

in the presence of more number of proteins causing metastasis and hence more inhibitors are required to immobilize these proteins.

The value of lambda chosen here is 0.33 for which value of lambda cut set is 0.123 which is then compared with the each value in column of table 3. If the corresponding value is greater than lambda cut set level, then this value is defuzzified to 1 else 0. This is tabulated in the table 4.

Table 2: The value of proteins corresponding to first distant metastasis

	BONE	LIVER	LUNG	SKIN	BRAIN	OTHERS
COX2	0.313	0.16	0.2133	0.0733	0.0466	0.1933
HER2	0.318	0.1978	0.1978	0.098	0.01	0.1758
ER	0.4427	0.1614	0.1041	0.088	0.0156	0.1875
PgR	0.4335	0.1678	0.0909	0.0769	0.0069	0.2237
EGFR	0.25	0.1718	0.2343	0.093	0.04687	0.2031
CK5	0.3	0.1	0.233	0.0333	0.1333	0.2
Nestin	0.37	0.111	0.1481	0.074	0.111	0.1851
Prominin1	0.26	0.130	0.1739	0.043	0.1304	0.2608
SMA	0.3076	0.1538	0.1538	0	0.1538	0.2307
SNAI1	0.435	0.14	0.11	0.085	0.025	0.205
SNAI2	0.407	0.1604	0.1604	0.037	0.037	0.1975
CK18	0.3877	0.1802	0.1326	0.074	0.034	0.1904
Ecadherin	0.401	0.1776	0.1312	0.0617	0.0368	0.196
GATA3	0.421	0.1818	0.1	0.0765	0.023	0.196

Table 3: Normalization value 'x' for different proteins

PROTEINS	X
COX2	0.4655
HER2	0.2812
ER	0.612
PgR	0.46
EGFR	0.1836
CK5	0.1014
Nestin	0.0923
Prominin1	0.0833
SMA	0.041
SNAI1	0.0677
SNAI2	0.2657
CK18	0.9684
E- cadherin	0.8957
GATA3	0.6875

Table 4: Normalized protein value

	BONE	LIVER	LUNG	SKIN	BRAIN	OTHERS
COX2	0.1443	0.07448	0.09929	0.034	0.0216	0.0899
HER2	0.089	0.05562	0.05562	0.0028	0.0028	0.04934
ER	0.2709	0.0987	0.0637	0.0538	0.0095	0.1147
PgR	0.1997	0.077	0.0419	0.0354	0.00318	0.1031
EGFR	0.0459	0.0318	0.043	0.017	0.0086	0.037
CK5	0.03	0.01014	0.0236	0.00337	0.0134	0.02028
Nestin	0.0344	0.0102	0.01366	0.0068	0.0102	0.017
Prominin1	0.0216	0.0108	0.1448	0.00358	0.0108	0.0217
SMA	0.0126	0.0063	0.0063	0	0.0063	0.00945
SNAI1	0.294	0.0947	0.0744	0.0575	0.0169	0.1387
SNAI2	0.108	0.0426	0.0426	0.0098	0.0098	0.052
CK18	0.375	0.1745	0.128	0.071	0.0329	0.1843
Ecadherin	0.359	0.159	0.1175	0.055	0.0275	0.1755
GATA3	0.29	0.125	0.0689	0.0527	0.0158	0.135

Table 5: Defuzzification results

	BONE	LIVER	LUNG
COX2	1	0	0
HER2	0	0	0
ER	1	0	0
PgR	1	0	0
EGFR	0	0	0
CK5	0	0	0
Nestin	0	0	0
Prominin1	0	0	1
SMA	0	0	0
SNAI1	1	0	0
SNAI2	0	0	0
CK18	1	1	1
Ecadherin	1	1	1
GATA3	1	1	0

Inference: Proteins CK18 and E-Cadherin are expressed in bone, liver and lung metastasis. Hence a single inhibitor which binds with both these proteins has to be selected to prevent these metastasis. This reduces the number of prescriptions given to an individual patient resulting in a tailor made drug delivery. Protein GATA3 is expressed in both liver and lung metastasis. Proteins such as SNAI1, COX2, ER and PgR are expressed in bone metastasis and prominin-1 is expressed only in lung metastasis. The combination of proteins is represented pictorially by the Venn diagram as shown in Fig. 7. Hence conclusions of the proteins which have an impact on the development of a particular metastasis can be drawn.

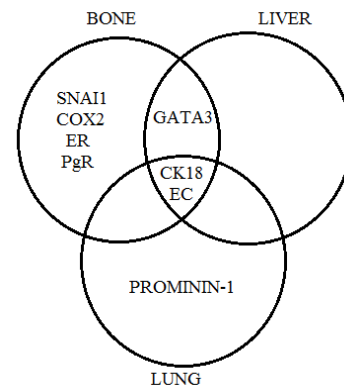


Figure 7: Venn diagram

5. Conclusion

In our paper we developed a prediction model for the first site of breast cancer metastasis. Membership functions for overly expressed proteins are developed. The Trained neural network is tested with different inputs. These results are found to be restricted for limited number of proteins. Hence fuzzy arithmetic is used to get the results for more number of proteins using lambda cut sets. These results were compared to that obtained from the survey paper's inference and were found to be very useful for the practitioner to propose the individual therapy

6. Future work

Clinical trials based on the above results if carried out and the resulting results incorporated in the input data sets used

in the above algorithm, still better prediction models can be developed.

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