

Supplementary Information

for

IPECnet: ML model for predicting the area of water solubility of interpolyelectrolyte complexes

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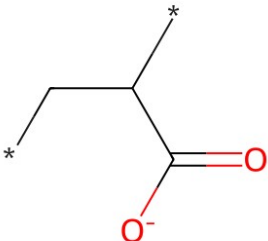
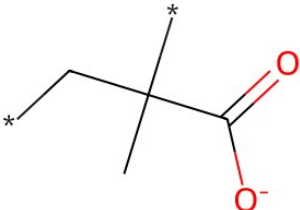
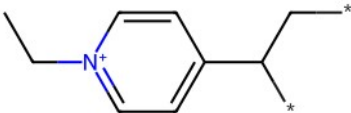
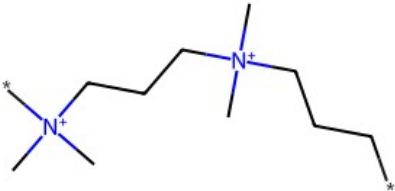
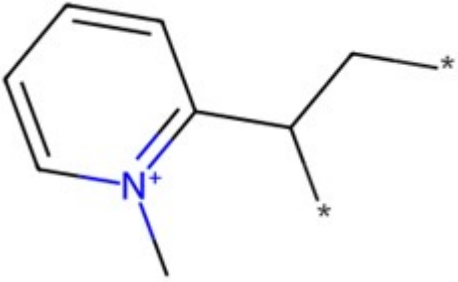
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Table S1. The structures of monomers of polymers studied in the work. Visualizations are obtained using the RDKit library. The chemical structure of the monomer is presented in the pSMILES format

PC/PA index	Polymer	
1	Sodium poly(acrylate) <chem>[*]C(C[*])C(=O)[O-]</chem>	
2	Sodium poly(methacrylate) <chem>[*]C(C)(C[*])C(=O)[O-]</chem>	
3	Poly-N-ethyl-4-vinylpyridinium bromide <chem>[*]CC([*])c1cc[n+](CC)cc1</chem>	
4	3,3'-ionene bromide <chem>[*][N+](C)(C)CCC[N+](C)(C)CCC[*]</chem>	
5	Poly-N-methyl-2-vinylpyridinium <chem>[*]CC([*])c1[n+](C)c(C)ccc1</chem>	

PC/PA index	Polymer	
6	2,4-ionene bromide <chem>[*][N+](C)(C)CC[N+](C)(C)CCCC[*]</chem>	
7	2,8-ionene bromide <chem>[*][N+](C)(C)CC[N+](C)(C)CCCCCCCC[*]</chem>	
8	Poly(allylamine) hydrochloride <chem>[*]CC([*])C[N+]</chem>	
9	Sodium poly(styrenesulfonate) <chem>[*]CC([*])c1ccc(S(=O)(=O)[O-])cc1</chem>	
10	Poly(4-vinylpyridinium) <chem>[*]CC([*])c1cc[n+]cc1</chem>	
11	Poly(diallyldimethylammonium chloride) solution == PDADMAC <chem>C1[n+](C)(C)CC(C[*])C1C[*]</chem>	

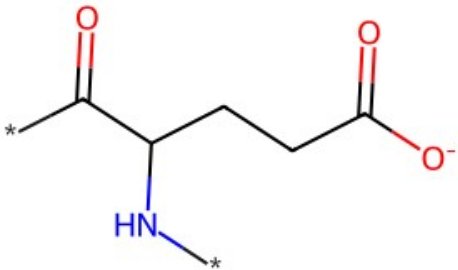
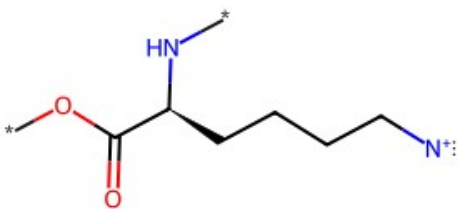
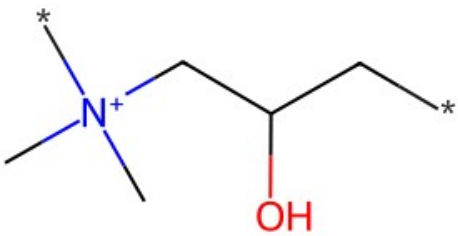
PC/PA index	Polymer	
12	Poly-L-glutamic acid sodium salt == PGA-Na <chem>[*]C(C(CCC([O-])=O)N[*])=O</chem>	 <p>The structure shows a glutamic acid residue in its sodium salt form. It consists of a central carbon atom bonded to a hydrogen atom (not shown), an amino group (NH) in blue, and two carboxylate groups. One carboxylate group is at the end of a three-carbon chain, and the other is at the end of a two-carbon chain. The amino group and one of the carboxylate groups are connected to a polymer chain, indicated by asterisks (*).</p>
13	Poly-L-lysine hydrobromide == polylysHBr <chem>C(CC[N+])C[C@@H](C(=O)O[*])N[*]</chem>	 <p>The structure shows a lysine residue in its hydrobromide form. It consists of a central carbon atom bonded to a hydrogen atom (not shown), an amino group (NH) in blue, and two carboxyl groups. One carboxyl group is at the end of a three-carbon chain, and the other is at the end of a two-carbon chain. The amino group and one of the carboxyl groups are connected to a polymer chain, indicated by asterisks (*).</p>
14	Hyperbranched Kaustamin == FL <chem>[N+]([*])(CC(O)C[*])(C)C</chem>	 <p>The structure shows a hyperbranched Kaustamin repeat unit. It consists of a central carbon atom bonded to a hydrogen atom (not shown), a hydroxyl group (OH) in red, and two carboxyl groups. One carboxyl group is at the end of a three-carbon chain, and the other is at the end of a two-carbon chain. The amino group and one of the carboxyl groups are connected to a polymer chain, indicated by asterisks (*).</p>

Figure S1. The Bootstrap AUC-score, F1-score and Accuracy with 90% confidence intervals for the models described above. Statistical significance according to the nonparametric Mann-Whitney U test is indicated in small Latin letters directly next to the graphs. “IPECnet polyBERT” – original “IPECnet” model described in article with polyBERT as molecular embedding, “IPECnet MFP” – “IPECnet” with Morgan Fingerprint as molecular embedding instead of polyBERT, “IPECnet GNN” - “IPECnet” with graph neural network as molecular embedding instead of polyBERT, “IPECnet OHE” - “IPECnet” with one-hot encoding as molecular embedding instead of polyBERT

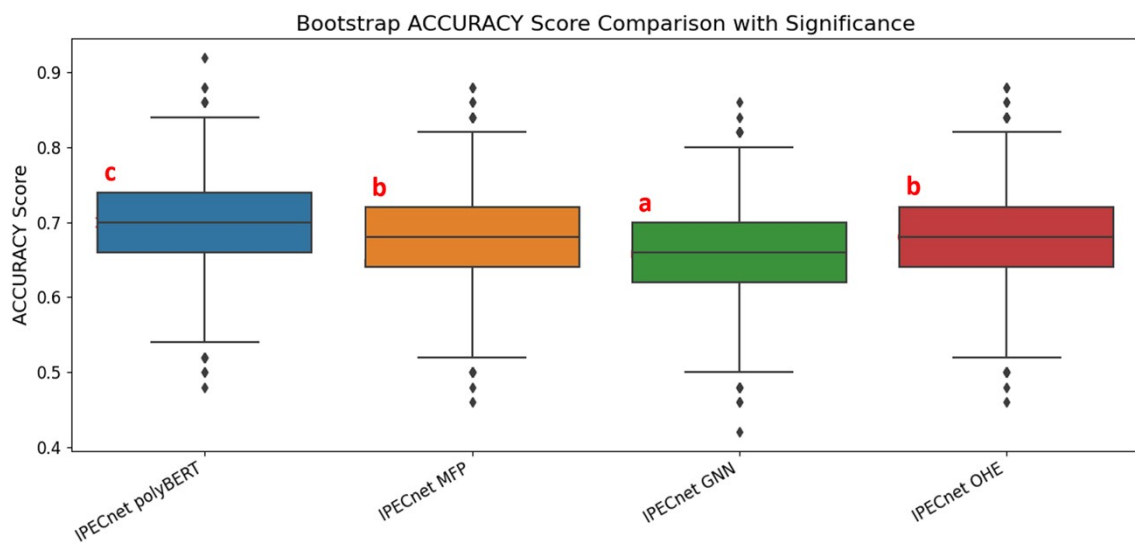
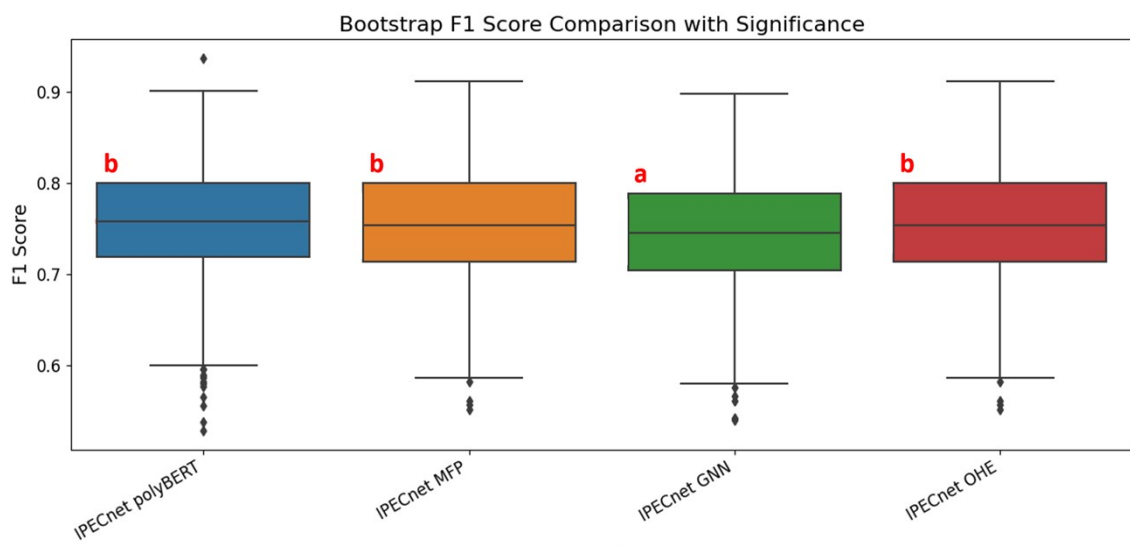
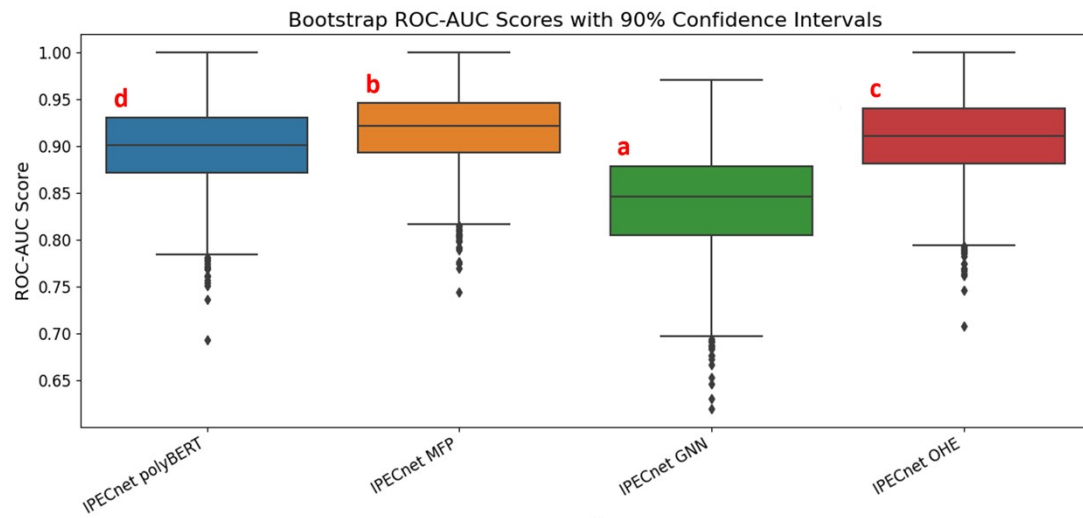


Figure S2. Trade-offs analysis between model complexity performance for “No chemistry model”, “IPECnet light”, “IPECnet” and “IPECnet without chemistry”

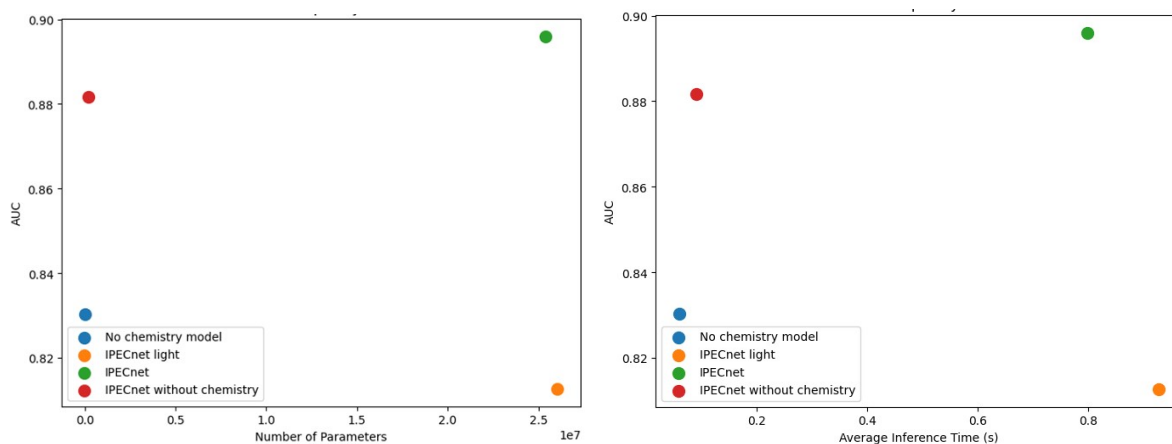


Figure S3. The results of comparing the “IPECnet” architecture model with various chemical embeddings (polyBERT, MorganFingerptint, GNN, OHE) trained on the initial and augmented datasets. As part of the application of the augmentation technique in our task, we examined samples increased in size by 4, 16 and 36 times. The results of the models trained on such datasets are marked on the graphs below as x4, x16 and x36, respectively. The method of compiling datasets using augmentation techniques is such that x2 means that each SMILES representation of GPE and HPE has been doubled, thereby increasing the total size of the dataset to x4. The rest of the changes were made according to the same rule. Augmentation technology was implemented based on [<https://arxiv.org/abs/1703.07076>].

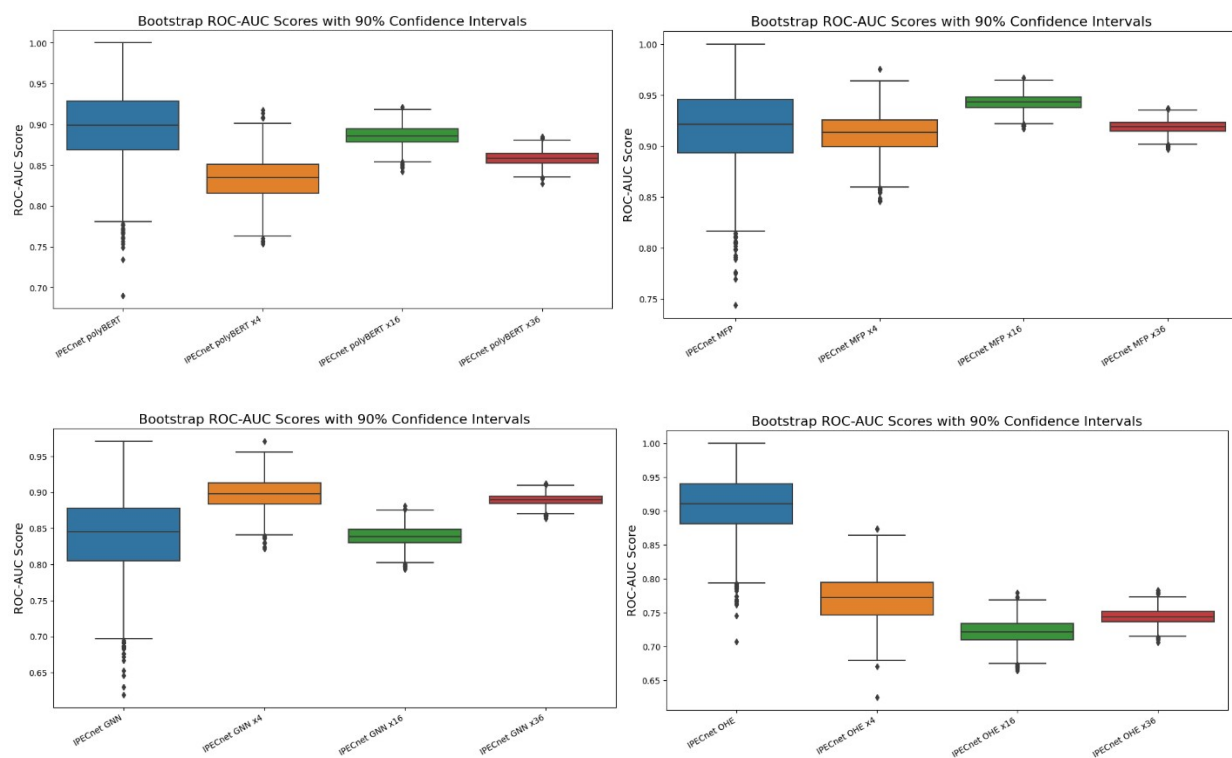


Figure S4. Average impact on model output magnitude for 20 most important (by mean ($|SHAP$ value)) features for “No chemistry model” (left) and “IPECnet without chemistry” (right). “PA_” features are properties related to the HPE polymer present in excess in the system. “PC_” features are properties related to the GPE polymer present in the defect in the system. Features designations are available on GitHub.

