


RQ1 & RQ3

Variables	ADM_Order	Delegator_ID	Delegator_grp	Delegator_mil	Delegator_Role	TA1_Name	Trial_ID	Attribute	Scenario
Source	Delegation survey loading log	Delegation survey response log	Delegation survey response log	Delegation survey response log	Delegation survey response log	Delegation survey loading log	Delegation survey loading log	Delegation survey loading log	Delegation survey loading log
Definition	One of four orders for presentation of the TA2 ADM responses to attribute scenarios	Used to track and identify participants, also called participant ID		Does this individual have a military background?	Professional medical role	Origin of scenario	Trial number within participant presentation		Scenario presented to the delegators in DM observation materials
Levels	1-4 		Military or civilian	Yes or no	EMT, paramedic, resident, physician, or other	ADEPT SoarTech	1-16	Moral Judgement (MJ) Ingroup/Outgroup (IO) Value of Life (VOL) Quality of Life (QOL)	1-3

ORDER 1	ORDER 2	ORDER 3	ORDER 4
Kitware – ADEPT MJ	Kitware – ST QoL	Parallax – ADEPT MJ	Parallax – ST VoL
Parallax – ST QoL	Kitware – ADEPT IG	Parallax – ST QoL	Kitware – ST QoL
Parallax – ADEPT IG	Parallax – ST VoL	Kitware – ADEPT IG	Parallax – ADEPT IG
Kitware – ST VoL	Parallax – ADEPT MJ	Kitware – ST VoL	Kitware – ADEPT MJ

RQ1 & RQ3 (con.)

Variables	TA2_Name	ADM_Type	Target	Alignment score (ADM target)	Alignment score (Delegator target)	Server Session ID (Delegator)	ADM_Aligned_Status (Baseline/Misaligned/Aligned)	ADM Loading
Source	Delegation survey loading log	Delegation survey loading log	Delegation survey loading log	TA1 server via Delegation survey loading log	TA1 server via Delegation survey loading log	Text Scenario Output / TA1 Server	Delegation survey loading log	Delegation survey loading log
Definition			Target against which the presented ADM was run For baseline ADMs, established a priori (most aligned) For aligned ADMs, determined by alignment with delegator text alignment scores	Calculated alignment score between the KDMA measurement of the ADM aligned to a particular target and that target	Calculated alignment score between the KDMA measurement of a delegator and a target	The session id used to get the delegator's alignment score from the TA1 server for the text scenarios	Assigned to the presented ADM based on baseline vs. aligned; and then based on the alignment score between the delegator and the target where aligned is the most aligned and misaligned is the least aligned (see exceptions)	Exceptions are noted when the presented ADM was not the most aligned or least aligned. This occurs in cases when the baseline matched the most aligned or where either the baseline or the aligned matched the least aligned.
Levels	Parallax Kitware	Baseline Aligned	ADEPT 0.0-1.0 Soartech: unique file	0.0-1.0	0.0-1.0		Baseline Aligned Misaligned	Normal Exceptions

RQ1 & RQ3 (con.)

Variables	Alignment score (Delegator Observed_ADM _(target))	Trust_Rating	Delegation preference (A/B)	Delegation preference (A/M)	Trustworthy_Rating	Agreement_Rating	SRAalign_Rating
Source	TA1 server post experiment	Delegation survey response log	Delegation survey response log	Delegation survey response log	Delegation survey response log	Delegation survey response log	Delegation survey response log
Definition	compares the KDMA measurement based on delegator responses to the subset of probes from an ADM they observed in the delegation survey	Delegator rating in response to individual DM	Delegation preference indicated by the delegator between the aligned ADM and baseline ADM on comparison trials	Delegation preference indicated by the delegator between the aligned ADM and misaligned ADM on comparison trials	Delegator rating in response to individual DM	Delegator rating in response to individual DM	Delegator rating in response to individual DM
Levels	0.0-1.0	1-5	For comparison trials: A = aligned B = baseline For individual DM trials: Y = chosen N = not chosen <i>Note: this is derived from the comparison trial at the end of each block</i>	For comparison trials: A = aligned B = baseline For individual DM trials: Y = chosen N = not chosen <i>Note: this is derived from the comparison trial at the end of each block</i>	1-5	1-5	1-5