MCDA/SMAA R Shiny Application

Brief Explainer and Demo

MCDA, Probabilistic MCDA and SMAA

- MCDA calculates overall utility in each treatment group i as:

$$U_i = w_1 u_1(\xi_{i1}) + \cdots + w_n u_n(\xi_{in})$$

  - ξ_{ij} - Performance of treatment i on criterion j
  - $u_j(.)$- Linear value function that maps the performance on criterion j to [0,1] scale
  - w_j - Weight (relative importance) given to criterion j
- Probabilistic MCDA (pMCDA) accounts for uncertainty in ξ_{ij} values by:
  - Drawing from the posterior distribution of these values
  - Calculating a posterior $Prob(U_i > U_{i'})$
- SMAA builds on pMCDA by accounting for uncertainty in weights, drawing w_j from a simplex such that:
  - $a < \frac{w_j}{w_{j'}} < b$, where $w_{j'}$ is the weight for most important criterion, a , b specified and $\sum_j w_j = 1$

Borrowing through priors: Mixture Priors

- Borrow from a prior study data but control amount of information borrowed using a mixture prior
- Imagine a scenario where performances, ξ_{ij}, are rates, we use a conjugate Gamma-Poisson model and specify priors:
  - $\xi_{ij} \sim d_{ij} * Gamma\left(a_{0j}, b_{0j}\right) + \left(1 - d_{ij}\right) * Gamma(0.001, 0.001)$
  - d_{ij} is the weight (between 0 and 1) we want to put on the prior coming from prior study, usually with $a_{0j}, \mathrm{b_{0j}}$ such that a_{0j}/b_{0j} was the rate observed in this prior study
- Similarly for Beta-Binomial (proportions) and Normal-Normal (continuous) models

Data Source

Select source of data

- Example dataset
- Upload dataset

Please upload your data

Browse... voyagermcdafc

Upload complete

File should be in .csv format

Use dataset

Range and Utility functions

Weights

MCDA

Probabilistic MCDA

SMAA

Generate Report

Select column containing alternatives

trt

Benefit criteria

alldth, mi, ischemic, amp, ali, revasc

Input Data must have ordered all Benefits first and all risks after

Risk criteria

bleed, ich, minor, reqmed, minbld

Select column containing number of subjects

n_alldth, n_mi, n_ischemic, n_amp, n_ali, n_revasc, n_bleed, n_ich, n_minor, n_reqmed, n_minbld

Select columns containing variance(s)

v_alldth, v_mi, v_ischemic, v_amp, v_ali, v_revasc, v_bleed, v_ich, v_minor, v_reqmed, v_minbld

Columns for Number of subjects (n_) and Variance (v_) should be in same order as endpoints

Prior Study Indicator

Pstudy

Prior study indicator should take value of 0 for current study 1 for prior study

Pstudy

Select criteria which are event counts

Nothing selected

For rate endpoints do not select either counts or continuous scores

Select criteria with continuous scores

Nothing selected

Endpoints are entered such that dividing by corresponding n_ column gives group mean (e.g., alldth/n_alldth = mean rate (or proportion) of all cause death in group

Select criteria where lower scores are better

alldth, mi, ischemic, amp, ali, revasc, bleed, ich, minor, reqmed, minbld

Select criteria where lower scores are better

alldth, mi, ischemic, amp, ali, revasc, bleed, ich, minor, reqmed, minbld

Select most important criterion

alldth

Arrange dataset

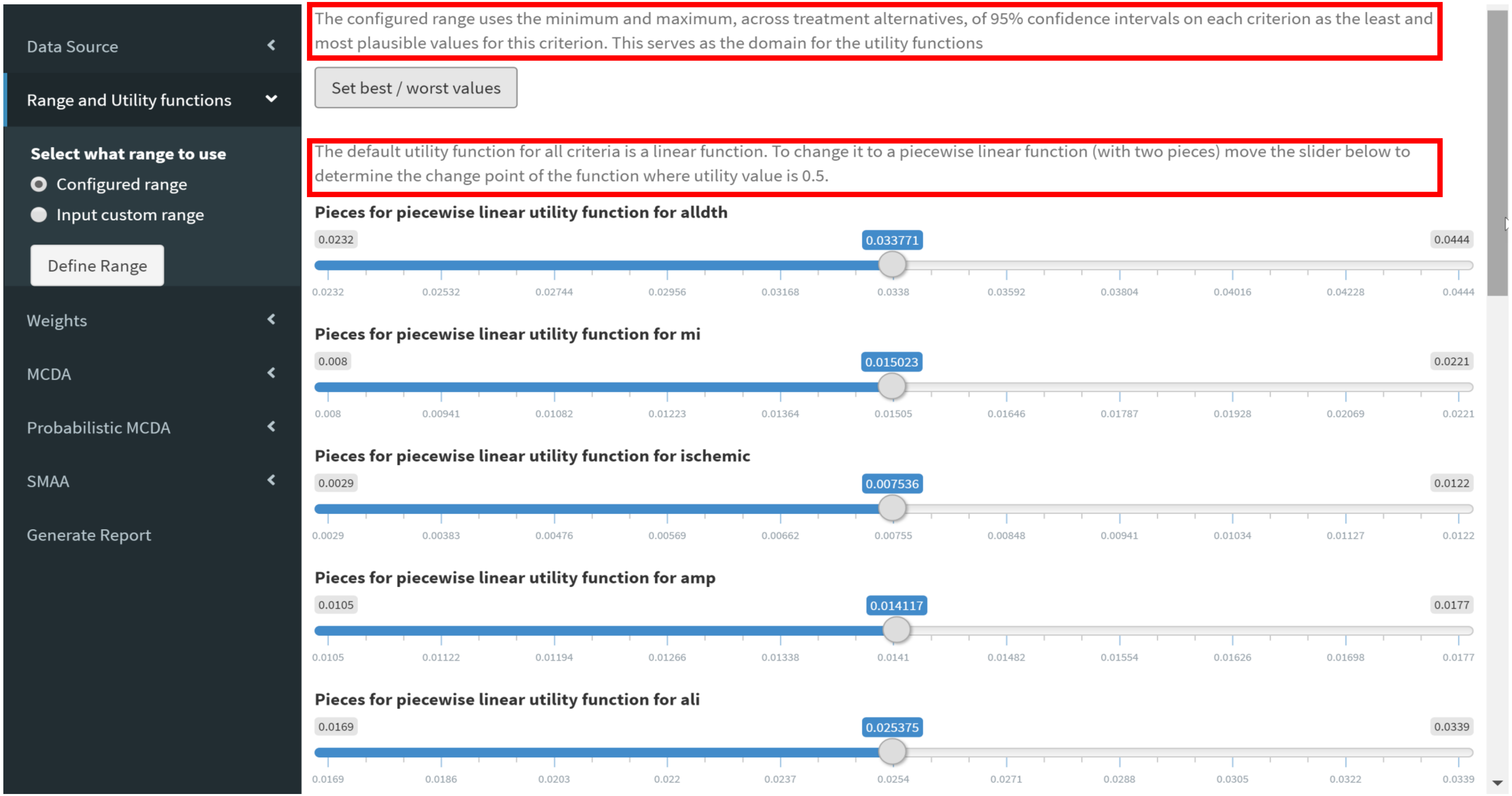
Copy | Download

Columns with green colour define criteria which are benefits, whereas columns with red colour define criteria which are risks.

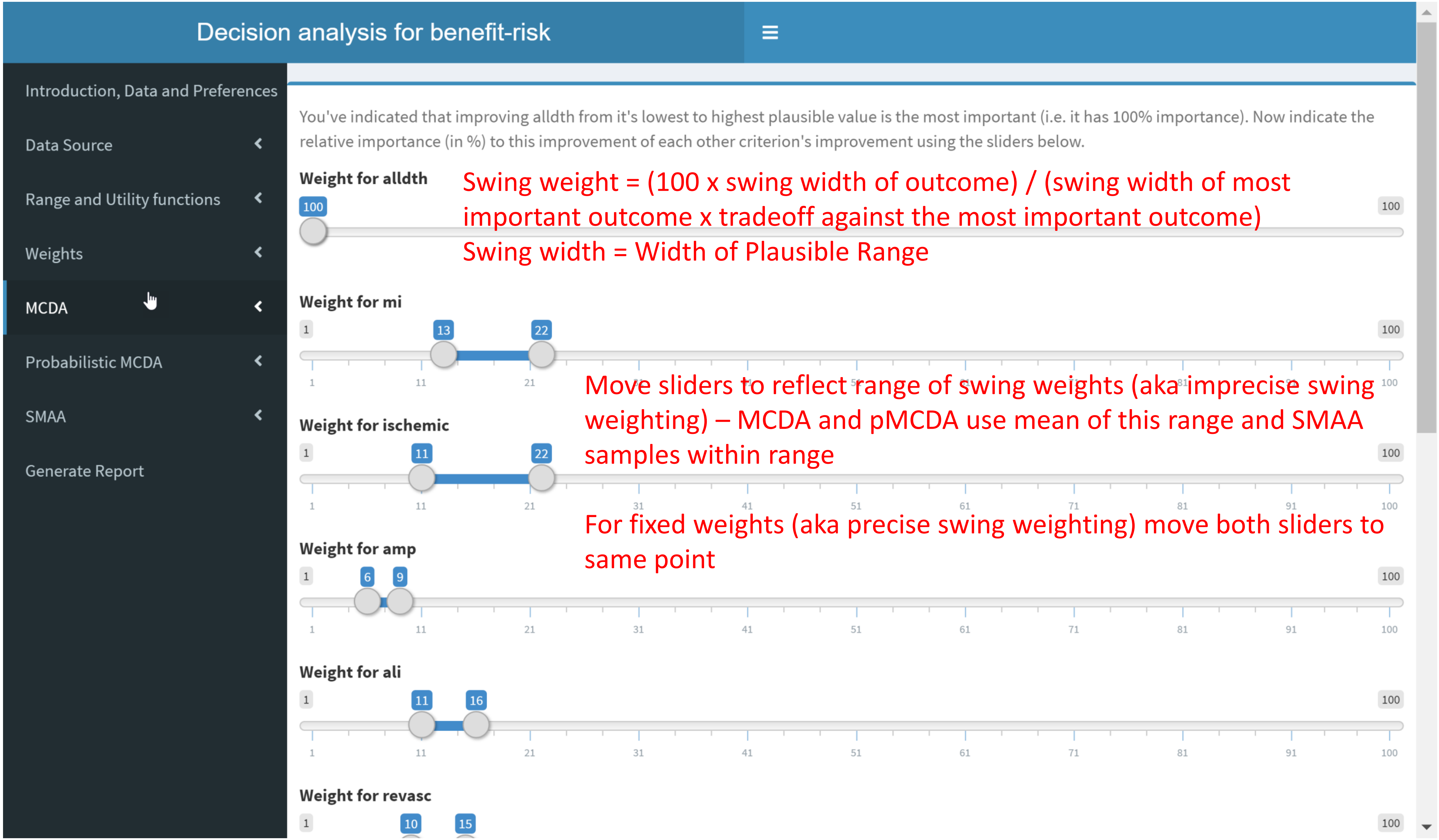
trt	alldth	n_alldth	v_alldth	mi	n_mi	v_mi	ischemic	n_ischemic	v_ischemic	amp
rivaroxaban	321	8025	4.98e-06	131	7706	2.21e-06	71	7889	1.14e-06	103
asa	297	8027	4.61e-06	148	7789	2.44e-06	82	8200	1.22e-06	115
rivaroxaban	129	4607	6.08e-06	51	4636	2.37e-06	22	4400	1.14e-06	NA
asa	142	4581	6.77e-06	67	4467	3.36e-06	40	4444	2.03e-06	NA

If prior study has no data on any endpoint, values are set to NA

Use scroller to visualized entire arranged dataset



Sliders determining next two change points of piecewise linear function will appear below

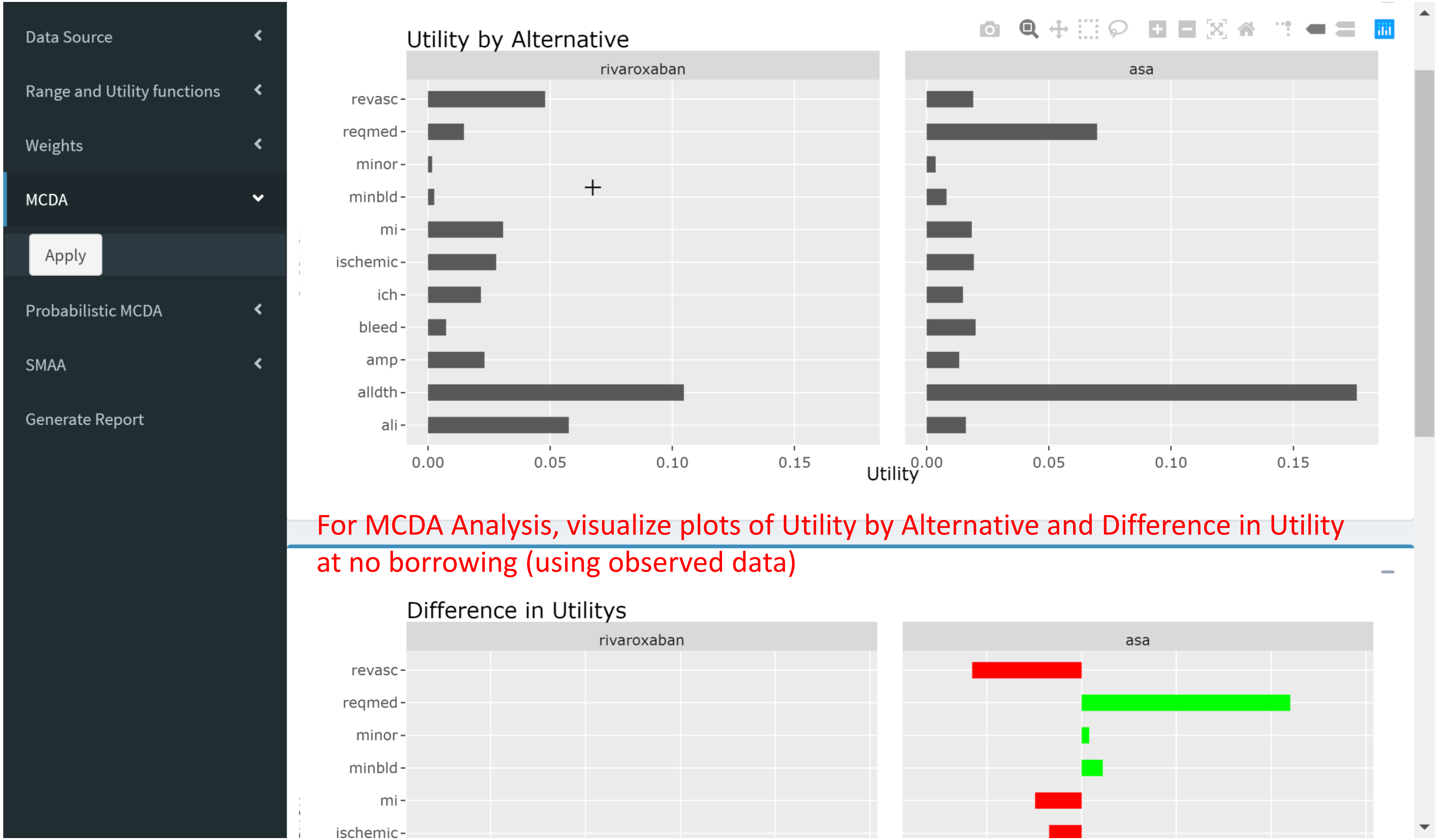


Swing weight = (100 x swing width of outcome) / (swing width of most important outcome x tradeoff against the most important outcome)

Swing width = Width of Plausible Range

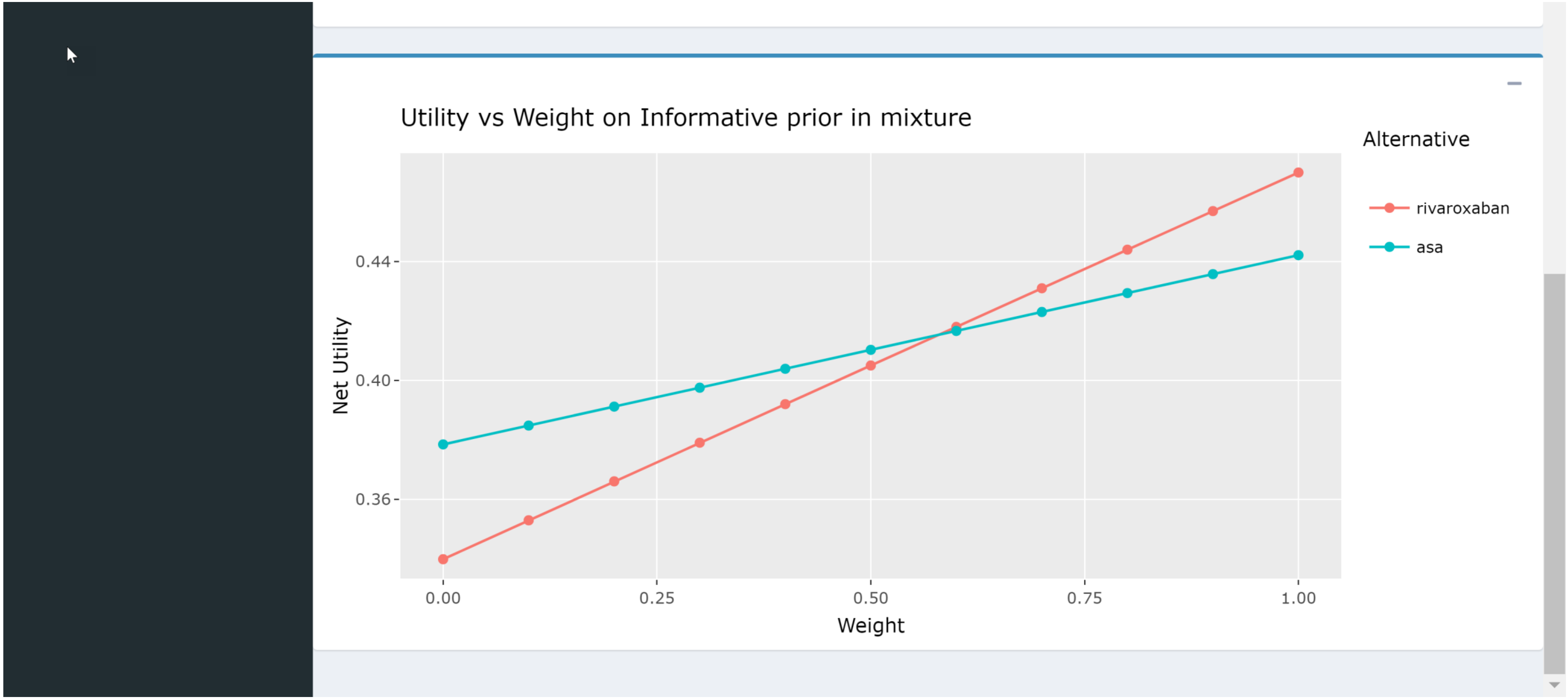
Move sliders to reflect range of swing weights (aka imprecise swing weighting) – MCDA and pMCDA use mean of this range and SMAA samples within range

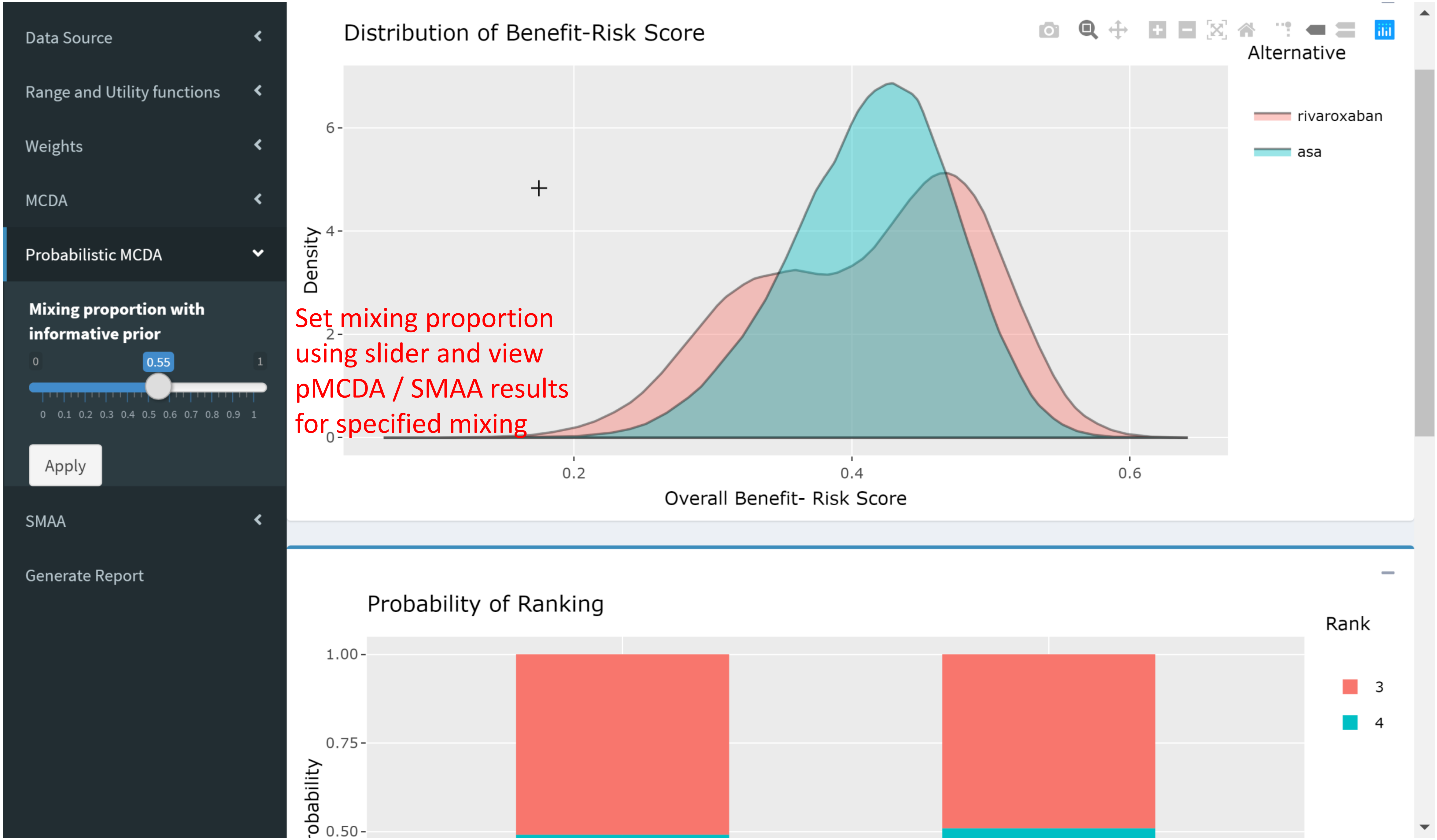
For fixed weights (aka precise swing weighting) move both sliders to same point



Data Source
Range and Utility functions
Weights
MCDA
Apply
Probabilistic MCDA
SMAA
Generate Report
Utility by Alternative
rivaroxaban
asa
revasc
reqmed
minor
minbld
mi
ischemic
ich
bleed
amp
alldth
ali
0.00
0.05
0.10
0.15
Utility
For MCDA Analysis, visualize plots of Utility by Alternative and Difference in Utility at no borrowing (using observed data)
Difference in Utilitys
rivaroxaban
asa
revasc
reqmed
minor
minbld
mi
ischemic

Scroll down on MCDA results to visualize the net utility by arm as weight on informative prior varies; point at which lines cross indicate weight at which rank preference for treatment groups change




Data Source
Range and Utility functions
Weights
MCDA
Probabilistic MCDA
Mixing proportion with informative prior
0
0.55
1
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1
Apply
SMAA
Generate Report
Distribution of Benefit-Risk Score
Alternative
rivaroxaban
asa
Density
0
2
4
6
0.2
0.4
0.6
Overall Benefit- Risk Score
Set mixing proportion using slider and view pMCDA / SMAA results for specified mixing
Probability of Ranking
Rank
3
4
1.00
0.75
0.50
obability