

Discriminate the response of Acute Myeloid Leukemia patients to treatment by using Proteomics Data and Answer Set Programming

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Additional file 1 : ASP implementation for readouts maximization

1- Dataset representation for readouts maximization

`prot(Z).`

`affinite(L1,L2).`

`r(L1,Z,X).`

We represent the set of readouts nodes with the the predicate `prot/1` namely `prot(Z)`

for all the readouts nodes.

The predicate `affinity(L1,L2)` is the result of the program in the Listing 2 (Methods

Section - Protein Selection – main paper). It means that the patient `L1` and patient

`L2` have the same values for the `k` choosen proteins.

`r(L1,Z,X)` means that the value of the readout `Z` for the patient `L1` is `X`.

2- ASP Implementation of the maximization of the readouts

`1.diff(L1,L2,Z,D) :- affinite(L1,L2), r(L1,Z,X), r(L2,Z,Y), gene(Z), D=X-Y, X>Y.`

`2.diff(L1,L2,Z,D) :- affinite(L1,L2), r(L1,Z,X), r(L2,Z,Y), gene(Z), D=Y-X, Y>X.`

`3.somme(L1,L2,M) :- M = #sum {D: diff(L1,L2,Z,D)}, affinite(L1,L2).`

`4.choix(L1,L2) :- {somme (L3,L2,M): M>X}0, {somme (L1,L3,M): M>X}0, somme (L1,L2,X).`

`5.sommedsommes(S) :- S = #sum {M: somme(L1,L2,M)}.`

`6.#show somme/3.`

`7.#show choix/2.`

8.#show sommedsommest/1.

In line 1 and line 2, we calculate the difference between the readouts for all pairs of patients over the predicate diff/4, namely $\text{diff}(L1, L2, Z, D)$ which means that the difference between the patient L1 and the patient L2 is D for the readout node Z.

Then in line 3, we sum the difference between L1 and L2 for all the readouts nodes with the predicate somme/3 namely $\text{somme}(L1, L2, M)$ which means that the sum of differences between L1 and L2 for all readouts is M.

In line 4, we choose the patients that have the largest difference in the readouts vector between patients L1 and L2, with the predicate choix/2 namely $\text{choix}(L1, L2)$.

In line 5, if we had more than one answer set that maximize the differences, we choose the one that maximize the sum of differences.

Line 6,7 and 8 display the results in the terminal.