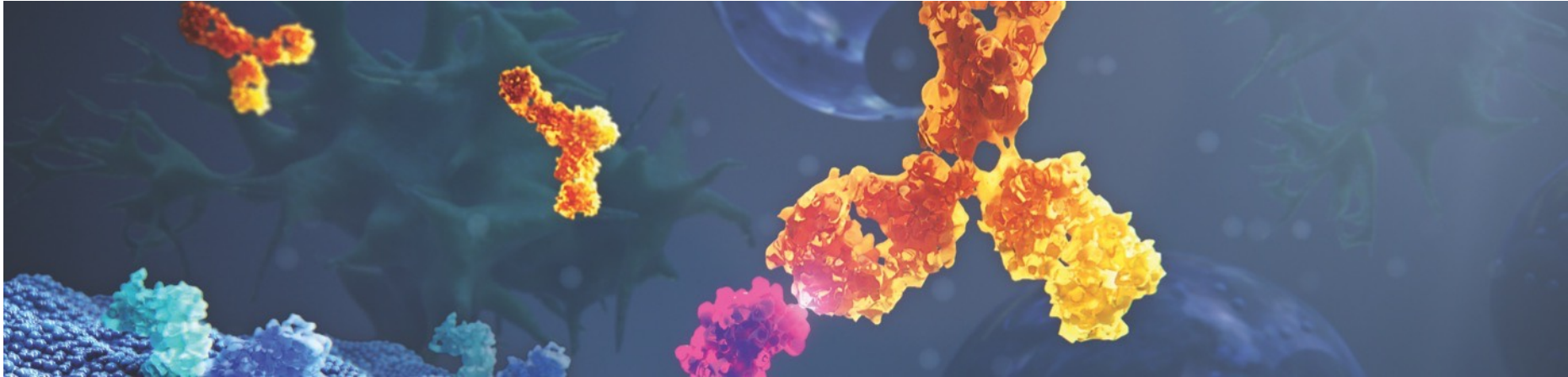


Difficulties with network meta-analysis when starting to use PD-L1 thresholds



Disclaimer

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Summary presentation

- Objective: To compare nivolumab with pembrolizumab within NSCLC 2nd line or later
- PD-L1 is an important effect modifier for immuno oncology treatments in NSCLC
- As such, the Network Meta Analysis of Kim et al (2018) compared nivolumab with pembrolizumab per PD-L1 level
- However, Kim et al (2018) used hazard ratios where the proportional hazards assumption is violated
- In this presentation, non-proportionality is accounted for by the use of splines
- Results of the spline approach will be presented and seem to contradict conclusions of Kim et al (2018)



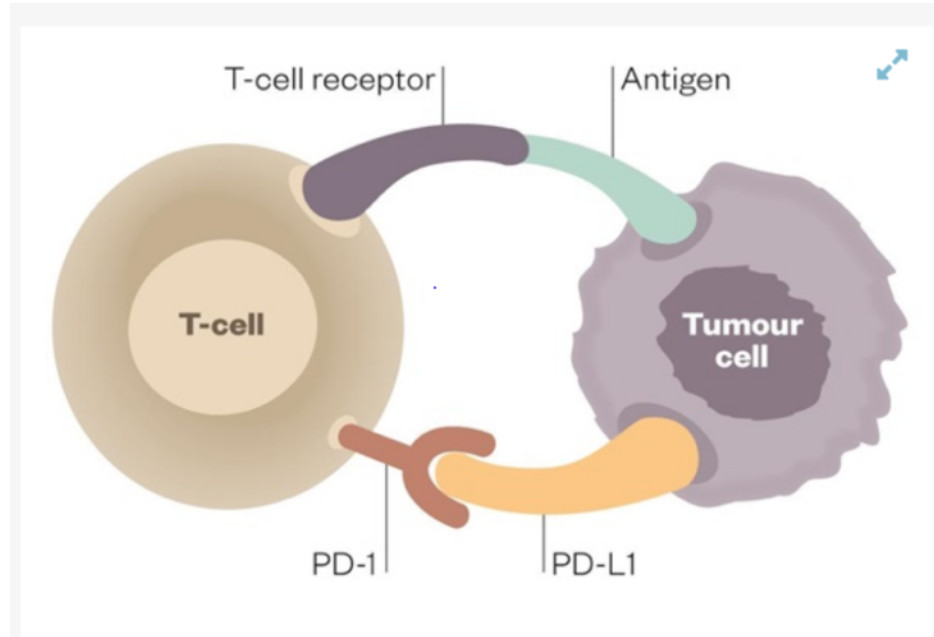
Lung cancer (NSCLC) and its treatment

- Lung cancer (NSCLC) is the leading cause of cancer death
- Docetaxel is the standard of care for second-line or third-line NSCLC treatment
- PD-1 and PD-L1 inhibitors (Immuno Oncology treatments) have become available or are under investigation offering improved efficacy



Immuno-oncology: PD-1 and PD-L1 inhibitors

PD1 and PD-L1 inhibitors:
Different mode of Action to docetaxel



Docetaxel

Docetaxel blocks the growth of the cancer by stopping the cancer cells from dividing and multiplying.

PD1 and PD-L1 inhibitors

PD1 and PD-L1 inhibitors block response of the tumour cells generated via PD-L1 or PD-1 to T cells and

prevent against inactivation of T-cells, which themselves are scanning the body for abnormalities and infections



NMA: 2018 scientific report comparing atezolizumab, nivolumab and pembrolizumab at different PD-L1 levels

Jinchul Kim, Jinhyun Cho, Moon Hee Lee, Joo Han Lim, Relative Efficacy of Checkpoint inhibitors for advanced NSCLC According to Programmed Death-Ligand-1 Expression: A Systematic Review and Network Meta-Analysis. [Sci Rep](#). 2018; 8: 11738.

Objective: Network meta-analysis aimed to assess the survival benefit and comparative efficacy of checkpoint inhibitors according to PD-L1 expression level: <1%, 1–49%, and ≥50%.

Method: A fixed-effects Bayesian network meta-analysis (NMA) was performed to estimate **hazard ratios (HRs)** for overall survival (OS) with 95% credible intervals (CrIs).

Conclusion: Atezolizumab, nivolumab, and nivolumab were the most effective agents for second- or later-line settings in the PD-L1 < 1%, PD-L1 1–49%, and PD-L1 ≥ 50% subgroups, respectively.



2nd line or later nivolumab and pembrolizumab trials included in Kim et al (2018)

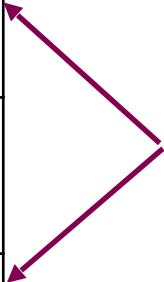
2nd line or later nivolumab and pembrolizumab trials included in Kim et al (2018):

- Nivolumab: Checkmate 017 squamous and Checkmate 057 non squamous
- Pembrolizumab: Keynote 010 79% non-squamous
- Same docetaxel prescription and only ECOG 0/1 for all trials



PD-L1 levels

Study	N	PD-L1 inclusion	Pre-specified PD-L1 levels
CM 017 Squamous	135 nivolumab 137 docetaxel	All comers	<ul style="list-style-type: none">• $\geq 1\%$• $\geq 5\%$• $\geq 10\%$
CM 057 Non-squamous	292 nivolumab 290 docetaxel	All comers	<ul style="list-style-type: none">• $\geq 1\%$• $\geq 5\%$• $\geq 10\%$
KN 010 79% non-squamous	345 pembro 2mg 346 pembro 10mg 343 docetaxel	$\geq 1\%$	<ul style="list-style-type: none">• $\geq 1\%$• $\geq 50\%$



Only for these levels, KM data are publically available



HR second line or later nivolumab and pembrolizumab; PD-L1 dependency

HR 1-49%:

Nivolumab versus docetaxel

- Checkmate 017: 0.75 [0.49, 1.16]
- Checkmate 057: 0.77 [0.55, 1.08]

Pembrolizumab versus docetaxel

- Keynote 010: 0.76 [0.64, 0.89]

- Checkmate 017 Squamous showing much less change than Checkmate 057 Non-squamous
- Pembrolizumab in between with 79% non-squamous

HR 50%+

Nivolumab versus docetaxel

Checkmate 017: 0.68 [0.27, 1.66]

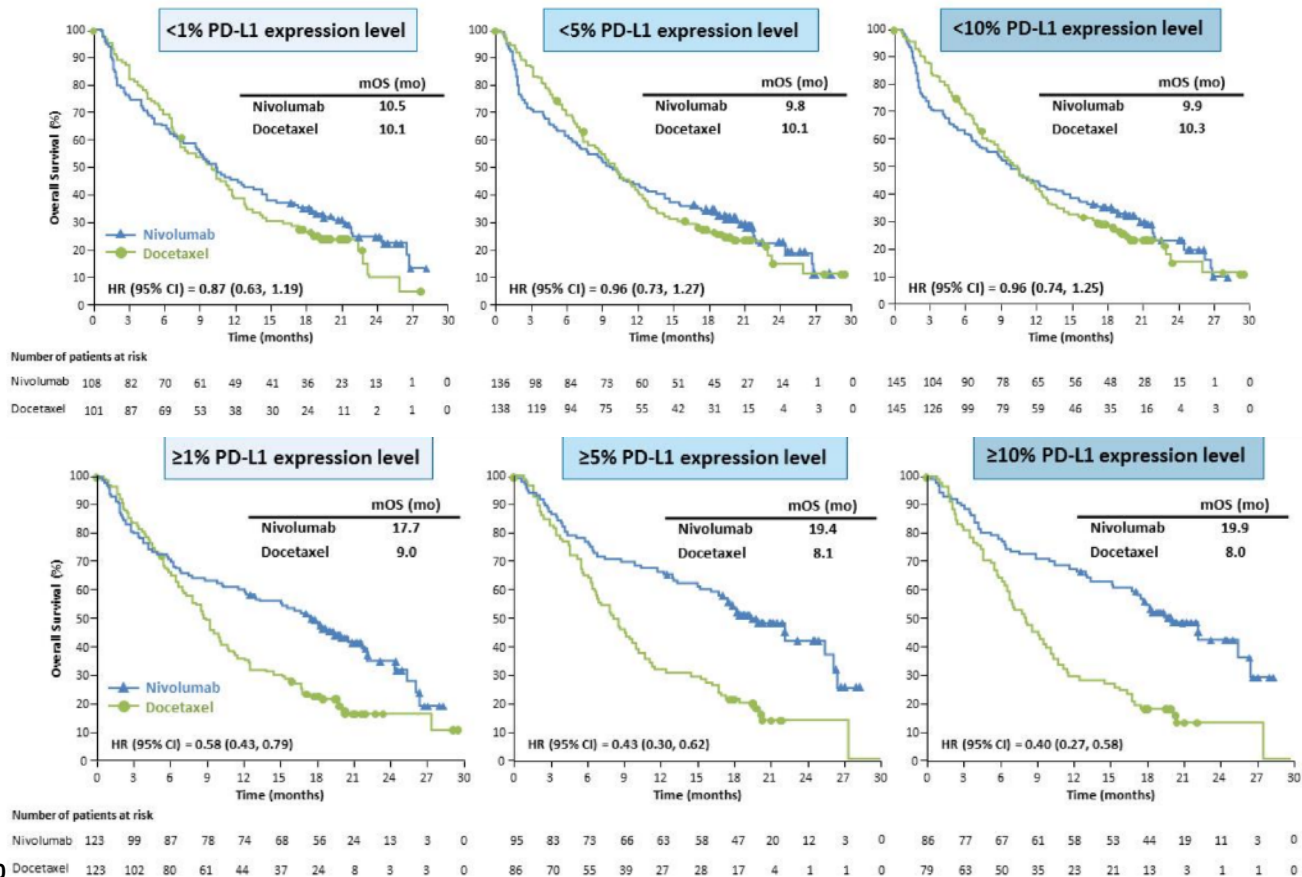
Checkmate 057: 0.35 [0.22, 0.55]

Pembrolizumab versus docetaxel

Keynote 010: 0.51 [0.41, 0.64]

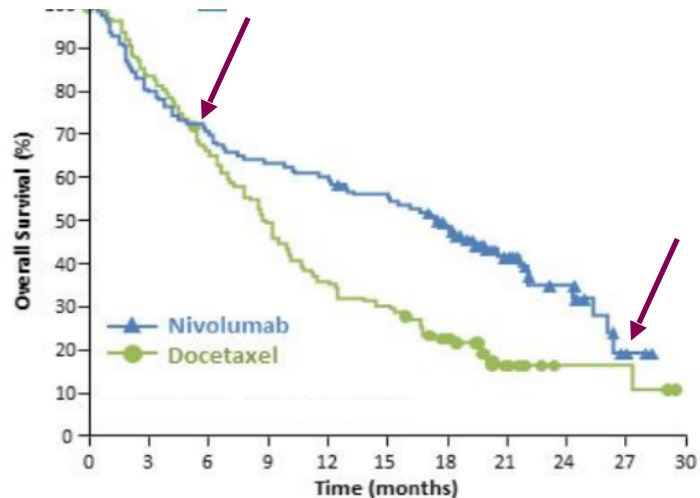


PD-L1 dependent treatment effect in Checkmate 057



Included Kaplan Meiers Nivolumab for PD-L1 $\geq 1\%$

Checkmate 057 Non-squamous



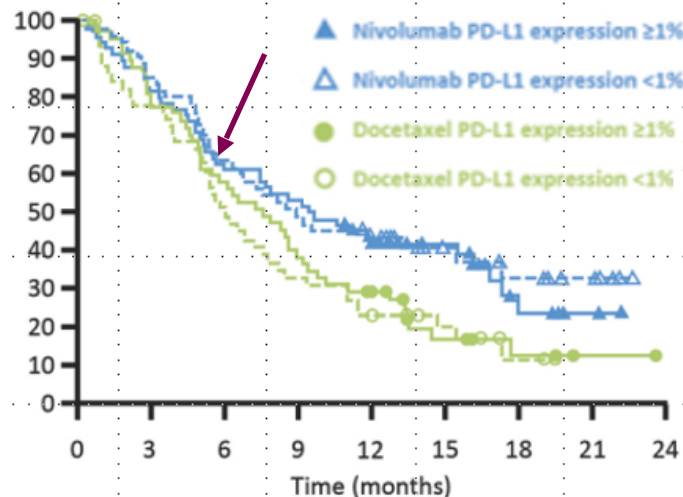
Number of patients at risk

Nivolumab	123	99	87	78	74	68	56	24	13	3	0
Docetaxel	123	102	80	61	44	37	24	8	3	3	0

HR $\geq 1\%$ 0.58 [0.43, 0.79]

Median: nivo 17.7, docetaxel 9.0

Checkmate 017 Squamous



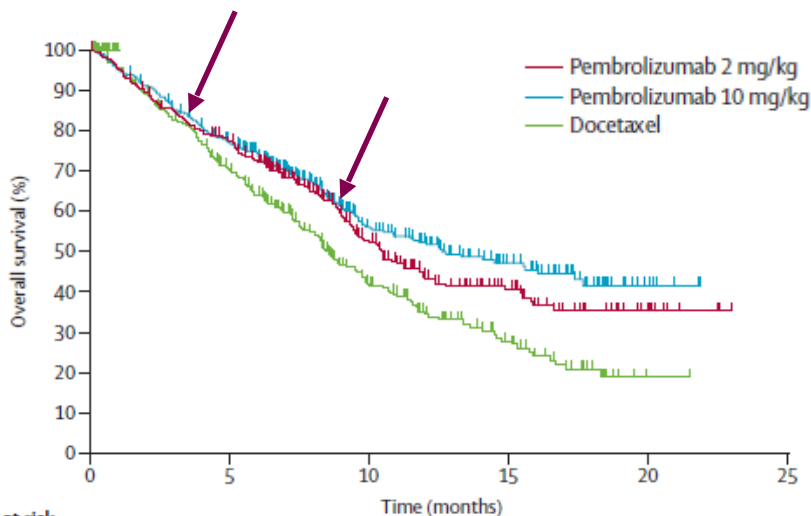
63	51	38	32	23	15	5	2	0
54	46	34	26	21	11	8	5	0
56	43	31	21	14	6	3	1	0
52	39	25	16	11	6	2	0	0

HR $\geq 1\%$ 0.69 [0.45, 1.10]

Median: nivo 9.3, docetaxel 7.2



Included Kaplan Meiers Pembrolizumab for PD-L1 $\geq 1\%$



Number at risk

Pembrolizumab 2 mg/kg	344	259	115	49	12	0
Pembrolizumab 10 mg/kg	346	255	124	56	6	0
Docetaxel	343	212	79	33	1	0

Pembrolizumab 10mg
HR $\geq 1\%$ 0.61 [0.49, 0.75]
Median: pembro 12.7, docetaxel 8.5

Pembrolizumab 2mg
HR $\geq 1\%$ 0.71 [0.58, 0.88]
Median: pembro 10.4, docetaxel 8.5



Kaplan Meier extraction

- We extracted the KM of the previous slides based on

Guyot, Ades, **Ouwens** and Welton (2012) Enhanced secondary analysis of survival data: reconstructing the data from published Kaplan-Meier survival curves; BMC Medical Research Methodology 2012 12:9

- And wanted to apply the approach discussed in Ouwens et al based on standard extrapolation distributions:

- Network meta-analysis of parametric survival curves

Ouwens, Philips, Jansen **accepted by NICE and referred in TSD 14**

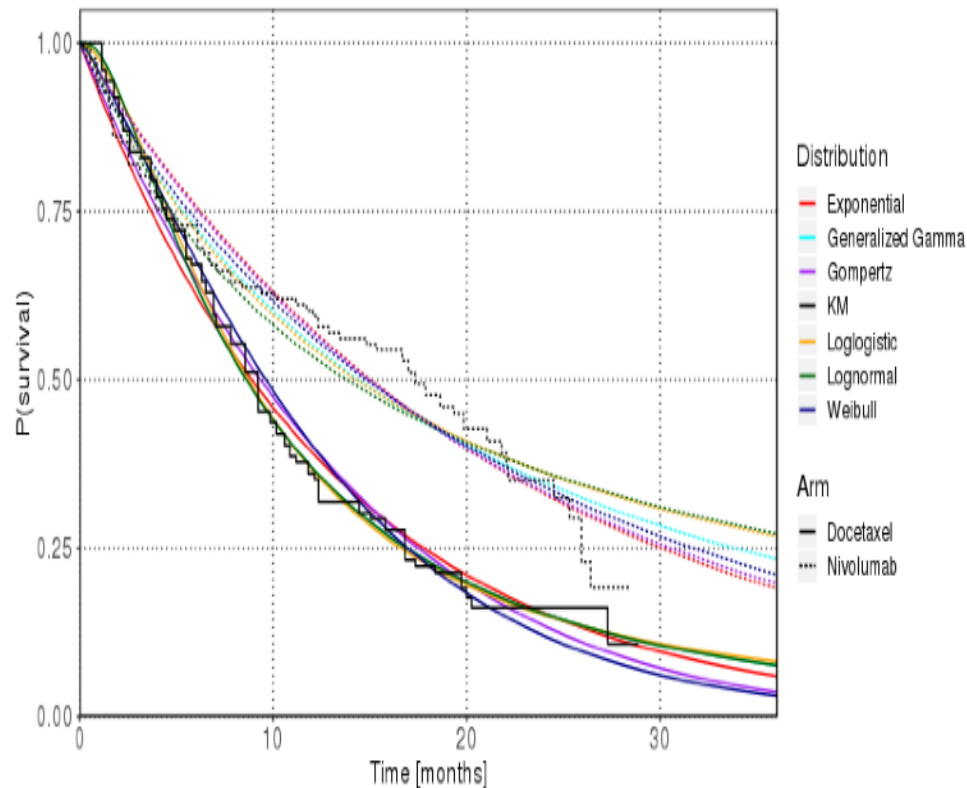
[Res Synth Methods](#), 2010 Jul;1(3-4):298-71. doi: 10.1002/rsm.25. Epub 2011 Mar 11.

- Network meta-analysis of survival data with fractional polynomials Jansen **not selected as 4 out of 7 rejected by NICE (found in systematic review of NICE submissions)**

[Stat Med](#), 2015 Jul 10;34(15):2294-311. doi: 10.1002/sim.6492. Epub 2015 Apr 15.



Fit of parametric distributions to Checkmate 057

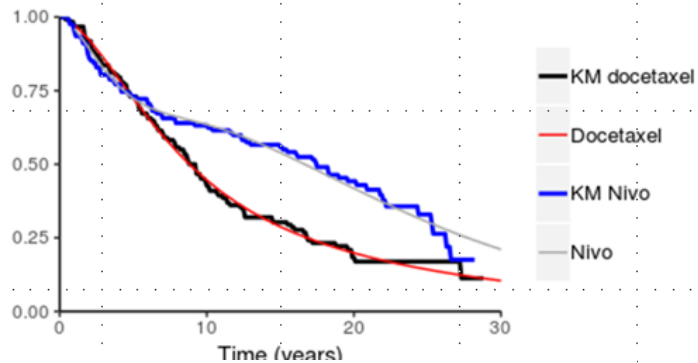


- Standard distributions provided a poor fit to the nivolumab data
- Alternative: Splines
 - Arbitrarily chosen knots:
half a year and a whole year
 - Simple NMA based on inverse variance weighting of each of the coefficients
 - Log(-log(S)) as survival percentage transformation

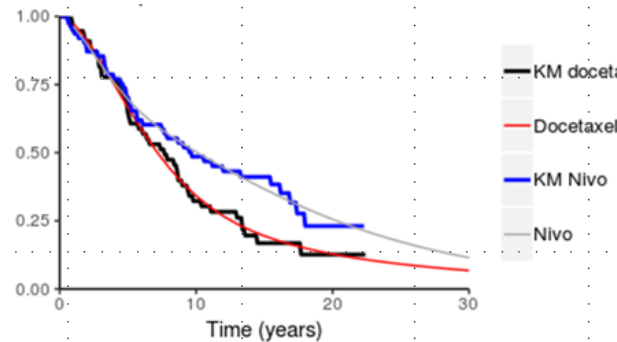


Fit of splines (PD-L1 $\geq 1\%$)

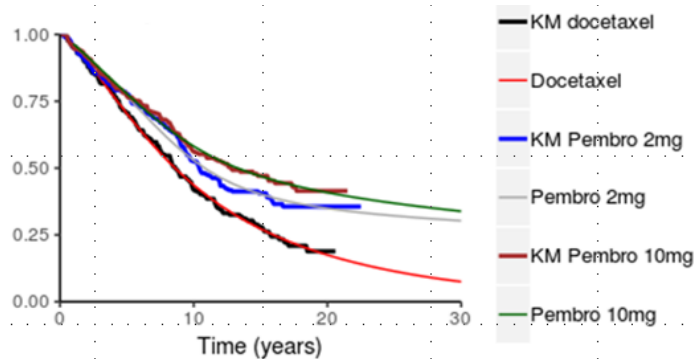
Checkmate 17



Checkmate 57



Keynote 10



Simple NMA: Combining vectors ignoring covariance

Checkmate 17

	Docetaxel		Nivolumab		Difference		
	EST	SE	EST	SE	Diff	SE	VAR
gamma0	-3.6	0.7	-3.3	0.6	0.3	0.9	0.75
gamma1	1.8	0.5	1.6	0.4	-0.2	0.7	0.47
gamma2	-0.1	0.4	0.4	0.4	0.5	0.6	0.33
gamma3	0.3	0.6	-0.4	0.5	-0.7	0.8	0.59

Simple version used

(for illustrational purposes):
inverse variance per coefficient

$$(0.3/0.75 + 0.4/0.35)/(1/0.75 + 1/0.35) = 0.37$$

Adding to Keynote 10 docetaxel:
 $-3.23 + 0.37 = -2.86$

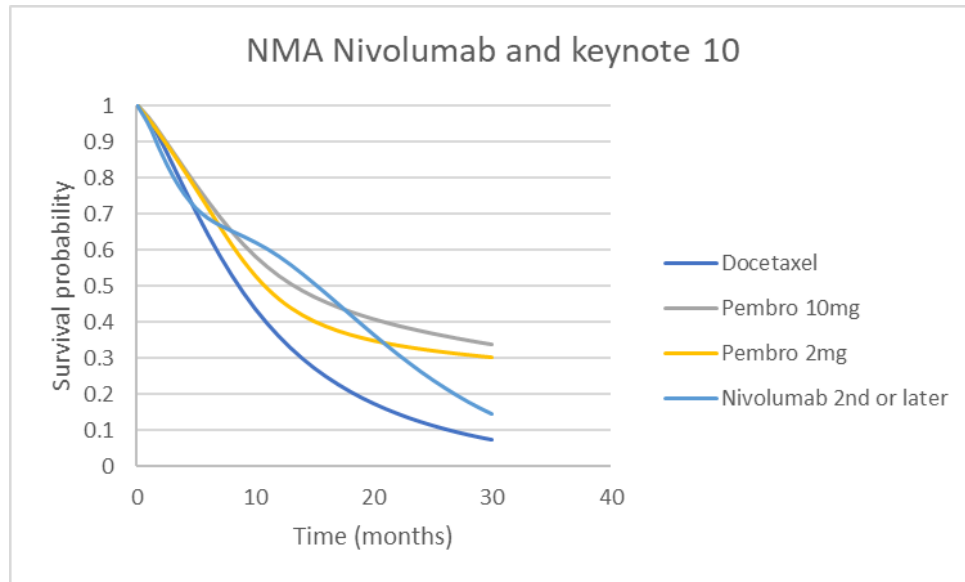
Checkmate 57

	Docetaxel		Nivolumab		Difference		
	EST	SE	EST	SE	Diff	SE	VAR
gamma0	-3.6	0.5	-3.2	0.4	0.4	0.6	0.35
gamma1	1.6	0.3	1.6	0.3	0.0	0.4	0.20
gamma2	0.0	0.2	0.8	0.2	0.8	0.3	0.10
gamma3	0.2	0.3	-1.0	0.2	-1.2	0.4	0.15

Keynote 10	Docetaxel	Diff Nivo Doce	Nivo
	EST	EST	EST
gamma0	-3.23	0.37	-2.86
gamma1	1.39	-0.08	1.31
gamma2	-0.03	0.75	0.72
gamma3	0.10	-1.06	-0.96



Results for PD-L1 $\geq 1\%$ for 2nd line and later



- Conclusion:
 - Crossing curves
 - In the long term, rather than nivolumab, pembrolizumab may be preferred



Take home message

- Comparing efficacy across PD-L1 levels is important, but use of HR is questionable
- Spline approaches, among others, can be used when Kaplan Meiers are presented for different PD-L1 levels
- Data may not be available at a sufficient granularity to model impact of the characteristic
- Sample sizes are decreased when evaluating subgroups



Personal opinion

- In areas where biomarkers are influencing end results, we need to have consistent definitions of biomarkers and present Kaplan Meiers for all relevant categories in a consistent way across trials.
- Spline approaches may be valid per category, even while the choice of number and place of knots is subjective (may require clinical validation)
- However, insufficient information may be present to pool data across trials at all



Background slides

Accounting for PD-L1 level when Individual Patient Data are available from the own trial

- A few possible approaches would exist when individual patient data would be available
 - PD-L1 subgroup analysis
 - Estimating a PD-L1 enhancement factor from our data and applying to comparator trial in cases where equivalent PD-L1 subgroup data for the comparator are not available
 - Weighting our data using the percentages in each of the categories of the comparator trial; Estimating a beta-distribution based on the percentages in the comparator trial to get a more refined impression of the distribution of PD-L1 in the comparator trial and using this beta-distribution to reweight our data
 - Using PD-L1 as a covariate in our models for our own trial and validating the assumed relationship. Then using Simulated Treatment Comparison approaches to link our trial with the comparator trial (NICE TSD 18)



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