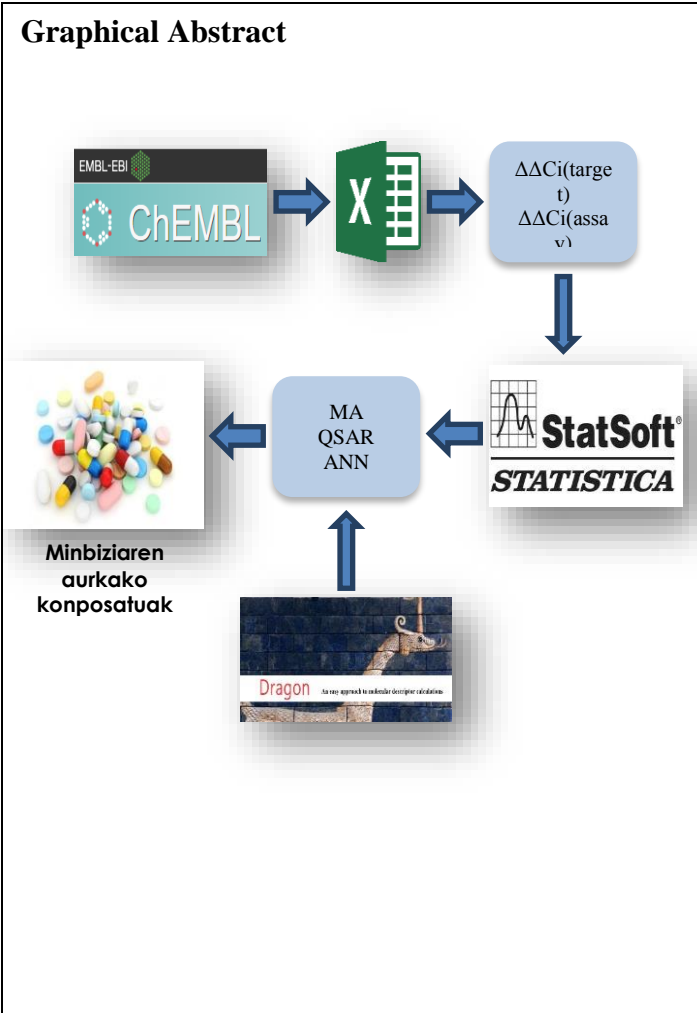


## Predicting preclinical activity values with PTML Model

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Graphical Abstract	Abstract.
 <p>The diagram illustrates the PTML model workflow. It starts with ChEMBL data (EMBL-EBI) being processed by X (Excel) to calculate <math>\Delta\Delta C_i(\text{target})</math> and <math>\Delta\Delta C_i(\text{assa})</math>. This data is then used by StatSoft STATISTICA for MA QSAR ANN modeling, which is supported by Dragon software. The final output is 'Minbiziaren aurkako konposatuak' (Compounds against cancer).</p>	<p><b>Abstract.</b></p> <p>ChEMBL-tik datu basea lortuta, perturbazio teoria (PT) eta Machine Learning (ML) teknikak erabilia PTML eredu bat eraiki da, zein perturbazioen efektua kuantifikatzeko erabili daitekeen konplexuak diren sistema biomolekularretan.</p> <p>Eredua hau erabilia konposatu berri batek minbiziaren aurkako parametron klinikoan (<math>k_i</math>, <math>LD_{50}</math>, etab.) balioak aurrean ditzakegu.</p> <p>After obtaining the database from ChEMBL to combine Perturbation Theory (PT) and Machine Learning (ML) we obtain PTML Model, it has been created to quantify the perturbations of complex biomolecular systems.</p> <p>Using this model we can predict preclinical (<math>k_i</math>, <math>LD_{50}</math>, etc.) values of new compounds against cancer.</p>

### References

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