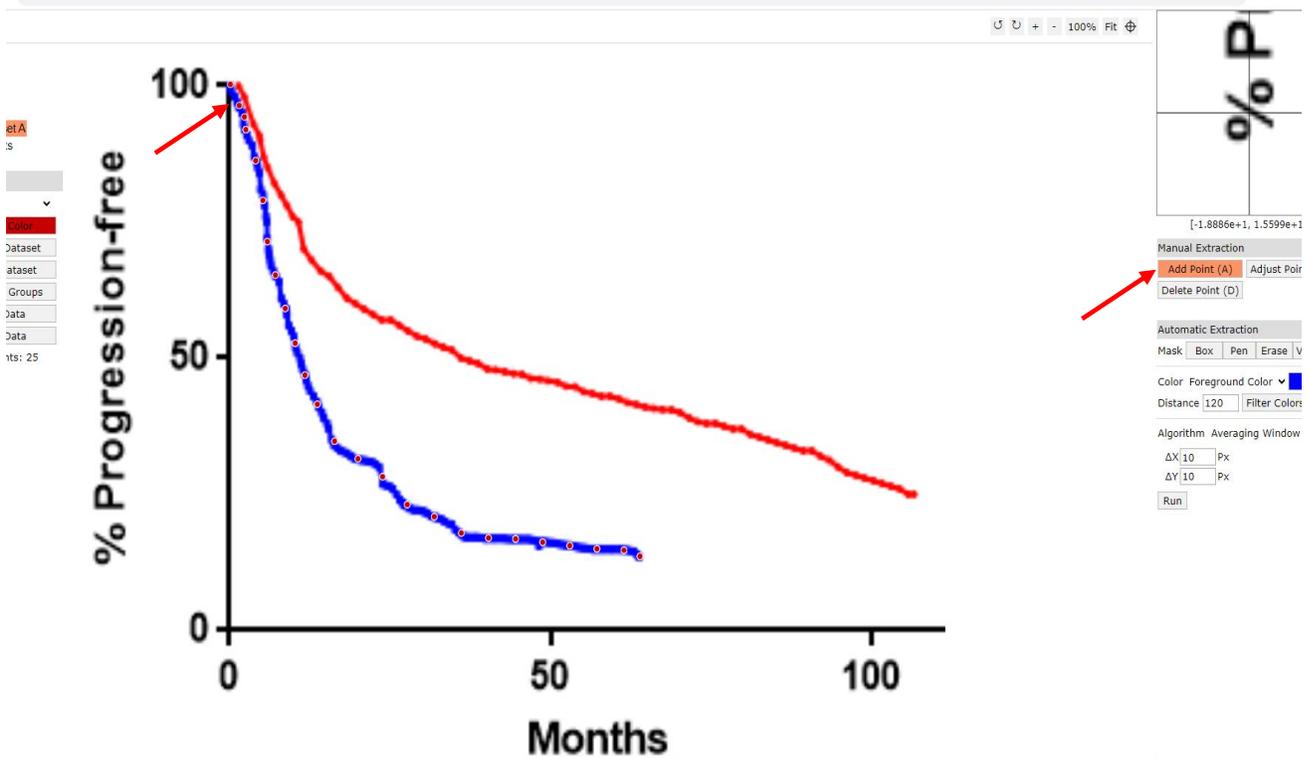
23. The data points appear as new red points along the curve. In this case, 4 points were added erroneously to the black y axis, and no points were added to the upper part of the blue curve.



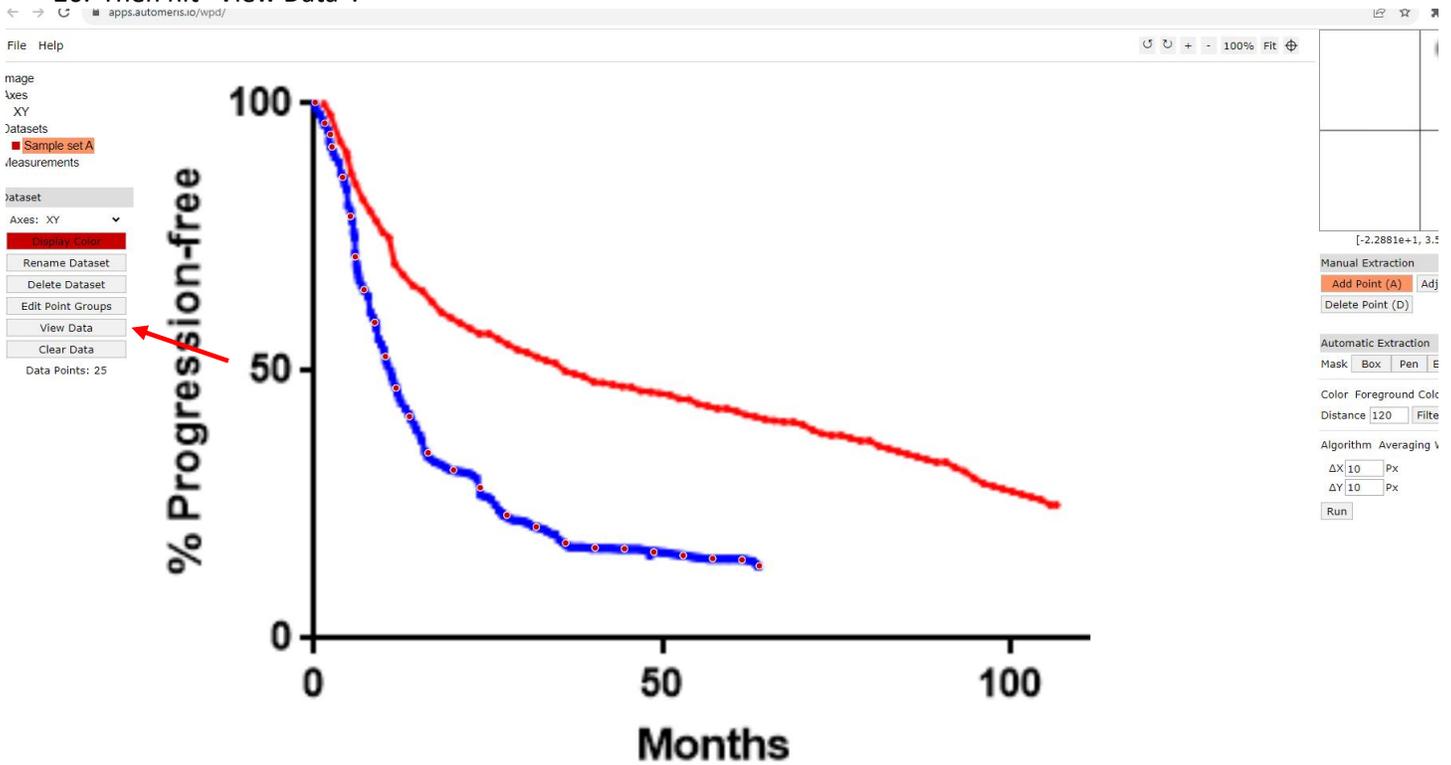
24. To remove the erroneous points, click on "Delete Point", then place the cursor near the erroneous point and click enter. Here, the extra points have now been removed.



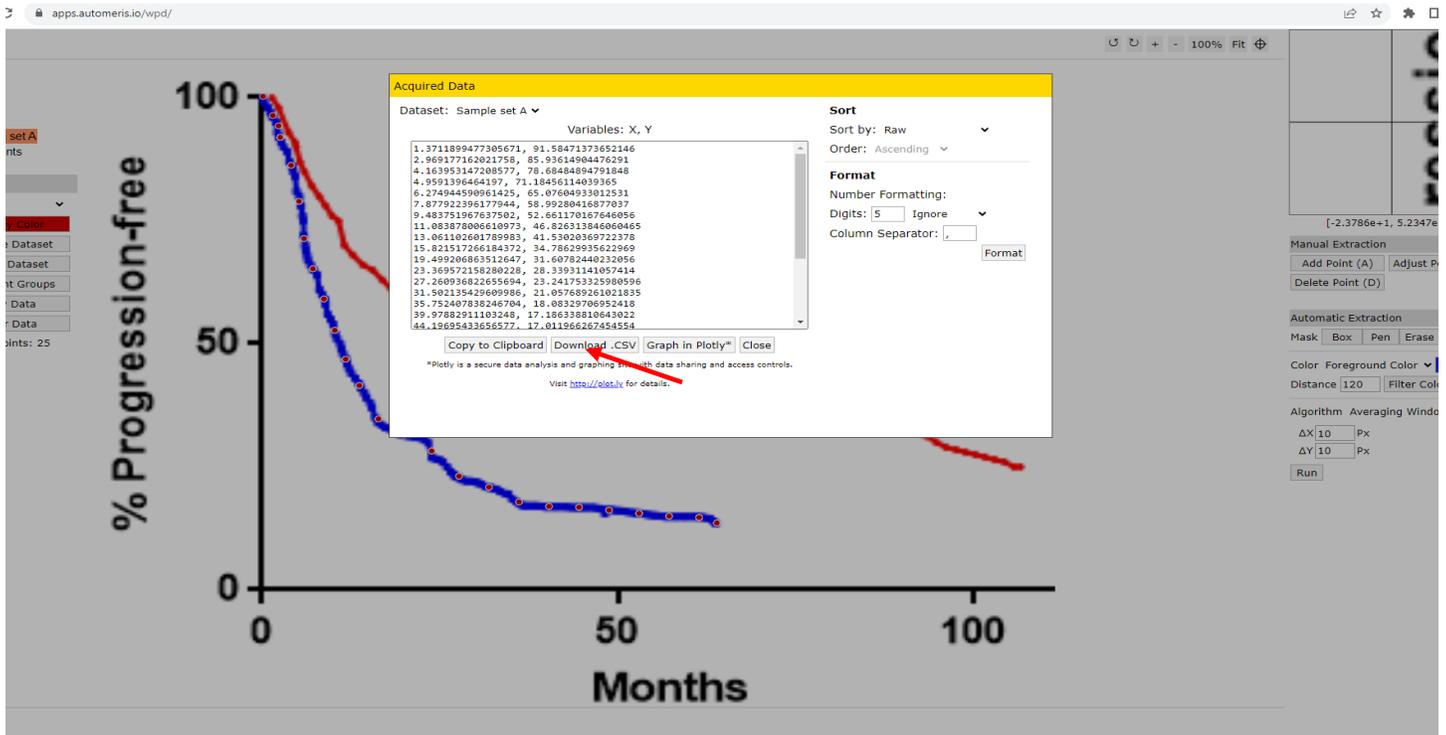
25. To add missing points, click on "Add Point". Then place the cursor where you want a point added and click enter. We have now added 3 points to the upper part of the blue curve.



26. Then hit "View Data".



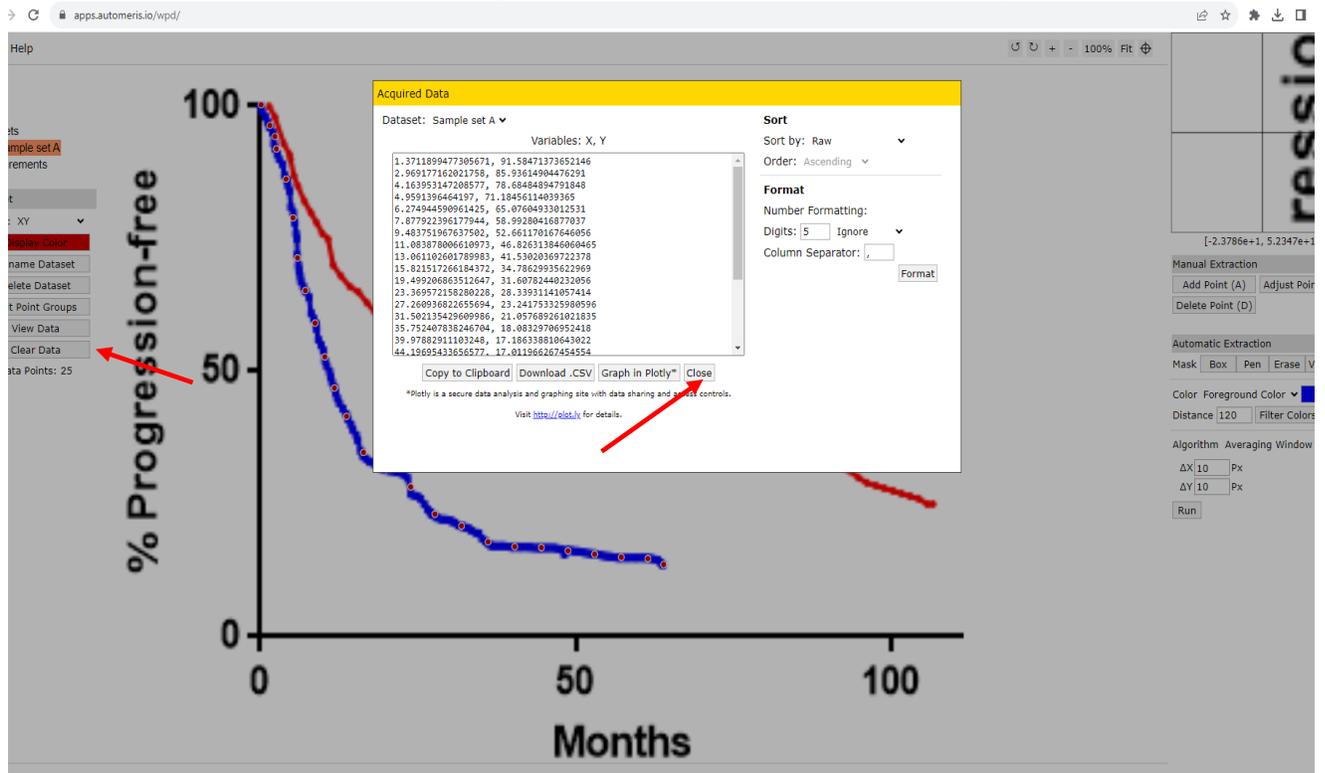
27. After hitting "View Data", the data co-ordinates are displayed. Once they are displayed, hit "Download .CSV".



28. The downloaded .CSV data are displayed below. They can then be saved as an Excel file, and the data can be sorted by column A (time in months). We correct to 0 any time points that may have been reported as being slightly less than 0, and we correct to 100% any survival values that may have been reported as being slightly above 100%. These data can now be used with GraphPad Prism.

	A	B	C	D
1	1.37119	91.58471		
2	2.969177	85.93615		
3	4.163953	78.68485		
4	4.95914	71.18456		
5	6.274945	65.07605		
6	7.877922	58.9928		
7	9.483752	52.66117		
8	11.08388	46.82631		
9	13.0611	41.5302		
10	15.82152	34.7863		
11	19.49921	31.60782		
12	23.36957	28.33931		
13	27.26094	23.24175		
14	31.50214	21.05769		
15	35.75241	18.0833		
16	39.97883	17.18634		
17	44.19695	17.01197		
18	48.42001	16.40856		
19	52.64332	15.78257		
20	56.86585	15.22432		
21	61.08475	14.98221		
22	63.58889	13.86817		
23	0	99.85136		
24	0.28258	95.98443		
25	1.110158	93.90233		
26				
27				
28				
29				
30				

29. Once data for Sample Set A have been saved, the data set can be closed. When “Clear Data” is clicked, the data for Sample Set A are cleared. The Dataset can then be renamed (eg, Sample Set B), the color of the other curve (red) can be selected using the Color Picker, and the process can be repeated to obtain the data co-ordinates for the red curve. Once familiar with the program, it typically takes 10-20 minutes to digitize a curve.



How to replot data on a log-linear curve and perform exponential decay nonlinear regression analysis:

1. We typically use GraphPad Prism Version 7 for these analyses, although other nonlinear regression analysis programs could also potentially be used. We have not compared other programs to GraphPad Prism.
2. After GraphPad is opened, click on "XY" in the left-hand column, and then click on "Y: enter and plot a single Y value for each point", then on "Create".

The screenshot shows the GraphPad Prism interface with the 'New Data Table and Graph' dialog box open. The dialog box is titled 'XY tables: Each point is defined by an X and Y coordinate'. It contains a table with the following structure:

	X	A			B		
Minutes		Control	Treated				
	X	A:Y1	A:Y2	A:Y3	B:Y1	B:Y2	B:Y3
1	Title						
2	Title						
3	Title						

The dialog also includes a 'Y:' section with the following options:

- Numbers
- Numbers with error values to plot horizontal error bars
- Dates
- Elapsed times
- Y: Enter and plot a single Y value for each point
- Enter 2 replicate values in side-by-side subcolumns
- Enter and plot error values already calculated elsewhere

The 'Use tutorial data:' section includes the following options:

- Linear regression - Compare slopes
- Nonlinear regression -- One phase exponential decay
- Dose-response - X is log(dose)
- Interpolate unknowns from a linear standard curve
- Correlation
- Entering dates into the X column
- Entering elapsed times into the X column
- More tutorial data...

At the bottom of the dialog, there are buttons for 'Prism Tips', 'Free update available', 'Cancel', and 'Create'. A red arrow points to the 'Create' button.

- Enter the digitized survival data in GraphPad. The “x” column is time in months and the “y” column is proportion of patients who are event-free (eg, alive) at that time. Click on “Data 1” to name the data set, then click on “Analyze” to begin the analysis.

GraphPad Prism 7.04 - [Project2:Data 1]

File Edit View Insert Change Arrange Family Window Help

Prism File Sheet Undo Clipboard Analysis Change Import Draw Write Text

Prism File Sheet Undo Clipboard Analysis Change Import Draw Write Text

Family Search results Data Tables Data 1 Info Project info 1 Results Graphs Data 1 Layouts

Table format: XY		X	Group A	Group B	Group C	Group D	Group E	Group F
	X Title	Y Title						
1	Title	0.000000	99.85136					
2	Title	0.282580	95.98443					
3	Title	1.110158	93.90233					
4	Title	1.371190	91.58471					
5	Title	2.969177	85.93615					
6	Title	4.163953	78.68485					
7	Title	4.959140	71.18456					
8	Title	6.274945	65.07605					
9	Title	7.877922	58.99280					
10	Title	9.483752	52.66117					
11	Title	11.083880	46.82631					
12	Title	13.061100	41.53020					
13	Title	15.821520	34.78630					
14	Title	19.499210	31.60782					
15	Title	23.369570	28.33931					
16	Title	27.260940	23.24175					
17	Title	31.502140	21.05769					
18	Title	35.752410	18.08330					
19	Title	39.978830	17.18634					
20	Title	44.196950	17.01197					
21	Title	48.420010	16.40856					
22	Title	52.643320	15.78257					
23	Title	56.865850	15.22432					
24	Title	61.084750	14.98221					
25	Title	63.588890	13.86817					
26	Title							
27	Title							
28	Title							
29	Title							
30	Title							
31	Title							

4. We have named the dataset "Sample dataset A". Next, click on "Nonlinear regression" and then on "OK".

GraphPad Prism 7.04 - [Project2:Sample dataset A]

File Edit View Insert Change Arrange Family Window Help

Prism File Sheet Undo Clipboard Analysis Change Import Draw Write Text Export

Family
Search results
Data Tables
Sample dataset A
Info
Project info 1
Results
Graphs
Sample dataset A
Layouts

Table format:	X	Group A	Group B	Group C	Group D	Group E	Group F	Group G	G
XY	X Title	Data Set-A	Title	Title	Title	Title	Title	Title	
	X	Y	Y	Y	Y	Y	Y	Y	
1	Title	0.000000	99.86136						
2	Title	0.282580							
3	Title	1.110158							
4	Title	1.371190							
5	Title	2.969177							
6	Title	4.163953							
7	Title	4.959140							
8	Title	6.274945							
9	Title	7.877922							
10	Title	9.483752							
11	Title	11.083880							
12	Title	13.061100							
13	Title	15.821520							
14	Title	19.499210							
15	Title	23.369570							
16	Title	27.260940							
17	Title	31.502140							
18	Title	35.752410							
19	Title	39.978830							
20	Title	44.196950							
21	Title	48.420010							
22	Title	52.643320							
23	Title	56.865850							
24	Title	61.084750							
25	Title	63.588890							
26	Title								
27	Title								
28	Title								
29	Title								
30	Title								
31	Title								

Analyze Data

Built-in analysis

Which analysis?

- Transform, Normalize...
 - Transform
 - Transform Concentrations (X)
 - Normalize
 - Prune rows
 - Remove baseline and column math
 - Transpose X and Y
 - Fraction of total
- XY analyses
 - Nonlinear regression (curve fit)
 - Linear regression
 - Fit spline/LOWESS
 - Smooth, differentiate or integrate curve
 - Area under curve
 - Deming (Model II) linear regression
 - Column statistics
 - Row means with SD or SEM
 - Correlation
 - Interpolate a standard curve
- Column analyses
- Grouped analyses
- Contingency table analyses

Analyze which data sets?

A

When you analyze tables or graphs with more than one data set, use this space to select which data set(s) to analyze.

Select All Deselect All

Help Cancel OK

5. Click on "One phase decay" and then on "Constrain".

The screenshot displays the GraphPad Prism interface. On the left, a navigation pane shows 'Sample dataset A' selected. The main window shows a data table with the following columns: X, Group A, Group B, Group C, Group D, Group E, Group F, Group G, and Group H. The data points are as follows:

Row	X	Y
1	0.000000	Title
2	0.282580	Title
3	1.110158	Title
4	1.371190	Title
5	2.969177	Title
6	4.163953	Title
7	4.959140	Title
8	6.274945	Title
9	7.877922	Title
10	9.483752	Title
11	11.083880	Title
12	13.061100	Title
13	15.821520	Title
14	19.499210	Title
15	23.369570	Title
16	27.260940	Title
17	31.502140	Title
18	35.752410	Title
19	39.978830	Title
20	44.196950	Title
21	48.420010	Title
22	52.643320	Title
23	56.865850	Title
24	61.084750	Title
25	63.588890	Title
26		
27		
28		
29		
30		

The 'Parameters: Nonlinear Regression' dialog box is open, with the 'Constrain' tab selected. Under 'Choose an equation', the 'Standard curves to interpolate' category is expanded, and 'One phase decay' is selected. The 'Fitting method' section has 'Least squares (ordinary) fit' selected. The 'Interpolate' section has 'Interpolate unknowns from standard curve' checked, with a 'Confidence interval' dropdown set to 'None'. Buttons for 'Learn', 'Cancel', and 'OK' are visible at the bottom of the dialog.

6. For Y0, change constraints from “No constraint” to “constraint equal to 100” and for Plateau, change constraints from “No constraint” to “constraint equal to 0”, then hit “OK”.

Parameters: Nonlinear Regression

Parameter Name	Constraint Type	Value	Hook
Y0	Constant equal to	100	
Plateau	Constant equal to	0	
K	Must be greater than	0	

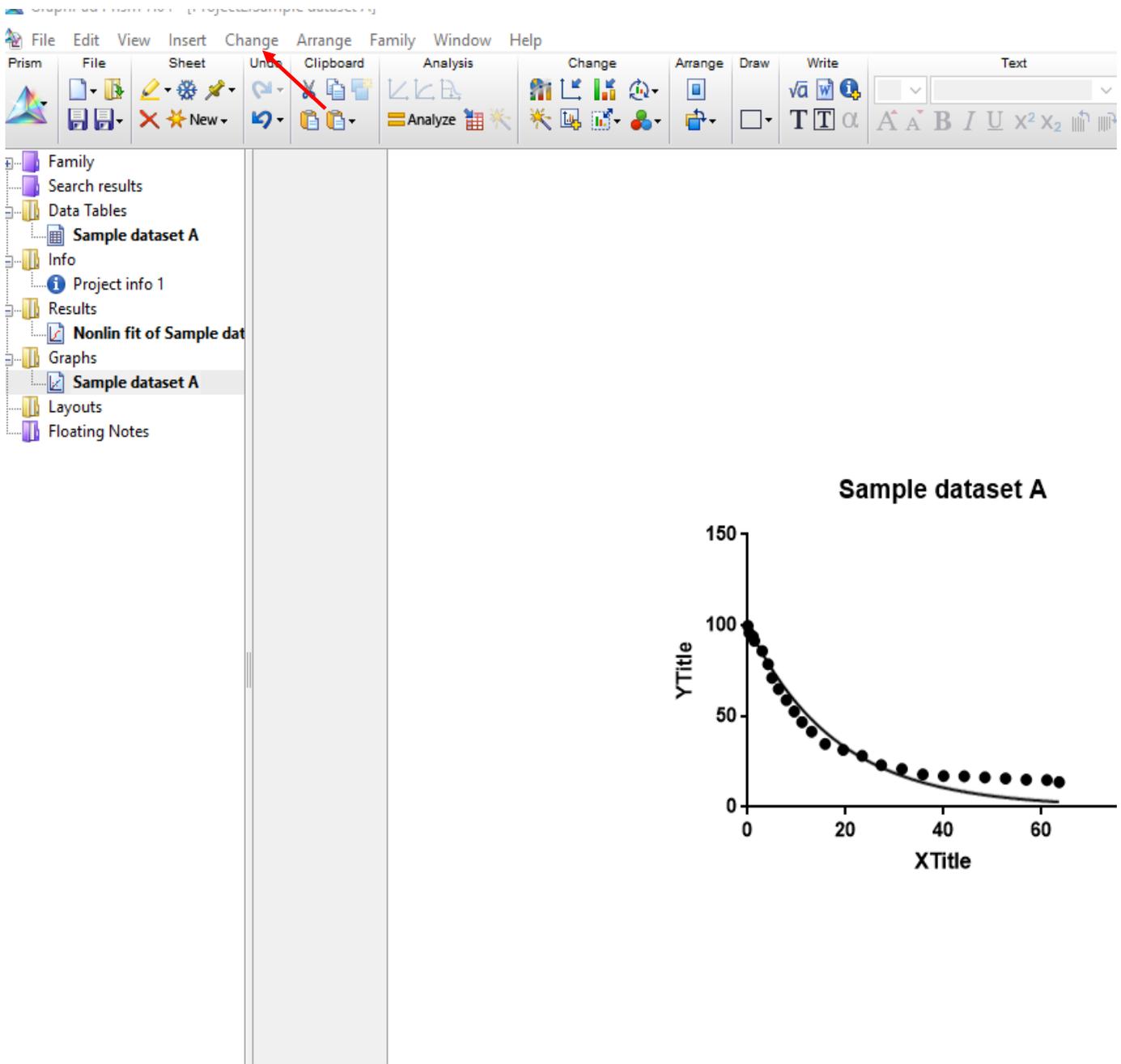
Constrain one parameter relative to another

must be greater than 1 times

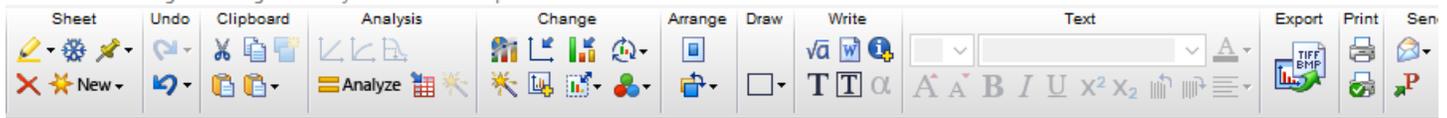
must be greater than 1 times

Learn Cancel OK

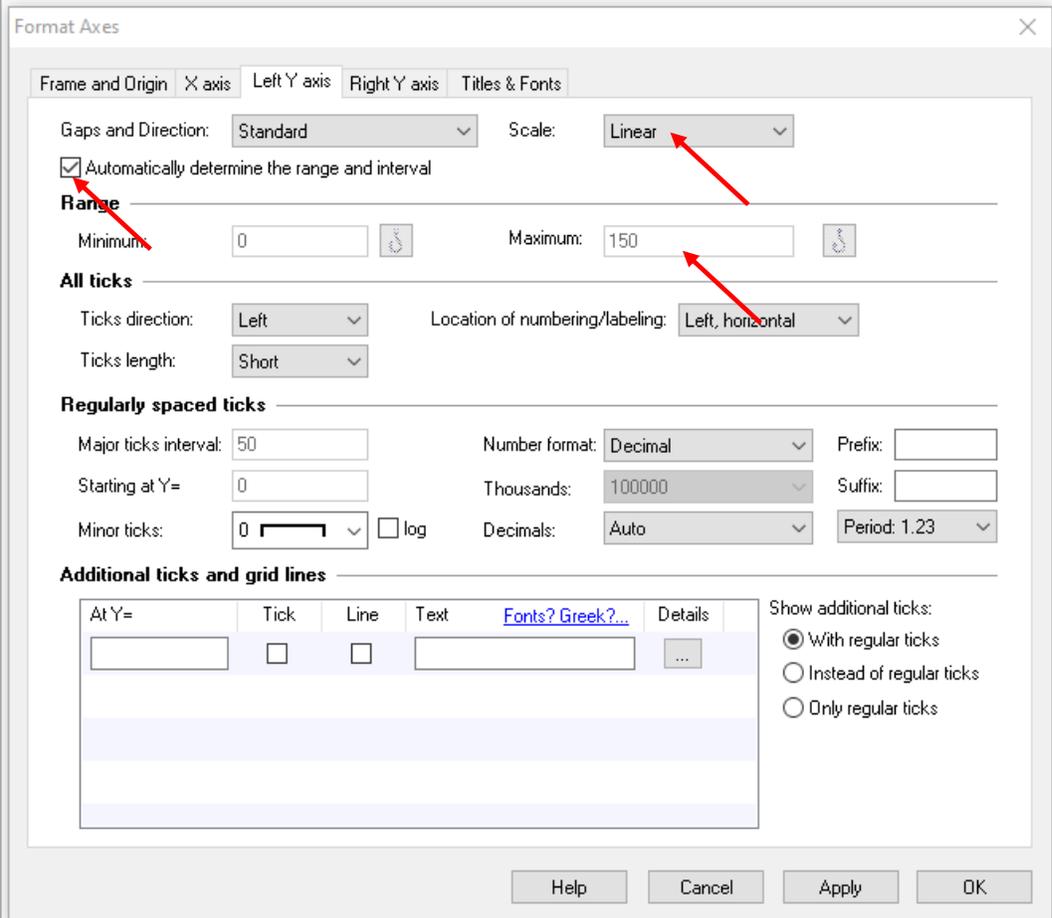
8. These are the data plotted on a linear-linear scale. Click on “Change” on the top line to convert it to log-linear.



9. On the drop-down menu, click on “Y axis (left)”. From the pull-down menu for “Scale”, change “Linear” to “Log 10”. Click on “Automatically determine the range and interval” to turn it off. Then set the “Maximum” at 100. Then click “OK”.



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dataset A
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dataset A
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Format Axes

Frame and Origin | X axis | **Left Y axis** | Right Y axis | Titles & Fonts

Gaps and Direction: Standard | Scale: Log 10

Automatically determine the range and interval

Range

Minimum: 1 | Maximum: 100

All ticks

Ticks direction: Left | Location of numbering/labeling: Left, horizontal

Ticks length: Short

Regularly spaced ticks

Major ticks interval: 1 powers of 10 | Number format: Antilog | Prefix: | Starting at Y= 1 | Thousands: 100000 | Suffix: | Minor ticks: 9 log | Decimals: 0.01, 0.1, 1, 10, ... | Period: 1.23

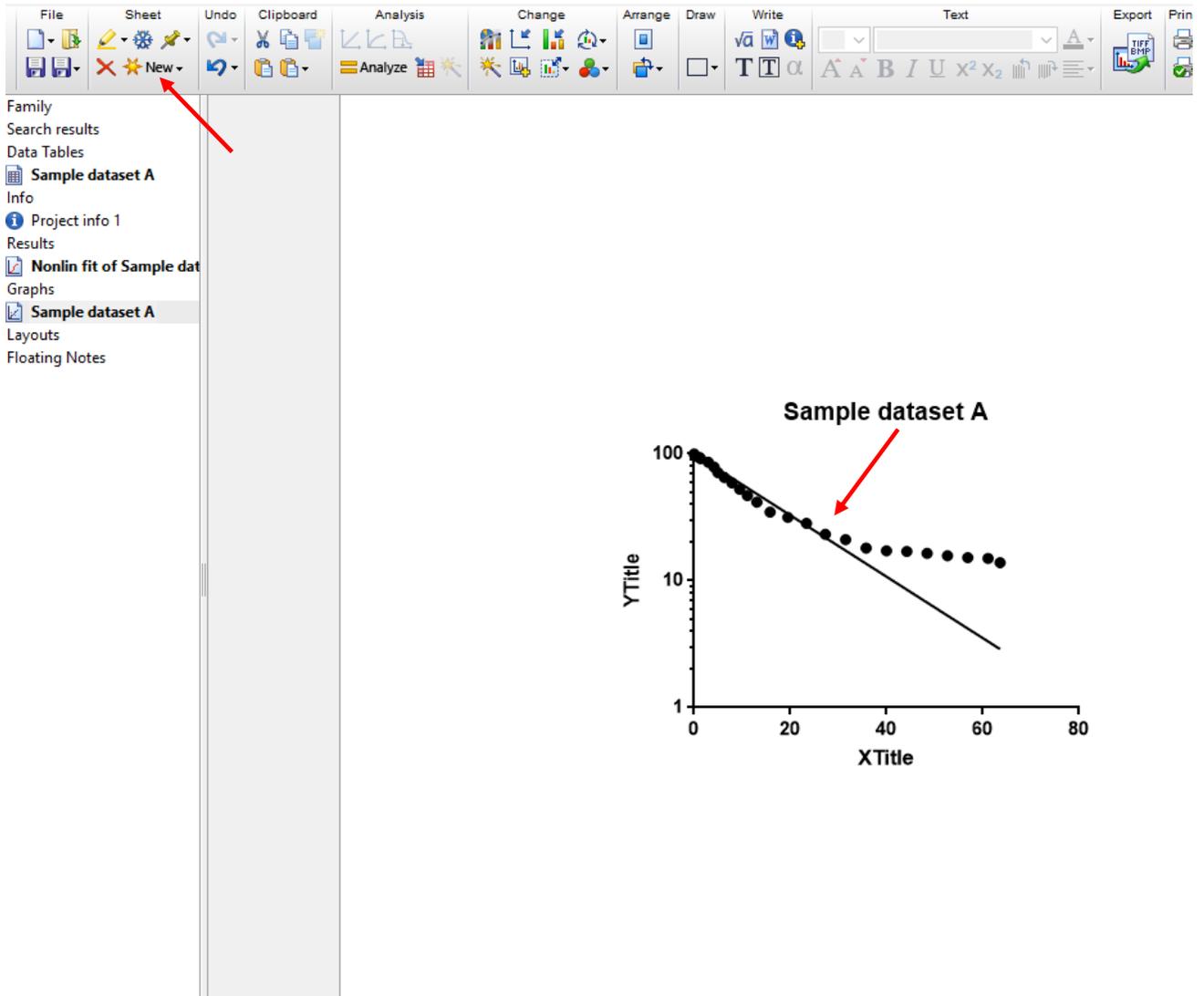
Additional ticks and grid lines

At Y=	Tick	Line	Text	Fonts? Greek?...	Details
	<input type="checkbox"/>	<input type="checkbox"/>			...

Show additional ticks:
 With regular ticks
 Instead of regular ticks
 Only regular ticks

Help | Cancel | Apply | OK

10. Below is the log-linear plot. The deviation of the log-linear plot to the right indicates that this curve is following 2-phase exponential decay. Next, click on “New” at the top to re-enter the same data to permit 2-phase decay EDNLRA.



11. Again, click on “XY”, then on “Enter and plot a single Y value for each point”, then on “Create”.

XY tables: Each point is defined by an X and Y coordinate

	X	A			B		
	Minutes	Control		Treated			
	X	A:Y1	A:Y2	A:Y3	B:Y1	B:Y2	B:Y3
1	Title						
2	Title						
3	Title						

Enter/import data:

X: Numbers
 Numbers with error values to plot horizontal error bars
 Dates
 Elapsed times

Y: Enter and plot a single Y value for each point
 Enter 2 replicate values in side-by-side subcolumns
 Enter and plot error values already calculated elsewhere
Enter: Mean, SD, N

Use tutorial data: Linear regression - Compare slopes
 Nonlinear regression -- One phase exponential decay
 Dose-response - X is log(dose)
 Interpolate unknowns from a linear standard curve
 Correlation
 Entering dates into the X column
 Entering elapsed times into the X column
 More tutorial data...

Prism Tips Free update available Cancel Create

12. Enter the same data as for 1-phase decay, and rename the dataset indicating that it is for 2-phase decay analysis, then click on “Analyze”.

GraphPad Prism 7.04 - [Project2:Sample dataset A]

File Edit View Insert Change Arrange Family Window Help

File Sheet Undo Clipboard Analysis Change Imp

Family

Search results

Data Tables

- Sample dataset A 1-phase
- Sample dataset A 2-phase

Info

- Project info 1

Results

- Nonlin fit of Sample dataset A 1-

Graphs

- Sample dataset A 1-phase
- Sample dataset A 2-phase

Layouts

Floating Notes

Table format: XY		X	Group A	Group
		X	Y	Y
1	Title	0.000000	99.85136	
2	Title	0.282580	95.98443	
3	Title	1.110158	93.90233	
4	Title	1.371190	91.58471	
5	Title	2.969177	85.93615	
6	Title	4.163953	78.68485	
7	Title	4.959140	71.18456	
8	Title	6.274945	65.07605	
9	Title	7.877922	58.99280	
10	Title	9.483752	52.66117	
11	Title	11.083880	46.82631	
12	Title	13.061100	41.53020	
13	Title	15.821520	34.78630	
14	Title	19.499210	31.60782	
15	Title	23.369570	28.33931	
16	Title	27.260940	23.24175	
17	Title	31.502140	21.05769	
18	Title	35.752410	18.08330	
19	Title	39.978830	17.18634	
20	Title	44.196950	17.01197	
21	Title	48.420010	16.40856	
22	Title	52.643320	15.78257	
23	Title	56.865850	15.22432	
24	Title	61.084750	14.98221	
25	Title	63.588890	13.86817	
26	Title			

13. Click on "Nonlinear regression", then on "OK".

The screenshot shows a software interface with a menu bar (File, Edit, View, Insert, Change, Arrange, Family, Window, Help) and a toolbar. A spreadsheet is visible in the background with columns labeled X, Group A, Group B, Group C, Group D, Group E, and Group F. The 'Analyze Data' dialog box is open, showing a list of analysis options. The 'XY analyses' section is expanded, and 'Nonlinear regression (curve fit)' is selected. The 'Analyze which data sets?' section has a checkbox for 'A' checked. The 'OK' button is highlighted with a red arrow.

Table format: XY

	X	Group A	Group B	Group C	Group D	Group E	Group F
1	Title	0.000000	99.85136				
2	Title	0.000000					
3	Title	1.000000					
4	Title	1.000000					
5	Title	2.000000					
6	Title	4.000000					
7	Title	4.000000					
8	Title	6.000000					
9	Title	7.000000					
10	Title	9.000000					
11	Title	11.000000					
12	Title	13.000000					
13	Title	15.000000					
14	Title	19.000000					
15	Title	23.000000					
16	Title	27.000000					
17	Title	31.000000					
18	Title	35.000000					
19	Title	39.000000					
20	Title	44.000000					
21	Title	48.000000					
22	Title	52.000000					
23	Title	56.000000					
24	Title	61.000000					
25	Title	63.000000					
26	Title						
27	Title						
28	Title						
29	Title						

Family

Search results

Data Tables

- Sample dataset A 1-phase
- Sample dataset A 2-phase

Info

- Project info 1

Results

- Nonlin fit of Sample dataset A 1-phase

Graphs

- Sample dataset A 1-phase
- Sample dataset A 2-phase

Layouts

Floating Notes

Analyze Data

Built-in analysis

Which analysis?

- Transform, Normalize...
 - Transform
 - Transform Concentrations (X)
 - Normalize
 - Prune rows
 - Remove baseline and column math
 - Transpose X and Y
 - Fraction of total
- XY analyses
 - Nonlinear regression (curve fit)
 - Linear regression
 - Fit spline/LOWESS
 - Smooth, differentiate or integrate curve
 - Area under curve
 - Deming (Model II) linear regression
 - Column statistics
 - Row means with SD or SEM
 - Correlation
 - Interpolate a standard curve
- Column analyses
- Grouped analyses
- Contingency table analyses

Analyze which data sets?

A

When you analyze tables or graphs with more than one data set, use this space to select which data set(s) to analyze.

Select All Deselect All

Help Cancel OK

14. Click on "Two phase decay", then on "Constrain".

The image shows the Prism software interface with the 'Parameters: Nonlinear Regression' dialog box open. The 'Constrain' tab is selected, and 'Two phase decay' is chosen from the 'Recently used' list. The 'Fitting method' is set to 'Least squares (ordinary) fit'.

Table format: XY

	X	Group A	Group B	Group C	Group D	Group E	Group F	Gr
1	Title							
2	Title							
3	Title							
4	Title							
5	Title							
6	Title							
7	Title							
8	Title							
9	Title							
10	Title							
11	Title	1						
12	Title	1						
13	Title	1						
14	Title	1						
15	Title	2						
16	Title	2						
17	Title	3						
18	Title	3						
19	Title	3						
20	Title	4						
21	Title	4						
22	Title	5						
23	Title	5						
24	Title	6						
25	Title	6						
26	Title							
27	Title							
28	Title							
29	Title							

Parameters: Nonlinear Regression

Fit Compare **Constrain** Weights Initial values Range Output Confidence Diagnostics Flag

Choose an equation

- Recently used**
 - Three phase decay
 - Two phase decay
 - One phase decay
- Standard curves to interpolate**
- Dose-response - Stimulation**
- Dose-response - Inhibition**
- Dose-response - Special**
- Binding - Saturation**
- Binding - Competitive**
- Binding - Kinetics**
- Enzyme kinetics - Inhibition**
- Enzyme kinetics - Substrate vs. Velocity**
- Exponential**
- Lines**
- Polynomial**
- Gaussian**
- Sine waves**
- Classic equations from prior versions of Prism**

Sum of two decay processes -- one fast, one slow.

Two phase decay [Learn about this equation](#)

Fitting method

Least squares (ordinary) fit Robust fit Automatic outlier elimination

Interpolate

Interpolate unknowns from standard curve. Confidence interval: None

Learn Cancel OK

15. For Y0, change constraints from “No constraint” to “constraint equal to 100” and for Plateau, change constraints from “No constraint” to “constraint equal to 0”, then click on “OK”.

The screenshot shows a software interface with a spreadsheet background and a dialog box titled "Parameters: Nonlinear Regression". The spreadsheet has columns labeled "X", "Group A", "Group B", "Group C", "Group D", "Group E", "Group F", and "Group G", and rows numbered 1 to 30. The dialog box has several tabs: "Fit", "Compare", "Constrain", "Weights", "Initial values", "Range", "Output", "Confidence", "Diagnostics", and "Flag". The "Constrain" tab is selected, displaying a table with the following data:

Parameter Name	Constraint Type	Value	Hook
Y0	Constant equal to	100	
Plateau	Constant equal to	0	
PercentFast	Must be between zero and	100	
KFast	No constraint		
KSlow	Must be greater than	0	

Below the table, there is a section titled "Constrain one parameter relative to another" with two rows of options:

- KFast must be greater than 1 times KSlow
- must be greater than 1 times

At the bottom of the dialog box, there are three buttons: "Learn", "Cancel", and "OK". Red arrows in the image point to the "Value" column for Y0 and Plateau, and to the "OK" button.

16. The 2-phase decay exponential decay nonlinear regression analysis fit our definition for a curve fitting a 2-phase decay model. We have defined curves as fitting 2-phase decay models if the “Percent Fast” is $\geq 1\%$ and $\leq 99\%$ (meaning that each of the “fast” and “slow” subpopulations will constitute at least 1% of the entire population. Note that most analyses will provide a value for “Percent Fast”, but we do not define it as fitting a 2-phase decay model if this value is $<1\%$ or $>99\%$. We also have required that the “Half Life (Slow)” be \geq twice as long as the “Half Life (Fast).”

For this illustrative analysis, the proportion of the patients in the rapidly progressing group was 85.79%, with 95% confidence intervals of 78.2 to 87.14%. The PFS half-life for the rapidly progressing group was 8.4 months (7.5 to ? months). The PFS half-life for the slowly progressing group appears to be very long, but 95% confidence intervals cannot be defined since follow up is much too short. As in most of these analyses in patients with a potentially cured subpopulation, we can conclude that the PFS half-life for the potentially cured group overestimates the true PFS half-life for the group since the half-life is longer than human life expectancy.

		Nonlin fit		A	B
				Data Set-A	Title
				Y	Y
set A 1-phase		1	Two phase decay	Hit constraint	
set A 2-phase		2	Best-fit values		
1		3	Y0	= 100	
		4	Plateau	= 0	
Sample dataset A 1-ph		5	PercentFast	85.79	
Sample dataset A 2-		6	KFast	0.08261	
set A 1-phase		7	KSlow	~ 2.009e-016	
set A 2-phase		8	Half Life (Slow)	~ 3.45e+015	
		9	Half Life (Fast)	8.391	
		10	Tau (slow)	~ 4.978e+015	
		11	Tau (fast)	12.11	
		12	Rate constant ratio	~ 4.112e+014	
		13	Std. Error		
		14	PercentFast	4.03	
		15	KFast	0.004935	
		16	KSlow		
		17	Rate constant ratio		
		18	95% CI (profile likelihood)		
		19	PercentFast	78.2 to 87.14	
		20	KFast	??? to 0.09208	
		21	KSlow		
		22	Half Life (Slow)		
		23	Half Life (Fast)	7.528 to ???	
		24	Tau (slow)		
		25	Tau (fast)	10.86 to ???	
		26	Goodness of Fit		
		27	Degrees of Freedom	22	
		28	R square	0.9973	
		29	Absolute Sum of Squares	60.41	
		30	Sy.x	1.657	
		31	Constraints		

17. In this analysis, we also received the notification “hit constraint”. This indicates that the exponential decay nonlinear regression analysis calculations were impacted by one of our constraints (“Y=100” or “Plateau=0”). This is generally from the constraint “Plateau=0”. Removing the constraint usually eliminates the “hit constraint” notification, but it generally also results in the data no longer fitting a 2-phase decay model, even when log-linear plots display clear 2-phase decay with a deviation to the right at an inflection point. The calculation typically hits the constraint if the length of the PFS curve/ maximum patient follow-up is relatively short. When this constraint is hit, the program typically cannot calculate 95% confidence intervals for “Half-Life (Slow)”, but it generally can calculate 95% confidence intervals for “Percent Fast”. When constraints are hit, the program can generally calculate the lower boundary of 95% confidence intervals for “Half Life (Fast)” but could only calculate the upper boundary of 95% confidence intervals for “Half Life (Fast)” for 27% of curves hitting constraints in the analyses in this manuscript. The bottom line: as with calculations of medians or hazard ratios or assessment of any other clinical trial data, confidence in population survival kinetics estimates improves with longer follow up and more mature data.

		Nonlin fit	
		A	B
		Data Set-A	Title
		Y	Y
set A 1-phase set A 2-phase	1	Two phase decay	Hit constraint
	2	Best-fit values	
1	3	Y0	= 100
	4	Plateau	= 0
Sample dataset A 1-ph Sample dataset A 2-	5	PercentFast	85.79
	6	KFast	0.08261
set A 1-phase set A 2-phase	7	KSlow	~ 2.009e-016
	8	Half Life (Slow)	~ 3.45e+015
	9	Half Life (Fast)	8.391
	10	Tau (slow)	~ 4.978e+015
	11	Tau (fast)	12.11
	12	Rate constant ratio	~ 4.112e+014
	13	Std. Error	
	14	PercentFast	4.03
	15	KFast	0.004935
	16	KSlow	
	17	Rate constant ratio	
	18	95% CI (profile likelihood)	
	19	PercentFast	78.2 to 87.14
	20	KFast	??? to 0.09208
	21	KSlow	
	22	Half Life (Slow)	
	23	Half Life (Fast)	7.528 to ???
	24	Tau (slow)	
	25	Tau (fast)	10.86 to ???
	26	Goodness of Fit	
	27	Degrees of Freedom	22
	28	R square	0.9973
	29	Absolute Sum of Squares	60.41
	30	Sy.x	1.657
	31	Constraints	