

Supporting Information

for

**Orchestrating Explainable AI, ChatGPT, and Human Expertise: A Framework for
Extracting Polymer Design Guidelines**

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Building artificial neural network (ANN) models

The entire workflow/process to build artificial neural network (ANN) models (Models I, II) are written in details below. The steps were the same for Model I and II, except for the number of hidden layers used. Model II-mini was built based on Model II, trained upon a dimensionally reduced database obtained after feature selection using Model II.

Data pre-processing:

1. Original dataset containing 346 types of anion exchange membrane (AEM) polymers with chemical structures converted to 3,226 descriptors were preprocessed by removing columns with nonnumerical values and empty rows.
2. Standard scaler was applied to database obtained from 1. Standard scaler standardizes the value of explanatory variables present in the database via subtracting the mean, followed by scaling to unit variance (dividing all values by standard deviation).

Statistical feature selection:

3. Variance threshold (threshold = 0) was applied to the database obtained from 2. Variance threshold eliminates explanatory variables with low variance, which are typically constant or nearly constant throughout the whole database. Such variables provide minute information during prediction and might be taken as noise by the model, hence removing these low-variance features typically lead to improvement in model performance.
4. Maximum relevance — minimum redundancy (mRMR) was applied to the database from 3. MRMR was set to reduce the number of explanatory variables to 1,000 dimensions, while keeping “Block A (x)”, “Block B ($1-x$)”, “Block A/B ratio”, “Crosslinking [Yes/No]”, “alkaline stability temperature [$^{\circ}\text{C}$]”, “Concentration of alkaline solution soaked in [mol/dm^3]”, “alkaline stability [Days]”, “Conductivity Measuring Temperature [$^{\circ}\text{C}$]”, and “IEC” if not included in the database after mRMR. mRMR is a statistical-based feature selection method that identifies features with the highest relevance to the target variable while minimizing redundancy among selected features. It achieves this by maximizing mutual information between each feature and the target, and simultaneously minimizing mutual information among the features themselves, resulting in a compact and informative subset that preserves essential data characteristics.^{1,2} The same pre-processing steps 3. and 4. were applied to test database, a database containing AEM polymers not included in the train database (termed unseen AEM polymers), as well.

Construction of ANN And Explainable machine learning (ML)-Based Feature Selection:

5. The database from 4. was used to train two ANN models (Model I and II). The hyperparameters tuned using Optuna for both models include: the number of neurons for each hidden layer (ranging from 2 to 600), the activation function (Rectified Linear Unit (ReLU), tanh, or logistic), the solver (stochastic gradient descent (SGD) or Adam), the initial learning rate (0.00001–0.01 on a logarithmic scale), the regularization parameter α (0.1–5 on a logarithmic scale), and the batch size (64, 128, 256, 512 or 1024) were automatically optimized by trial suggestions. The optimized hyperparameters for each model are as follows:

- a. Model I used three hidden layers (Scheme S1a). The optimized hyperparameters are:

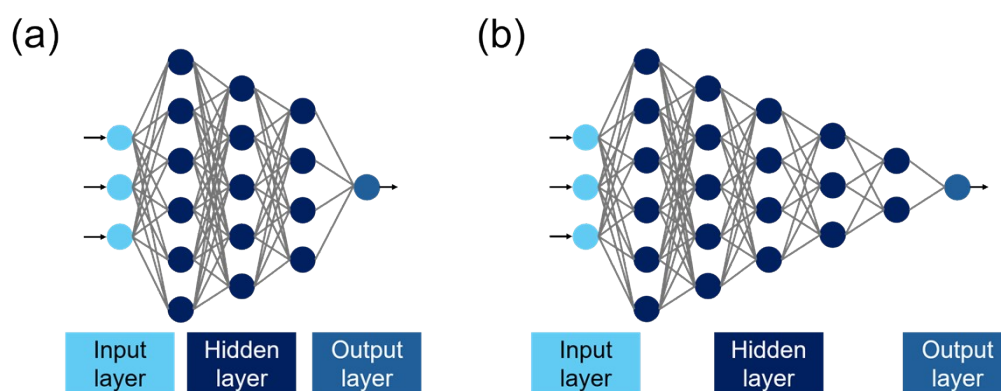
Table S1. Best hyperparameter settings of Model I.

Hyperparameter	Best Settings
Hidden Layer Sizes	512, 236, 64
Activation Function	tanh
Solver	adam
Initial Learning Rate	0.0001717234109928365
Regularization Parameter	4.446057291544881
Batch Size	1024

- b. Model II used five hidden layers (Scheme S1b). The optimized hyperparameters are:

Table S2. Best hyperparameter settings of Model II.

Hyperparameter	Best Settings
Hidden Layer Sizes	502, 372, 144, 66, 34
Activation Function	tanh
Solver	adam
Initial Learning Rate	0.0009447269296114181
Regularization Parameter	0.27577818216283784
Batch Size	512



Scheme S1. ANN with (a) 3 hidden layers (Model I), and (b) with 5 hidden layers (Model II and II-mini).

6. Predictive performance of Model I and II were evaluated, with their train-validation prediction accuracy shown in Figure S1, and the model to be used for the remaining of this study was chosen based on their predictive performance towards test AEM polymers. Model II was found to be superior to Model I, with root mean square error (RMSE) for test prediction of 0.0230 S cm^{-1} and 0.0349 S cm^{-1} , respectively. As such, Model II was used for explainable ML-based feature selection by applying ELI5 to Model II and selecting top 64 important explanatory variables.

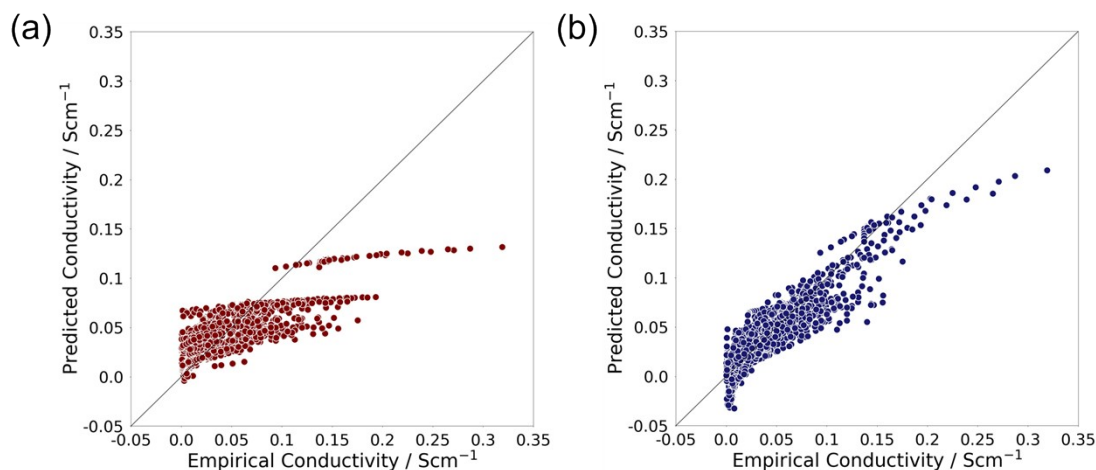


Figure S1. Predicted vs. actual anion conductivity plots from train-validation process of Models (a) I and (b) II.

ELI5 Global Explanation Explanatory Variable Importance

ELI5 provides a built-in Permutation Importance class that estimates each feature's significance by measuring the overall deterioration in predictive performance when that feature is shuffled across all samples in the validation set. For a trained model f and feature j :

1. Baseline Performance: Compute a baseline error metric E (e.g., mean squared error, accuracy) on the validation set D .
2. Feature Shuffling: Permute feature j across all samples in D , thereby destroying its original correlations.
3. Recompute Performance: Measure the new error E'_j under this shuffled condition.
4. Importance Scoring: Define global permutation importance of feature j as $\Delta_j = E'_j - E$, indicating how much the model's performance degrades when feature j is no longer informative.

Since the shuffling is performed at the dataset level, a single score Δ_j per feature is obtained, reflecting that feature's overall contribution to predictive performance. This procedure is repeated for each feature j , yielding a global ranking.

Table S3. Top 64 important explanatory variables obtained through applying ELI5 to Model II, listed in descending order according to their importance.

Explanatory Variable Names	Weight	Standard Deviation
Conductivity Measuring Temperature / °C	0.300825	0.004159
Ion Exchange Capacity (IEC)	0.099787	0.002317
MATS1i_B	0.020753	0.001089
MATS5d_B	0.018965	0.001024
alkaline stability / Days	0.018214	0.000721
MATS2s_B	0.01419	0.000832
AATS8Z_A	0.013021	0.000699
AATSC5d_B	0.012452	0.00094

MATS6c_A	0.010221	0.000725
AATS8v_A	0.009684	0.000208
VE3_DzZ_A	0.008531	0.001072
Block B (1-x)	0.008461	0.000515
AATS6d_A	0.008395	0.000902
Xc-5d_B	0.008303	0.000864
SpMax_A_A	0.008215	0.000911
AATSC1i_A	0.007873	0.001232
MATS4s_A	0.007784	0.000862
AATS7Z_A	0.00773	0.000948
AATS6p_A	0.007603	0.001123
TMWC10_B	0.007569	0.000927
GATS3se_A	0.007379	0.000373
MATS1i_A	0.007346	0.001328
ATSC5d_B	0.007268	0.00109
SpMAD_Dzm_B	0.007236	0.000366
AATS8se_A	0.007195	0.000782
ATSC6d_A	0.007067	0.000738
AATSC6c_A	0.007024	0.000198
AATSC2m_A	0.00698	0.000975
MATS1p_B	0.006968	0.00063
GATS3c_A	0.006823	0.000786
AATSC1i_B	0.006644	0.000236
MATS4se_B	0.006535	0.000244
MATS5i_A	0.006523	0.000624
MATS6s_A	0.006463	0.000855
AATS8are_A	0.006417	0.000358
MIC5_A	0.006338	0.000758
MATS4Z_B	0.005941	0.000719
MATS1c_A	0.00589	0.000372
Concentration of alkaline solution soaked in / mol dm⁻³	0.005599	0.000951
ATSC0s_B	0.005539	0.000567
GATS6p_A	0.005505	0.00042
Xpc-4dv_A	0.005505	0.001369
BalabanJ_A	0.005452	0.000881
AATS8d_A	0.005327	0.000549

AATSC5i_A	0.005321	0.000206
ATS3dv_A	0.005271	0.000468
GATS8s_A	0.005122	0.0004
AETA_eta_B_B	0.005017	0.000306
AATS3v_A	0.004992	0.001105
VSA_EState8_A	0.00497	0.000321
MATS5v_A	0.004944	0.000486
Block A (x)	0.004914	0.000314
AATSC2Z_A	0.004846	0.000207
AETA_eta_BR_B	0.004815	0.000585
MATS4pe_B	0.004802	0.000336
GATS8pe_A	0.00478	0.00043
bpol_A	0.004627	0.000922
SpAD_A_A	0.004499	0.000731
AATSC0m_A	0.004496	0.000724
SRW06_A	0.004485	0.000465
ATS4v_A	0.00448	0.000689
SpMAD_DzZ_B	0.004401	0.000877
GATS8are_A	0.004399	0.000411
SM1_Dzare_A	0.004377	0.000608

Table S4. Top 20 important explanatory variables obtained through applying ELI5 to Model II, and their explanations.

Explanatory Variable Name	Type	Property Used	Lag	Chemical Meaning
Conductivity Measuring Temperature / °C	Experimental condition	—	—	Measuring temperature of anion conductivity.
IEC	Polymer characteristic	—	—	Ion exchange capacity of a polymer.
MATS1i_B	Moran autocorrelation; block B	Ionization potential	1	Measures how similarly ionization potential is distributed among directly bonded atoms in block B.
MATS5d_B	Moran autocorrelation; block B	Sigma electrons	5	Evaluates how sigma electron density is related across atoms five bonds apart in block B.
alkaline stability / Days	Experimental condition	—	—	Duration of alkaline stability test.

MATS2s_B	Moran autocorrelation; block B	Intrinsic state	2	Captures how electronic configuration characteristics vary between atoms two bonds apart in block B.
AATS8Z_A	Averaged Moreau–Broto autocorrelation; block A	Atomic number	8	Assesses how atomic number varies across atom pairs eight bonds apart in block A.
AATSC5d_B	Centered avg. Moreau–Broto autocorrelation; block B	Sigma electrons	5	Evaluates variation in sigma electron density among atoms five bonds apart in block B, centered to mean.
MATS6c_A	Moran autocorrelation; block A	Gasteiger charge	6	Measures similarity in partial charges across atoms six bonds apart in block A.
AATS8v_A	Averaged Autocorrelation; block A	van der Waals volume	8	Atomic size spread over long range
VE3_DzZ_A	Eigenvector-based descriptor (Barysz matrix); block A	Atomic number	Eigenvector 3	Captures global shape and branching of the molecule using atomic number and 3rd eigenvector components.
Block B (1-x)	Polymer characteristics	—	—	Molar ratio of block B.
AATS6d_A	Averaged Moreau–Broto autocorrelation; block A	Sigma electrons	6	Assesses how sigma electron count varies over 6-bond atom pairs in block A.
Xc-5d_B	Chi cluster index; block B	Sigma electrons	Order 5	Reflects the local branching and electron density pattern in 5-atom clusters in block B.
SpMax_A_A	Spectral descriptor; block A	—	N/A	Indicates overall molecular branching through the largest eigenvalue of the adjacency matrix in block A.
AATSC1i_A	Centered avg. Moreau–Broto autocorrelation; block A	Ionization potential	1	Measures variation in ionization potential between bonded atoms in block A, normalized to mean.
MATS4s_A	Moran autocorrelation; block A	Intrinsic state	4	Describes how electronic configuration changes between atoms four bonds apart in block A.
AATS7Z_A	Averaged Moreau–Broto autocorrelation; block A	Atomic number	7	Shows how atomic number differences spread across 7-bond-separated atoms in block A.
AATS6p_A	Averaged Moreau–Broto autocorrelation;	Polarizability	6	Indicates how atomic polarizability varies across atoms six bonds apart in block

	block A		A.
TMWC10_B	Total walk count; block B	—	Walk length = 10 Quantifies the extent of atomic connectivity via the number of 10-step atom-atom paths in block B.

Model Prediction Logic Evaluation Using SHAP

After using ELI5 to select the top 64 (actual = 67) important variables, the obtained train database was used to train Model II-mini. The hyperparameters tuned using Optuna for Model II-mini include: the number of neurons for each hidden layer (ranging from 2 to 48), the activation function (Rectified Linear Unit (ReLU), tanh, or logistic), the solver (stochastic gradient descent (SGD) or Adam), the initial learning rate (0.000005–0.01 on a logarithmic scale), the regularization parameter α (0.001–1.2 on a logarithmic scale), and the batch size (64, 128, 256, 512 or 1024) were automatically optimized by trial suggestions. The optimized hyperparameters for each model are as follows:

Table S5. Best hyperparameter settings of Model II-mini.

Hyperparameter	Best Settings
Hidden Layer Sizes	34, 22, 16, 8, 2
Activation Function	tanh
Solver	adam
Initial Learning Rate	0.0019061299275277247
Regularization Parameter	0.005890339596103016
Batch Size	64

SHAP was applied to Model II-mini, but not to Model II directly because calculating SHAP value for each variable requires huge amount of computation resources (Fig. S2a).

(a)

```

MemoryError                                Traceback (most recent call last)
Cell In [5], line 9
      8 explainer_train = shap.KernelExplainer(final_model_full.predict, X_train_scaled_pre_RFE)
      9 # calculate SHAP values for the train set
----> 10 shap_values_train = explainer_train.shap_values(X_train_scaled_pre_RFE)
      11 # Visualize the summary plot to see feature importance
      12 shap.summary_plot(shap_values_train, features=X_train_scaled_pre_RFE, feature_names=column_name_full_train)

File ~\lib\site-packages\shap\explainers\kernel.py:190, in Kernel.shap_values(self, X, **kwargs)
    188 if self.keep_index:
    189     data = convert_to_instance_with_index(data, column_name, index_value[i:i + 1], index_name)
--> 190     explanations.append(self.explain(data, **kwargs))
    191 if kwargs.get("gc_collect", False):
    192     gc.collect()

File ~\lib\site-packages\shap\explainers\kernel.py:382, in Kernel.explain(self, incoming_instance, **kwargs)
    379 self.kernel_weights[nfixed_samples:] *= weight_left / self.kernel_weights[nfixed_samples:].sum()
    381 # execute the model on the synthetic samples we have created
--> 382 self.run()
    384 # solve then expand the feature importance (Shapley value) vector to contain the non-varying features
    385 phi = np.zeros((self.data.groups_size, self.D))

File ~\lib\site-packages\shap\explainers\kernel.py:521, in Kernel.run(self)
    519 if self.keep_index_ordered:
    ...
    602         layer_units[i + 1]))
    603 # forward propagate
    604 self._forward_pass(activations)

MemoryError: Unable to allocate 2.44 GiB for an array with shape (9635064, 34) and data type float64
Output is truncated. View as a scrollable element or open in a text editor. Adjust cell output settings...

```

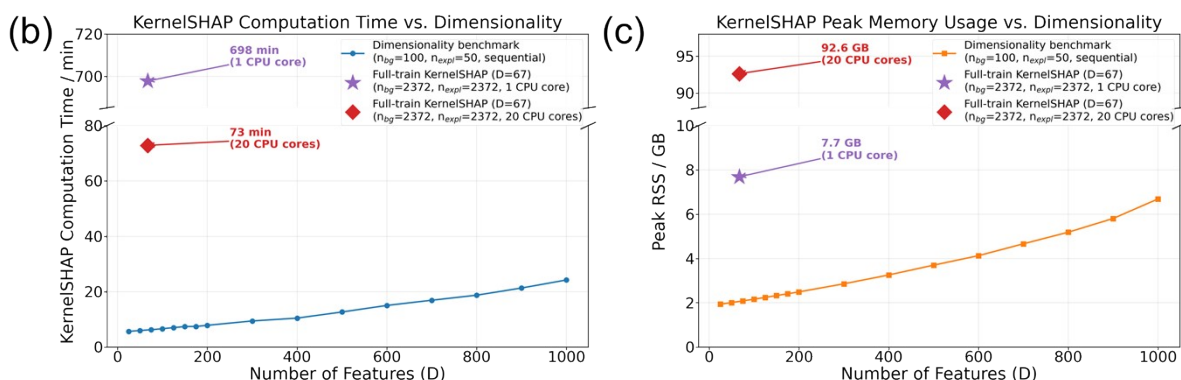


Figure S2. (a) Memory error message when trying to apply SHAP to Model II. Black boxes were placed over the portion of path directory to protect private information. The computation environment used was: Intel Core i9-11900K, 64 GB system memory, NVIDIA RTX 3060 graphics card. Python version: 3.9.7. KernelSHAP computational scaling with feature dimensionality. (b) Computation time and (c) peak memory usage (RSS) as a function of feature dimensionality D , benchmarked using an MLpregressor with the same hyperparameter settings as Model II, trained separately at each D using randomly selected descriptors ($n_{\text{background}} = 100$, $n_{\text{explain}} = 50$, $n_{\text{samples}} \approx 2D + 2048$). The dashed green line indicates $D = 67$ (Model II-mini, post-ELI5 feature selection). Both metrics increase monotonically with D , confirming that dimensionality reduction is essential for computationally feasible SHAP analysis of high-dimensional molecular descriptor datasets. The computational resource used for KernelSHAP computational scaling was: Intel Core i9-14900K, 192 GB (128 GB allocated for Windows Subsystem for Linux 2), NVIDIA RTX 4080 graphics card.

Table S6. KernelSHAP (KernelExplainer) computational benchmarks under controlled and manuscript-style settings. Runtime and peak RSS (Python process resident set size) were measured via subprocess monitoring of `/proc/[pid]/status` at 50 ms intervals. Per-thread Basic Linear Algebra Subprograms (BLAS) parallelism was limited (`OMP_NUM_THREADS = MKL_NUM_THREADS = OPENBLAS_NUM_THREADS = 1`) unless otherwise noted. Default KernelSHAP sampling was used ($n_{\text{samples}} \approx 2D + 2048$). Computational resource used: 192 GB (128 GB allocated for Windows Subsystem for Linux 2). (Panel A) Controlled scaling benchmark (fixed background and explained set). At each D , an MLP with the same hyperparameter settings as Model II was trained separately using randomly selected descriptors from the full feature set. $n_{\text{background}} = 100$ (k -means cluster centers); $n_{\text{explain}} = 50$; sequential (1 core). (Panel B) Manuscript-style feasibility benchmark (full training set). Model II-mini

architecture (hidden layers: 34, 22, 16, 8, 2) was used with the entire training set as both background and explained data. Parallel configuration distributed evaluation across 20 CPU cores using joblib.

Benchmark Regime	Setting	D	n _{samples}	n _{background}	n _{explain}	Cores	Time / min	Peak RSS / GB
Panel A — Controlled scaling benchmark								
Controlled	Sequential	25	2,098	100	50	1	5.67	1.94
Controlled	Sequential	50	2,148	100	50	1	5.98	2.01
Controlled	Sequential	100	2,248	100	50	1	6.63	2.16
Controlled	Sequential	200	2,448	100	50	1	7.86	2.49
Controlled	Sequential	400	2,848	100	50	1	10.46	3.26
Controlled	Sequential	600	3,248	100	50	1	15.04	4.13
Controlled	Sequential	800	3,648	100	50	1	18.74	5.19
Controlled	Sequential	1000	4,048	100	50	1	24.23	6.69
Panel B — Manuscript-style feasibility benchmark								
Manuscript-style	Sequential	67	2,182	2,372	2,372	1	697.7	7.69
Manuscript-style	Parallel	67	2,182	2,372	2,372	20	72.9	92.64

Parallelization achieved a 9.6× speed-up at the cost of a 12.0× increase in peak memory, as each parallel process (one per CPU core) instantiates its own KernelExplainer with associated internal allocations.

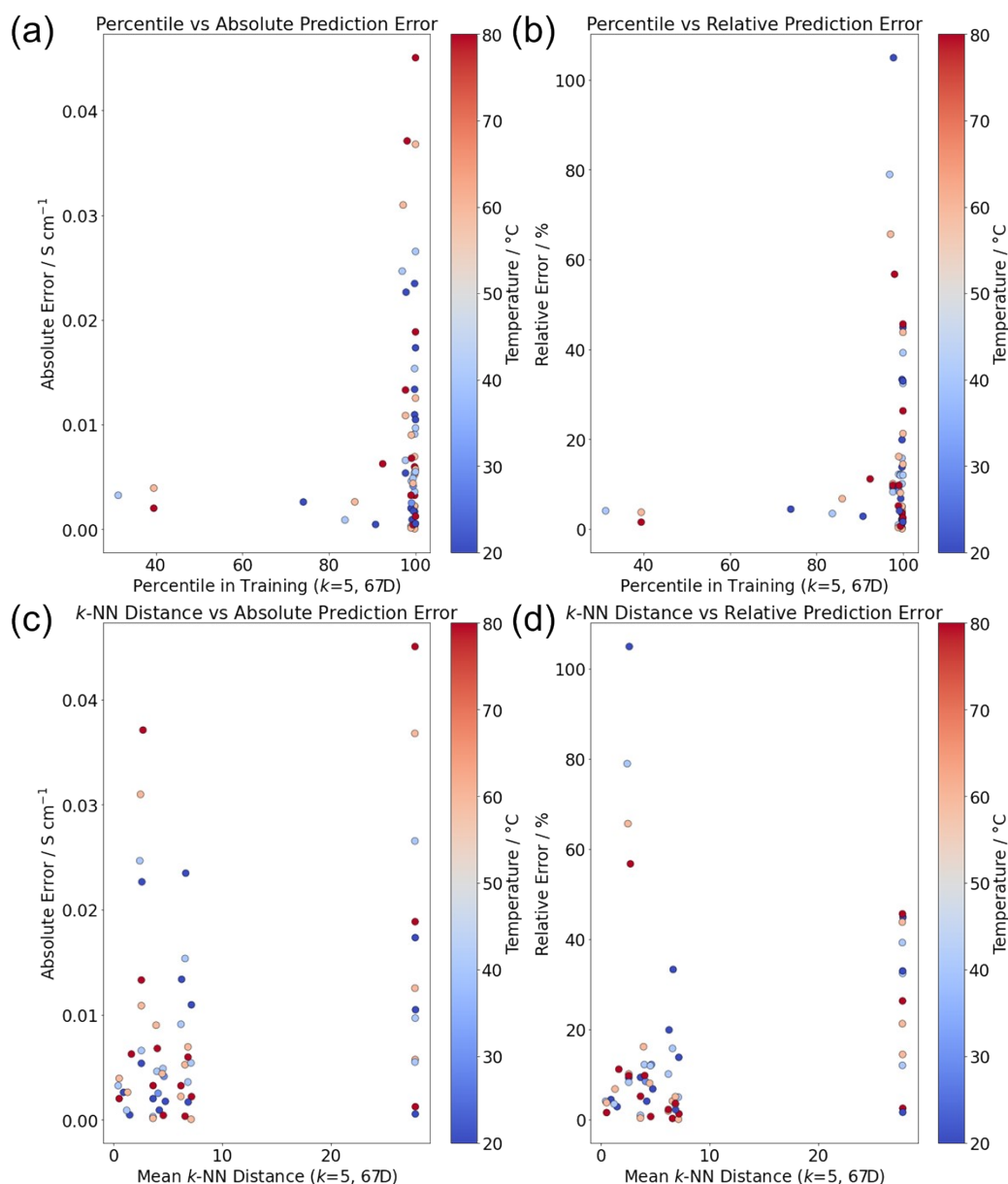


Figure S3. Relationship between applicability-domain metrics and prediction error for the 58 held-out test data points (14 polymers at multiple temperatures). (a) Percentile ranking (relative to training-set internal k -nearest neighbor (k -NN) distance distribution) vs. absolute prediction error. (b) Percentile ranking vs. relative prediction error. (c) Mean k -NN distance (standardized 67-dimensional descriptor space, $k = 5$ (default), Euclidean) vs. absolute prediction error. (d) Mean k -NN distance vs. relative prediction error. Points are colored by measurement temperature (colorbar). The analysis reveals that most test points cluster in the 97–100% percentile range with widely varying errors, whereas k -NN distance provides better separation: data points with k -NN distances ≤ 7.2 generally exhibit low absolute errors (MAE ≤ 0.015 S cm⁻¹), while those with substantially larger distances (~ 27.7 , PAEK-HQACz³ group) show elevated errors. The 95th percentile of the training-dataset internal k -NN distance distribution serves as a conservative reference; however, 50 of 58 test points exceed this threshold while the model retains strong overall predictive accuracy (test set RMSE = 0.0136 S cm⁻¹, MAE = 0.0089 S cm⁻¹), indicating that absolute k -NN distance is a more informative predictor of reliability than percentile ranking alone. Qualitative conclusions are unchanged for $k = 2$ –10.

Table S7. Applicability-domain analysis for held-out test polymers and conceptual AEM Polymer designs evaluated with Model II-mini. k -NN distances ($k = 5$, Euclidean) were computed in the standardized 67-dimensional descriptor space, with percentile rankings relative to the training-set internal k -NN distance distribution. The table reports mean, minimum, and maximum k -NN distances across the k nearest neighbors, along with the percentile rank and whether each data point falls within the 95th percentile reference threshold. Test polymers (14 unique polymers, 58 data points at multiple temperatures) are from four independent studies; conceptual AEM Polymer designs 1–4 are evaluated at 80 °C. Test polymers with k -NN distances ≤ 7.2 generally exhibit strong predictive accuracy, whereas those with substantially larger distances (~ 27.7 , PAEK-HQACz³ group) show degraded predictions. The four conceptual designs exhibit k -NN distances of 4.71–6.90, placing them within the range of well-predicted test polymers. Qualitative conclusions are unchanged for $k = 2$ –10.

DOI	Membrane Name	data set	Temperature / °C	Mean kNN distance	Min kNN distance	Max kNN distance	Percentile in train	Within 95pct
10.1039/D2TA03862E	PTPipQ100	test	20	0.935299	0.445259	1.55968	74.07251	TRUE
10.1039/D2TA03862E	PTPipQ100	test	40	0.445259	2.25E-14	0.890518	31.28162	TRUE
10.1039/D2TA03862E	PTPipQ100	test	60	0.534311	2.25E-14	0.890518	39.50253	TRUE
10.1039/D2TA03862E	PTPipQ100	test	80	0.534311	2.25E-14	1.335777	39.50253	TRUE
10.1039/D2TA03862E	PTPipQ83	test	20	2.571135	2.54561	2.588705	97.68128	FALSE
10.1039/D2TA03862E	PTPipQ83	test	40	2.570591	2.54561	2.588705	97.68128	FALSE
10.1039/D2TA03862E	PTPipQ83	test	60	2.570591	2.54561	2.588705	97.68128	FALSE
10.1039/D2TA03862E	PTPipQ83	test	80	2.570591	2.54561	2.588705	97.68128	FALSE
10.1039/D2TA03862E	PpTASU	test	20	6.652945	6.569944	6.717292	99.78921	FALSE
10.1039/D2TA03862E	PpTASU	test	40	6.593556	6.554839	6.658002	99.78921	FALSE
10.1039/D2TA03862E	PpTASU	test	60	6.584967	6.554839	6.615053	99.78921	FALSE
10.1039/D2TA03862E	PpTASU	test	80	6.593556	6.554839	6.658002	99.78921	FALSE
10.1039/D2TA03862E	PpTDMP	test	20	7.174089	7.051777	7.244613	99.78921	FALSE
10.1039/D2TA03862E	PpTDMP	test	40	7.131088	7.051777	7.215233	99.78921	FALSE
10.1039/D2TA03862E	PpTDMP	test	60	7.146744	7.037706	7.215233	99.78921	FALSE
10.1039/D2TA03862E	PpTDMP	test	80	7.187408	7.093823	7.230917	99.78921	FALSE
10.1039/D2TA03862E	PmTASU	test	20	6.275044	6.187005	6.343254	99.78921	FALSE
10.1039/D2TA03862E	PmTASU	test	40	6.212058	6.170962	6.280434	99.78921	FALSE
10.1039/D2TA03862E	PmTASU	test	60	6.202949	6.170962	6.234885	99.78921	FALSE

10.1039/D2TA 03862E	PmTASU	test	80	6.212058	6.170962	6.280434	99.78921	FALS E
10.1039/D2TA 03862E	PmTDM P	test	20	6.877332	6.8447	6.923903	99.78921	FALS E
10.1039/D2TA 03862E	PmTDM P	test	40	6.84993	6.830203	6.885345	99.78921	FALS E
10.1039/D2TA 03862E	PmTDM P	test	60	6.855709	6.830203	6.888011	99.78921	FALS E
10.1039/D2TA 03862E	PmTDM P	test	80	6.860538	6.830203	6.909571	99.78921	FALS E
10.1021/acs.iec r.1c04171	PPO-Pip	test	20	1.501055	0.313291	2.535559	90.76728	TRUE
10.1021/acs.iec r.1c04171	PPO-Pip	test	40	1.222339	0.313291	2.101985	83.68465	TRUE
10.1021/acs.iec r.1c04171	PPO-Pip	test	60	1.309054	0.313291	2.535559	85.96121	TRUE
10.1021/acs.iec r.1c04171	PPO-Pip	test	80	1.657729	0.313291	2.687393	92.41147	TRUE
10.1021/acs.iec r.1c04171	PPO- OPip	test	20	3.652812	3.557485	3.726523	98.94604	FALS E
10.1021/acs.iec r.1c04171	PPO- OPip	test	40	3.640957	3.557485	3.710622	98.94604	FALS E
10.1021/acs.iec r.1c04171	PPO- OPip	test	60	3.640957	3.557485	3.710622	98.94604	FALS E
10.1021/acs.iec r.1c04171	PPO- OPip	test	80	3.652812	3.557485	3.726523	98.94604	FALS E
10.1021/acs.iec r.1c04171	PPO- PipOH	test	20	2.61907	1.982621	3.253794	97.80776	FALS E
10.1021/acs.iec r.1c04171	PPO- PipOH	test	40	2.428706	1.982621	3.148925	96.92243	FALS E
10.1021/acs.iec r.1c04171	PPO- PipOH	test	60	2.492741	1.982621	3.469098	97.13322	FALS E
10.1021/acs.iec r.1c04171	PPO- PipOH	test	80	2.723426	1.982621	3.469098	98.06071	FALS E
10.1002/adfm.2 01902059	F20C9N	test	20	4.225305	3.76329	4.717406	99.19899	FALS E
10.1002/adfm.2 01902059	F20C9N	test	30	4.11201	3.78954	4.615144	99.07251	FALS E
10.1002/adfm.2 01902059	F20C9N	test	40	4.006738	3.76329	4.372499	99.03035	FALS E
10.1002/adfm.2 01902059	F20C9N	test	60	3.930904	3.76329	4.163465	99.03035	FALS E
10.1002/adfm.2 01902059	F20C9N	test	80	4.039732	3.76329	4.615144	99.07251	FALS E
10.1002/adfm.2 01902059	H22C9N	test	20	4.780602	4.345599	5.32397	99.4941	FALS E
10.1002/adfm.2 01902059	H22C9N	test	30	4.653355	4.368351	5.101121	99.45194	FALS E
10.1002/adfm.2 01902059	H22C9N	test	40	4.559302	4.345599	4.882686	99.40978	FALS E
10.1002/adfm.2 01902059	H22C9N	test	60	4.492018	4.345599	4.696416	99.40978	FALS E
10.1002/adfm.2 01902059	H22C9N	test	80	4.589478	4.345599	5.101121	99.45194	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.5	test	20	27.78548	27.7498	27.8354	100	FALS E
10.1016/j.mem sci.2021.11907	PAEK- HQACz-	test	40	27.75694	27.74623	27.77836	100	FALS E

9	0.5							
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.5	test	60	27.75337	27.74623	27.76052	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.5	test	80	27.76765	27.74623	27.80333	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.6	test	20	27.76484	27.72913	27.81479	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.6	test	40	27.73628	27.72555	27.75771	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.6	test	60	27.7327	27.72555	27.73985	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.6	test	80	27.74699	27.72555	27.7827	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.7	test	20	27.75665	27.72093	27.80662	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.7	test	40	27.72808	27.71735	27.74952	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.7	test	60	27.7245	27.71735	27.73165	100	FALS E
10.1016/j.mem sci.2021.11907 9	PAEK- HQACz- 0.7	test	80	27.73879	27.71735	27.77451	100	FALS E
—	AEM Polymer 1	conc eptua l	80	6.792802	6.780324	6.80264	99.78921	FALS E
—	AEM Polymer 2	conc eptua l	80	5.149477	5.060436	5.235003	99.70489	FALS E
—	AEM Polymer 3	conc eptua l	80	4.711315	4.631919	4.777318	99.4941	FALS E
—	AEM Polymer 4	conc eptua l	80	6.901414	6.84689	6.954268	99.78921	FALS E

Table S8. Top 20 important variables obtained from applying SHAP to Model II-mini, and their explanations.

Explanatory Variable Name	Type	Property Used	Lag	Chemical Meaning
AATSC5i_A	Averaged & Centered Autocorrelation; block A	Ionization potential	5	Electron distribution across 5-bond distances
AATS8v_A	Averaged Autocorrelation; block A	van der Waals volume	8	Atomic size spread over long range
Conductivity Measuring Temperature / °C	Experimental condition	—	—	Measuring temperature of anion conductivity.
SRW06_A	Self-Returning Walk Count; block A	Topological structure	6	Cyclicity and local structural complexity
AATSC2Z_A	Centered averaged Moreau-Broto autocorrelation; block A	Atomic number	2	Measures similarity in atomic number between atoms two bonds apart, normalized by mean.
TMWC10_B	Total walk count; block B	—	Walk length = 10	Reflects the extent of atomic connectivity via all possible paths of length 10.
GATS6p_A	Geary autocorrelation; block A	Polarizability	6	Evaluates how polarizability differs between atoms six bonds apart.
GATS8are_A	Geary autocorrelation; block A	Allred-Rochow electronegativity	8	Assesses difference in Allred-Rochow EN between distant atoms (8-bond distance).
AATSC5d_B	Centered averaged Moreau-Broto autocorrelation; block B	Sigma electrons	5	Describes variation in sigma electron count across atoms five bonds apart in block B.

ATS3dv_A	Moreau-Broto autocorrelation; block A	Valence electrons	3	Shows how valence electron counts are distributed between atoms three bonds apart.
AATSC2m_A	Centered averaged Moreau-Broto autocorrelation; block A	Mass	2	Describes mass similarity between atoms separated by two bonds.
IEC	Polymer characteristic	—	—	Ion exchange capacity of a polymer.
AATS7Z_A	Averaged Moreau-Broto autocorrelation; block A	Atomic number	7	Evaluates variation in atomic number across atoms seven bonds apart.
GATS3se_A	Geary autocorrelation; block A	Sanderson electronegativity	3	Measures difference in Sanderson EN between atoms three bonds apart.
SpMAD_DzZ_B	Spectral mean absolute deviation; block B	Atomic number	—	Captures variability of atomic number contributions from the Barysz matrix in block B.
MATS4se_B	Moran autocorrelation; block B	Sanderson electronegativity	4	Measures similarity in Sanderson EN between atoms four bonds apart in block B.
MATS5i_A	Moran autocorrelation; block A	Ionization potential	5	Describes how ionization potential correlates between atoms five bonds apart in block A.
GATS3c_A	Geary autocorrelation; block A	Gasteiger charge	3	Evaluates charge differences (Gasteiger) among atoms three bonds apart.
AETA_eta_BR_B	ETA branching index; block B	—	Ring count	Quantifies molecular branching in block B considering the number

of rings.

GATS8pe_A	Geary autocorrelation; block A	Pauling electronegativity	8	Quantifies long-range electronegativity dissimilarity at 8-bond separation (Geary Coefficient).
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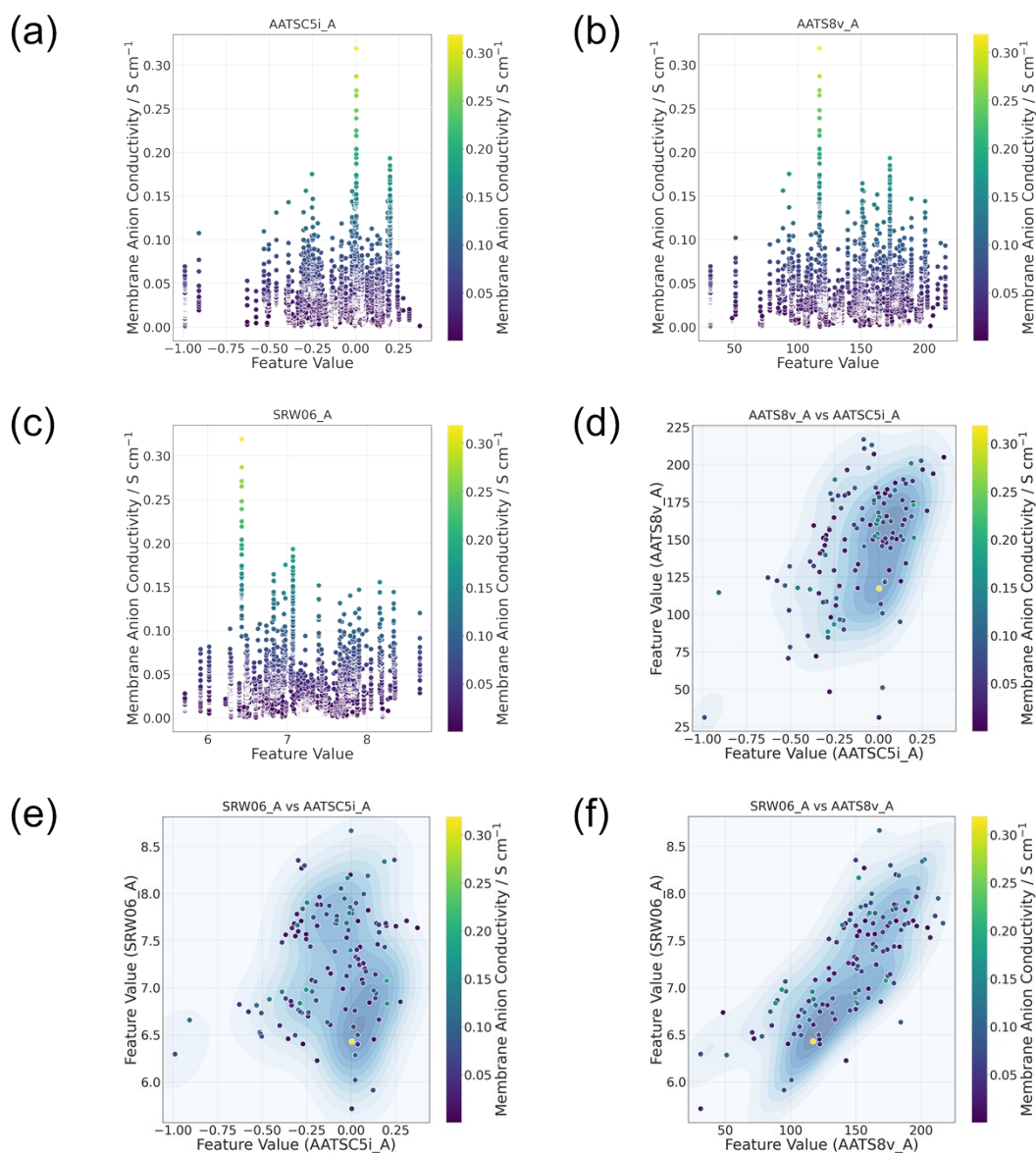


Figure S4. Scatter plot of descriptor value vs. anion conductivity for (a) AATSC5i_A, (b) AATS8v_A, and (c) SRW06_A. Scatter plot of descriptor value vs. descriptor value for the descriptor pairs (d) AATS8v_A vs. AATSC5i_A, (e) SRW06_A vs. AATSC5i_A, (f) SRW06_A vs. AATS8v_A. The color corresponds to anion conductivity value, with higher value shown in bright yellow, and lower value in dark purple. Blue color background represents density plot calculated according to datapoint count and their magnitude of anion conductivity, where darker blue represents higher density of datapoints with higher anion conductivity.

Table S9. Representative examples of ChatGPT output refinement through human-in-the-loop validation. ChatGPT served as an interpretive accelerator to generate initial draft explanations from source code and formal definitions; expert validation ensured scientific accuracy, appropriate epistemic humility, and practical relevance before incorporation into design guidelines.

Task	Typical LLM Tendency Observed	Expert Correction/Validation	Final Manuscript Outcome
Descriptor interpretation (AATSC5i_A, AATS8v_A)	Overconfident mechanistic narratives from correlation (e.g., "creates contiguous hydrophilic domains facilitating OH ⁻ transport")	Revised to hypothesis-level language; cross-checked against relevant AEM literature	Conservative phrasing: "consistent with," "may reflect," "suggests"
Design threshold identification	Screening-threshold heuristics (e.g., AATSC5i_A > 0, AATS8v_A > 140) implying monotonic improvement	Expert analysis of high-conductivity subset revealed non-monotonic tradeoffs	Refined to "optimal balance window" acknowledging upper limits
Length-scale significance (lag-5, lag-8)	Non-proactive: explanation provided only after explicit expert prompting	Domain knowledge required to formulate the appropriate question	Explicit connection to typical AEM side-chain architectures (7–8 σ -bonds)
Structural design suggestions	Generic suggestions without feasibility/stability context (e.g., "introduce heavier hetero-atoms")	Expert screening through established AEM synthesis knowledge	Retained only chemically plausible, synthetically accessible motifs
Statistical claims	Reports/derives statistics from supplied data without formal reproducibility context	Recomputed and confirmed in author scripts; only verified values reported	Statistics in manuscript derived from author-produced scripts

Table S10. Predicted anion conductivity profiles for AEM Polymers 1 and 3 under varying conditions. Temperature-dependent conductivity is shown at 20, 40, 60, and 80 °C (0 days alkaline exposure), followed by time-resolved alkaline degradation predictions at 80 °C over 0–100 days of exposure (1 M NaOH, 60 °C). Single-point predictions at 80 °C (0 days) are included for AEM Polymers 2 and 4 for reference. All predictions were performed using Model II-mini with IEC values calculated from the designed structures.

AEM Polymer No.	AATSC5i_A	AATS8v_A	IEC	alkaline stability / Days	Conductivity Measuring Temperature / °C	Predicted anion conductivity / S cm ⁻¹
1	0.07185	139.1117	2.40	0	20	0.04871
1	0.07185	139.1117	2.40	0	40	0.06682
1	0.07185	139.1117	2.40	0	60	0.08807
1	0.07185	139.1117	2.40	0	80	0.11244
1	0.07185	139.1117	2.40	1	80	0.11151
1	0.07185	139.1117	2.40	2	80	0.11059
1	0.07185	139.1117	2.40	3	80	0.10969
1	0.07185	139.1117	2.40	4	80	0.10881
1	0.07185	139.1117	2.40	5	80	0.10794
1	0.07185	139.1117	2.40	6	80	0.10709
1	0.07185	139.1117	2.40	7	80	0.10625
1	0.07185	139.1117	2.40	8	80	0.10543
1	0.07185	139.1117	2.40	9	80	0.10462
1	0.07185	139.1117	2.40	10	80	0.10383
1	0.07185	139.1117	2.40	100	80	0.07639
2	-0.06804	127.0347	2.08	0	80	0.07410
3	0.09846	161.8823	1.70	0	20	0.05211
3	0.09846	161.8823	1.70	0	40	0.06690
3	0.09846	161.8823	1.70	0	60	0.08368
3	0.09846	161.8823	1.70	0	80	0.10242
3	0.09846	161.8823	1.70	1	80	0.10157
3	0.09846	161.8823	1.70	2	80	0.10072
3	0.09846	161.8823	1.70	3	80	0.09989
3	0.09846	161.8823	1.70	4	80	0.09907
3	0.09846	161.8823	1.70	5	80	0.09827
3	0.09846	161.8823	1.70	6	80	0.09747
3	0.09846	161.8823	1.70	7	80	0.09668
3	0.09846	161.8823	1.70	8	80	0.09591
3	0.09846	161.8823	1.70	9	80	0.09515
3	0.09846	161.8823	1.70	10	80	0.09440
3	0.09846	161.8823	1.70	100	80	0.07306
4	0.1087	162.3189	1.56	0	80	0.07265

Table S11. Representative snapshot of the AEM polymer database showing raw experimental parameters. The complete database contains 2,452 entries from 346 unique polymers and is openly available on GitHub (https://github.com/KatoGroup-AppChemKU/AEM_Unsupervised-ML).⁴

Membrane Name (abbreviation)	Block A (x)	Block B (1-x)	Block A/B ratio	Polymer type	Conductivity Measuring Temperature [oC]	Membrane Anion Conductivity [S/cm]	ABC_A
PAEK-PYR50	0.198	0.802	0.247	1	80	0.00318	35.04061
PAEK-PYR75	0.502	0.498	1.008	1	80	0.00616	35.04061
PAEK-PYR100	0.7581	0.2419	3.134	1	80	0.01026	35.04061
PAEK-PYR125	0.967	0.033	29.303	1	80	0.01156	35.04061
⋮							

Data / Code Availability

The source code and database used in this study are available in GitHub (github.com/KatoGroup-AppChem-KU/AEM_Explained-ML_Workflow) to promote the introduction of machine learning within the community.

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