

Machine Learning-Guided Discovery of Polymer Membranes for CO₂ Separation

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Designing polymer membranes with high gas permeability and selectivity remains a grand challenge for energy, the environment, and economic sustainability. Increasing both the selectivity and permeability is a difficult multi-task constrained design problem for polymer membranes due to the trade-off between these two properties. The complexity of chemical composition and morphology of polymers makes this problem especially hard to attack with trial-and-error or intuition-based strategies. In this work, we instead present a machine learning (ML)-driven genetic algorithm to tackle the design problem of polymer membranes for CO₂ separation from N₂ and O₂. Using literature data of permeability for three gases, CO₂, N₂, and O₂, we constructed multiple ML models using different fingerprinting featurization schemes to predict all three gas permeabilities as well as the CO₂/N₂ and CO₂/O₂ selectivity values. Then, we employed a genetic algorithm to design new polymers and evaluated their performance with respect to the Robeson upper bounds using our machine learning models. We were able to identify new polymer membranes that are promising for both CO₂/N₂ and CO₂/O₂ separations. The

17 top discovered polymers are predicted to have high glass transition temperatures, T_g . Similarly,
18 the pyridine functionality was found in $\approx 20\%$ of the predicted polymers. Both of these facts
19 are well in line with currently accepted experimental wisdom for CO₂ based separations. The
20 framework developed here can be used to design polymers for any application involving con-
21 strained optimization. Finally, we outlined the strengths and limitations of this approach, as well
22 as the imminent challenges and opportunities with using machine learning guided data-driven
23 inverse design of polymers.

24 **Introduction**

25 The increased concentration of CO₂ in the atmosphere is the single most important anthro-
26 pogenic cause of global warming. Decreasing the release of CO₂ into the atmosphere requires
27 efficient CO₂ capture and separation technologies. Decades of research have been devoted to
28 improving existing gas separation technologies, but there is still an imminent need to find new
29 methodologies given the current course of climate change (1). Traditional unit operations have
30 the ability to isolate high-purity products, but they have a high carbon footprint due to the high
31 energy requirements. Membrane-based technologies are an attractive alternative because they
32 provide savings in capital and energy-related operating costs, and offer advantages related to the
33 ease of operation and compact environmental footprint (2–4). Polymer membranes have been
34 successfully investigated for H₂ recovery, N₂ generation, but there is still a significant opportu-
35 nity to improve polymer membrane technology for CO₂ separations. Although hundreds of new
36 materials are synthesized each year, most of the commercial membranes used today are from
37 the 1990s, and they rely on a dozen or so common polymer structures. This is largely because
38 the two properties that are important for a membrane material – high flux (permeability) and
39 high gas purity (selectivity) – are inversely correlated. This inverse relationship between gas se-
40 lectivity and permeability was first examined by Robeson in 1991 (5) and revisited in 2008 for

41 pure homopolymer membranes (6) and is famously known as the Robeson Upper Bound. Since
42 then, there have been considerable efforts in designing polymers that are above the empirically
43 determined upper bound for a given application (7–9).

44 Designing polymers with targeted structural and functional properties is challenging due
45 to the practically infinite polymer chemistry design space. Trial-and-error or intuition-based
46 strategies are not efficient, and they are likely to miss optimal solutions due to the complex-
47 ity of chemical composition and morphology of polymers. Furthermore, these strategies with
48 traditional experimental and computational routes are time and resource consuming. Machine
49 Learning (ML) models trained on polymer data sets can mitigate this problem, as it is possi-
50 ble to predict a new material's properties instantaneously by interpolating within an existing
51 dataset (10). There have been a number of studies in the recent literature that leveraged ML
52 to predict the properties of polymers. For example, Alves *et al.* developed models to discover
53 polymeric micelle formulations for poorly soluble drugs using micellar solubilization data (11).
54 Tao *et al.* used ML models to predict the glass transition temperature of a polymer based on
55 its structural formulation (12). Later, these authors also did a benchmarking study to compare
56 the predictive power of numerous ML models and showed the importance of structure and fea-
57 ture representations (13). Xu *et al.* used ML models to study swelling of polymer membranes
58 in different solvents with chemically informed molecular representations and descriptors (14).
59 Wang *et al.* used ML models to screen polymers for pervaporation separation (15) and devel-
60 oped a data-driven approach to predict the fractional free volume of polymers (16). There are
61 also excellent review articles published in the last couple of years that summarize the recent
62 developments in ML studies of polymer properties (17–26).

63 The success of applying ML models to design new polymer membranes for gas separation
64 has been comparatively lacking, largely owing to limitations in data availability. Barnett *et*
65 *al.* used experimental gas permeability data to develop a ML model to predict gas separation

66 in polymer membranes (27). They have successfully identified several polymers for improved
67 CO₂/CH₄ separation and synthesized two of them to experimentally validate the ML predic-
68 tions. Yuan *et al.* used ML algorithms to predict the missing values for the permeability of
69 different gases in the online Polymer Gas Separation Membrane Database of the Membrane
70 Society of Australasia (28). Yang *et al.* used the same data set and leveraged ML models to pre-
71 dict gas permeability based on the polymer chemistry (29). However, a ML model that predicts
72 polymer properties by itself does not lead to the discovery of new polymer membranes with op-
73 timal properties. In principle, one can propose many candidate polymers, possibly at random,
74 and use ML to predict their performance. This is obviously not an efficient strategy. A ML
75 “forward model” needs to be coupled with an inverse design/generative algorithm to efficiently
76 explore the polymer material space. Genetic algorithms (GA) are an example of a data-driven
77 inverse design method, which can be effectively coupled with an ML model. Srinivasan *et al.*
78 used GA to design single-stranded DNA grafted colloids (30). These authors were able to re-
79 produce the experimentally validated phase diagram and additionally identify the formation of
80 four previously unobserved crystal structures. Kim *et al.* demonstrated one of the first data-
81 driven inverse design methods of new polymers having high band gap and high glass transition
82 temperature that is relevant for high-temperature and high-energy density dielectrics (31). They
83 successfully identified new polymer structures with the desired properties.

84 In this work, we follow a similar procedure to Kim *et al.* to design new polymer membranes
85 with the desired selectivity and permeability for CO₂ separation from N₂ and O₂. First, we start
86 by assembling a library of gas permeabilities corresponding to the experimental studies of var-
87 ious polymers. Next, we train multiple ML models based on various fingerprints to determine
88 which ML model performs the best in predicting gas permeability. Then, we use our ML mod-
89 els to drive a GA for 100 generations and create more than 16000 new polymer structures. We
90 also use different fitness functions to design the best possible polymers given our initial data set.

91 Application of this combined ML-GA framework results in the discovery of more than 20 new
92 polymers that are above both the CO₂/N₂ and CO₂/O₂ Robeson upper bounds, many of which
93 contain aromatic functional groups along with oxygen- and nitrogen- motifs, aligning with ex-
94 perimental observations that show imines and polyethers as promising polymer membranes for
95 CO₂ separation (32–36).

96 Results

97 We compiled a literature database of permeability for three gases – CO₂, N₂, and O₂ – in a
98 variety of polymers at a temperature range of 300–330 K. The number of data points for each gas
99 is different due to the availability of data in the literature, so we only considered polymers that
100 have permeability measurements for all three gasses. This resulted in 780 different polymers
101 in our library, which represent a sizable portion of the polymers that are typically included in
102 the most up-to-date Robeson plots. The selectivity versus permeability data for CO₂/N₂ and
103 CO₂/O₂ are shown in Figure 1. We see that there are only three polymers that are above the
104 CO₂/N₂ Robeson upper bound (37, 38). These polymers have a benzene ring and ether oxygen
105 functional groups in common, which are known to be favorable for CO₂ separation. There are
106 more than ten polymers that are above the CO₂/O₂ upper bound as shown in Figure 1b. The list
107 of all polymers in our library and permeability measurements are provided in the SI.

108 The first step in applying ML models to evaluate physical properties is choosing an appro-
109 priate mathematical form to be used as input. This is commonly known as featurization (or
110 fingerprinting in the chemo-informatics literature) and it is of critical importance to the quality
111 and interpretability of the ML models. We start with generating the simplified molecular-input
112 line-entry system (SMILES) (39, 40) representations of our polymers based on their repeating
113 units. We cap the two ends of the monomer structure with hydrogen atoms to create a consistent
114 data set. Based on our SMILES strings, we use two common fingerprints in the literature, the

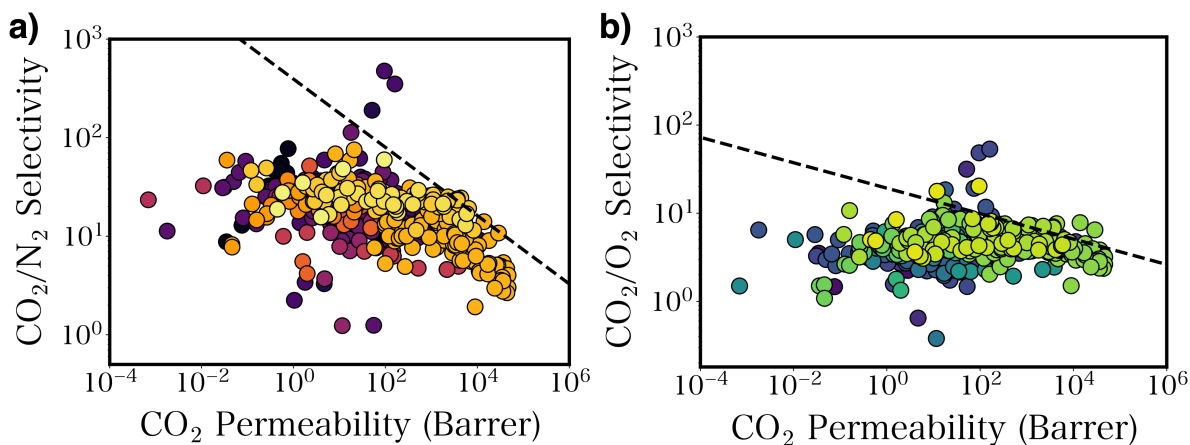


Figure 1: Robeson plot of selectivity versus permeability for (a) CO_2/N_2 and (b) CO_2/O_2 separations. The 2008 Robeson upper bounds (6) are shown as dashed black lines. Color code represents the different classes of polymers. Each data points represent a single polymer.

115 Extended Connectivity Fingerprint with bond diameter four Angstroms (ECFP4) (41, 42) and
 116 the Molecular ACCess System (MACCS) (43, 44) fingerprint. MACCS is a common substructure
 117 keys-based fingerprint consisting of a binary vector of 166 bits depending on the presence
 118 of certain substructures or features from a given list of structural keys (45). ECFP4 is an example
 119 of a topological fingerprint that is based on analyzing all the fragments of the molecule
 120 by looking at the environment of each atom up to a set radius, and then hashing every one of
 121 these environments to create the fingerprint. One needs to be careful when using hashed fingerprints
 122 because a bit cannot be traced back to a given feature, and this may result in a given bit
 123 corresponding to more than one different feature, which is called “bit collision” (46). We use
 124 ECFP4, based on the Morgan algorithm (47), which is a 2048 bit fingerprint as implemented in
 125 RDKit. Figure 2 shows the comparison for predicting CO_2 permeability with the random forest
 126 regression model using both fingerprints. We fit and plot the logarithmic permeability values to
 127 better visualize the data set. Both fingerprints result in R^2 value of 0.982 for the training set.
 128 However, R^2 for the test set is considerably higher when we use ECFP4 as shown in Figure 2.
 129 We also compare the root mean square error (RMSE) of the fits for both fingerprints. The test

130 set RMSE with ECFP4 fingerprint is 0.131, and the test set RMSE with MACCS fingerprint is
131 0.161. Thus, we use ECFP4 to train and test our ML models for the rest of this paper.

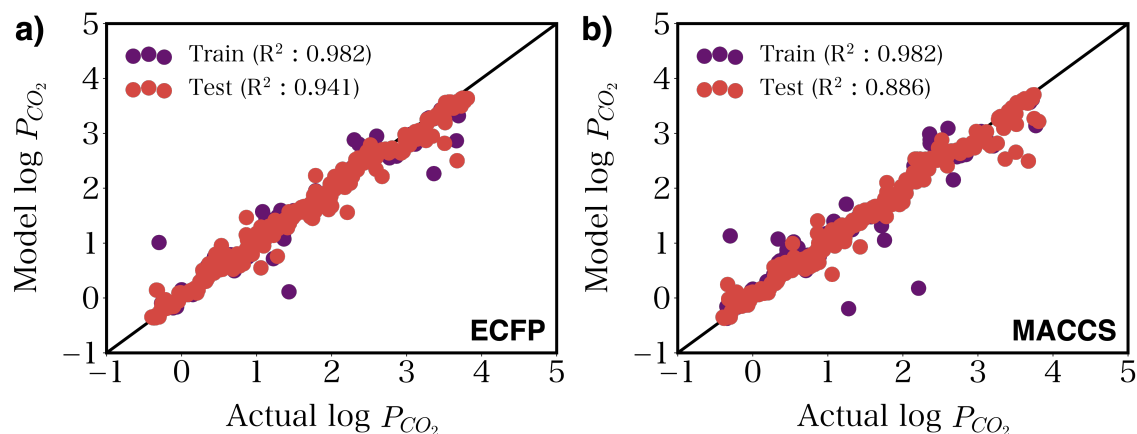


Figure 2: Comparison of CO₂ permeability model predictions using (a) ECFP and (b) MACCS fingerprints with random forest regression algorithm.

132 We start with randomly splitting our data set into one of two categories for each gas; one
133 is used for training the ML model, while the other is initially withheld during training. The
134 training data sets were 80% of our total database for each gas, which represents more than 600
135 polymers for each gas. We then apply the trained model to the remaining 20% of the polymers
136 (test set) and use these data as verification of the model's accuracy. Then, we employ various
137 ML models on the training sets including support vector regression (SVR), *k*-nearest neighbors
138 (KNN), decision tree, and random forest regression. Next, we compare the predictive power of
139 these popular ML regression models on CO₂ permeability values.

140 First we study SVR, which has the ability to consider non-linearity in the permeability
141 data (48). SVR results in R² value of 0.84 and 0.203 RMSE on the test set. KNN regression,
142 which predicts the target value by local interpolation of the targets associated with the nearest
143 neighbors in the training set, results in R² value of 0.822 and 0.242 RMSE on the test set. Then,
144 we employed a decision tree regression model, which uses a tree structure and inference layer to

145 achieve the final decision of the modeling results (18). Decision tree regression performs better
146 than both the SVR and KNN regression with R^2 value of 0.881 and 0.148 RMSE on the test set.
147 Finally, to make a more accurate prediction, we used a random forest regression model, which
148 is an ensemble learning method for regression that combines predictions from multiple decision
149 tree models. As expected, random forest predictions are better than all the other algorithms that
150 we have tried with R^2 value of 0.941 and 0.135 RMSE on the test set. Figure 3 summarizes the
151 different ML regression models that we have tried. We note that Yang *et al.* compared random
152 forest regression models with deep neural networks (DNN) and showed DNN model performs
153 better than the random forest regression model (29). However, DNNs typically require much
154 more data than what is available for this study.

155 To determine where on the Robeson plot a polymer is located, we need to be able to predict
156 the CO_2/N_2 and CO_2/O_2 selectivity as well as the CO_2 permeability. The ideal selectivity $\alpha_{i/j}$
157 for the gas pair is the ratio of the permeabilities P_i and P_j . Thus, we need ML models to predict
158 N_2 and O_2 permeability as well. Because the random forest regression model is the best per-
159 forming model for the CO_2 permeability, we have continued using random forest regression for
160 the N_2 and O_2 permeability. Figure 4 shows model predictions for the N_2 and O_2 permeability.
161 For both gases we can predict the gas permeability with R^2 values higher than 0.9. The RMSE
162 for N_2 and O_2 are 0.171 and 0.147, respectively. This demonstrates that we can predict all
163 three gas permeabilities accurately with the random forest regression model. Now that we have
164 established an accurate ML model to predict a polymer membrane's performance with respect
165 to the Robeson upper bounds, we start designing new polymers with a GA and evaluate their
166 performance on the fly with these ML models.

167 The first step of the GA is to construct the "gene pool" that will be used to create the initial
168 parent polymers. We used the "Breaking of Retrosynthetically Interesting Chemical Substruc-
169 tures" (BRICS) algorithm as implemented in the RDKit Python package to get the chemical

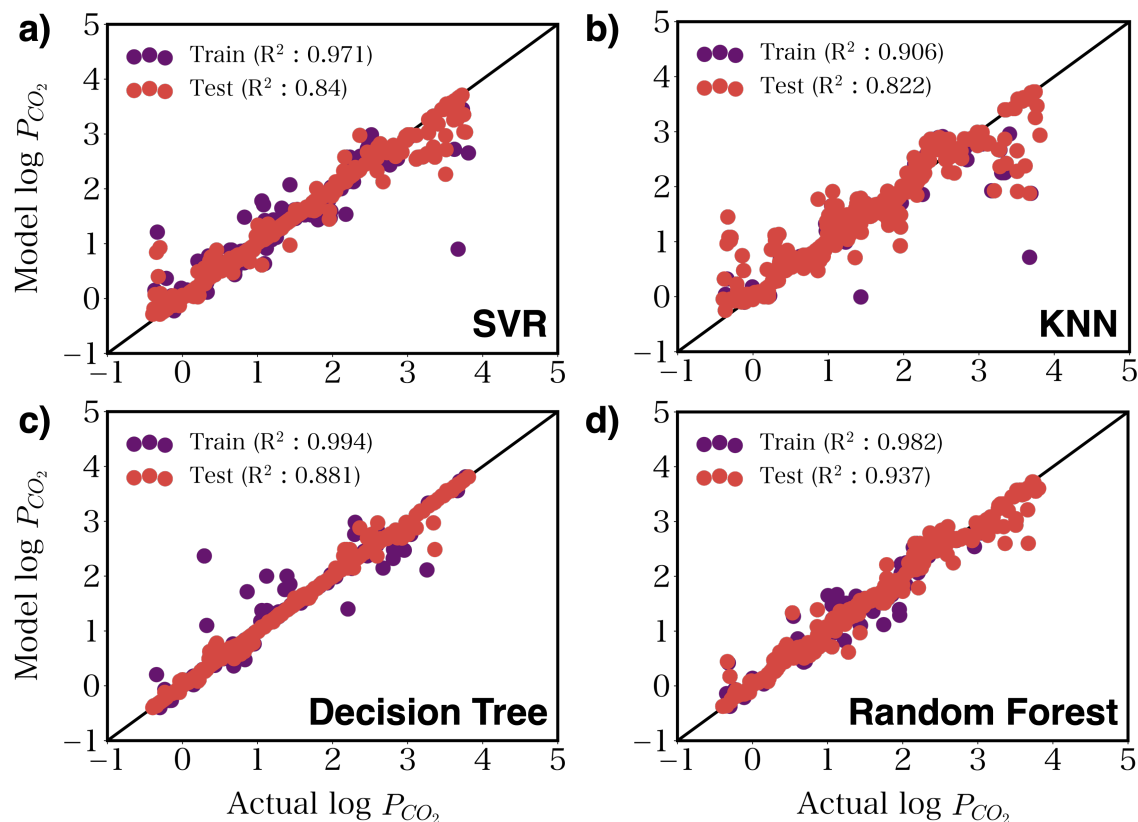


Figure 3: Comparison of CO₂ permeability model predictions using (a) SVR, (b) KNN regression, (c) Decision tree regression, and (d) Random forest regression models with ECFP fingerprints.

170 building blocks, or fragments, from our polymer library (49). A total of 79 unique fragments
 171 were extracted from 780 reference polymers. Figure 5 shows six functional groups that appear
 172 most frequently in our library. To initiate the GA process, 100 parent polymers consisting of 4
 173 building blocks in their monomer unit were created in the first generation. The fragments were
 174 chosen randomly from our gene pool of the 79 chemical fragments. Then, 15 families with the
 175 smallest Tanimoto similarity score (50), with 3 parents in each family, were chosen to perform
 176 crossover and mutation operations to alter their sequence of chemical building blocks, resulting
 177 in 12 offspring polymers in each family. During crossover, two parents generate an offspring
 178 by combining one random segment from a parent with another random segment from the other

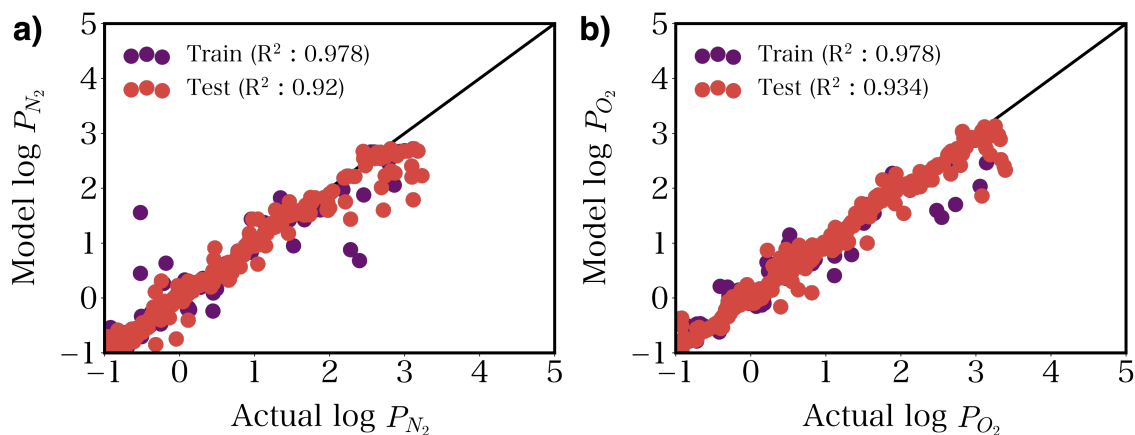


Figure 4: (a) N_2 and (b) O_2 permeability random forest regression model predictions with ECFP fingerprints.

179 parent. The segmentation point of a parent polymer was chosen according to a Gaussian dis-
 180 tribution with a mean at the center of the sequence and standard deviation of 0.3 blocks. We
 181 also applied mutation operations on 60% of the genes to increase the chemical diversity, where
 182 we randomly selected the building block in the sequence and replaced it with a new building
 183 block randomly chosen from the list of the 79 blocks. In each GA iteration, the top perform-
 184 ing offspring polymers with the highest fitness evaluation were retained as parents to create the
 185 next generation offspring polymers. We also assigned 10% migration rate between different
 186 families, whereby the highest-scoring polymers that were not selected as a parent migrated to
 187 a different family. An essential component in this evolutionary process is the polymer property
 188 estimation, which traditionally has been evaluated by experiments that are very time-consuming
 189 and expensive; here, we use our ML models for on-the-fly polymer property estimation.

190 We ran the GA for 100 generations and generated more than 16000 new polymer structures
 191 as shown in Figure 6. All the new polymers generated with the GA are reported in the SI,
 192 where we highlight the top performing 100 polymers. We optimized multiple parameters in
 193 the GA framework to guide the evolutionary process towards the targeted design area. First,

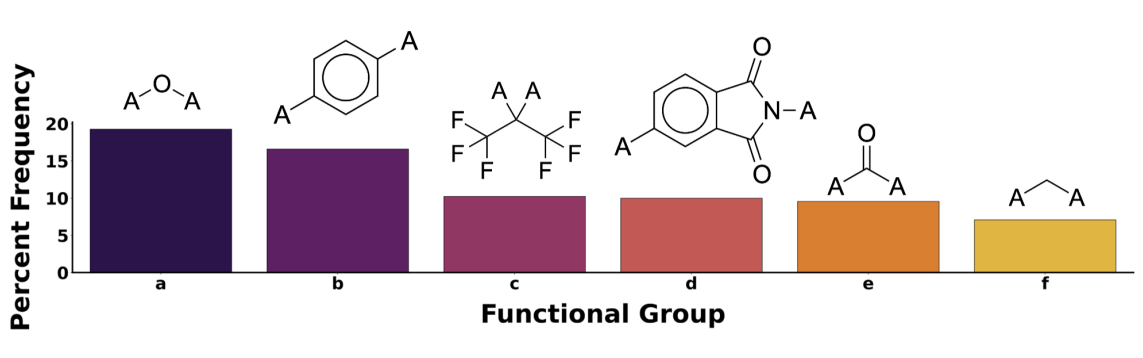


Figure 5: The six most chemical functional groups that appear in our library of experimental polymers using the BRICS algorithm. "A" represents the binding sites.

194 we ran the GA with an ML model trained with two different fingerprints, ECFP and MACCS
 195 keys, and found that the fingerprint used in the ML does not influence the top performing poly-
 196 mers identified from the GA framework. Next, we tried running the GA for an additional 100
 197 generations to see if running the GA for longer will result in better performing polymers, but
 198 found that the additional iterations did not result in any improved polymer structures. Finally,
 199 we tried multiple fitness functions to optimize the evolutionary trajectory. To optimize both
 200 CO_2/N_2 and CO_2/O_2 selectivity as well as CO_2 permeability, one needs a fitness function that
 201 includes all three metrics. However, the functional form of the fitness function is not clear *a*
 202 *priori*. We tried the fitness function $\log(P_{\text{CO}_2}) \times \alpha_{\text{CO}_2/\text{N}_2} \times \alpha_{\text{CO}_2/\text{O}_2}$ and showed that GAs
 203 using this fitness function failed to identify new polymer structures that are above both up-
 204 per bounds. We found that the fitness function based on the actual P_{CO_2} permeability values
 205 $(P_{\text{CO}_2} \times \alpha_{\text{CO}_2/\text{N}_2} \times \alpha_{\text{CO}_2/\text{O}_2})$ did result in several polymers that are above both the CO_2/N_2
 206 and CO_2/O_2 upper bounds as shown in Figure 6. Because CO_2 permeability values are gener-
 207 ally orders of magnitude larger than the selectivity values, this model favors the polymers that
 208 have higher permeability, thus biasing the GA towards better performing polymers.

209 We used the BRICS algorithm on the GA-generated polymers to understand which chemical
 210 building blocks are frequently observed in the top performing polymers. The top six frequently

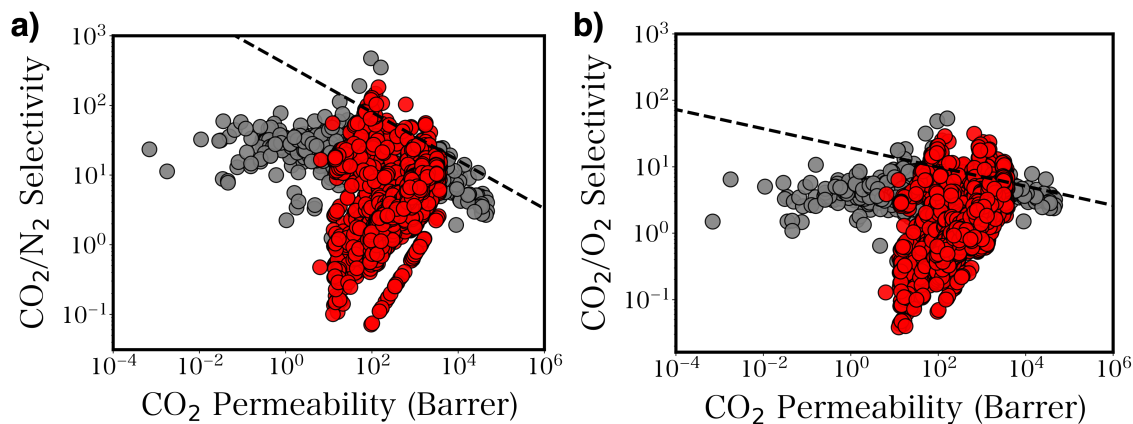


Figure 6: Robeson plot of selectivity versus permeability for (a) CO₂/N₂ and (b) CO₂/O₂ separations. The 2008 Robeson upper bounds are shown as dashed black lines (6). Colors represent experimental and GA generated polymers. Red color represents polymers generated with the GA. Each data point represents a single polymer.

211 observed functional groups with the 100 fittest GA-generated polymers are shown in Figure
 212 7. We identified a total of 464 chemical fragments within the fittest 100 polymers, and 18%
 213 of the fragments were pyridine functional groups. More than 70 polymers in the top perform-
 214 ing GA-generated polymers have the pyridine functional group in their repeating unit. This
 215 is by far the most frequently observed functional group, which is then followed by benzoxa-
 216 zole with 3%. We observe benzoxazole functional group in 13 polymers within the 100 fittest
 217 GA-generated polymers. Similarly, benzene, phosphonamidic acid, naphthalene, and dibro-
 218 mobenzene functional groups are also observed in the top performing polymers generated with
 219 the GA. We show six example polymer structures that have high fitness function values in Fig-
 220 ure 8. We note that these polymers have pyridine, benzoxazole, benzene, and phosphonamidic
 221 acid functional groups, which we identified as the most abundant functional groups with the
 222 BRICS algorithm. These polymers also include oxygen-, sulfur-, and nitrogen- containing
 223 motifs, similar to the three experimental polymers that are above the CO₂/N₂ upper bound.
 224 Oxygen- and nitrogen- containing motifs are reminiscent of imines and polyethers, which are

225 known to be high performing polymer membranes. Interestingly, our initial analysis using the
226 Polymer Genome software (51–54) suggests that most of the top 100 fittest polymers have high
227 glass transition temperature—well above the standard operating conditions (> 400 K). We note
228 that the three polymers in the experimental data set that are above the CO_2/N_2 upper bound also
229 have glass transition temperatures around 400 K. We speculate that the superior performance
230 of these glassy amorphous polymers for gas separation may be due to their high fractional free
231 volume and high number of microvoids (55, 56). It remains an open question whether or not
232 these polymers are easily synthesizable and easy to implement as membranes given their com-
233 plicated chemistry. Further computational and experimental studies will be required to better
234 understand these polymers and their efficacy as membrane materials.

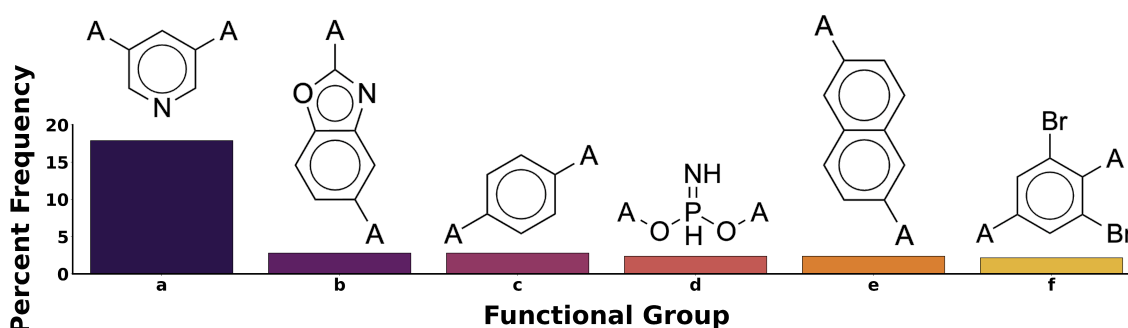


Figure 7: The six functional groups that appear most in the 100 fittest polymers generated with the GA using the BRICS algorithm. "A" represents the binding sites.

235 Discussion

236 We constructed an ML-driven GA to tackle the inverse design problem of polymer membranes
237 for CO_2 separation. We showed that the hashed-based ECFP4 yields lower predictive errors on
238 the test sets than the substructure keys-based fingerprints. We presented different regression-
239 based ML models, where random forest regression models resulted in the lowest RMSE and
240 highest R^2 values for both the test and the training set. Although random forest regression

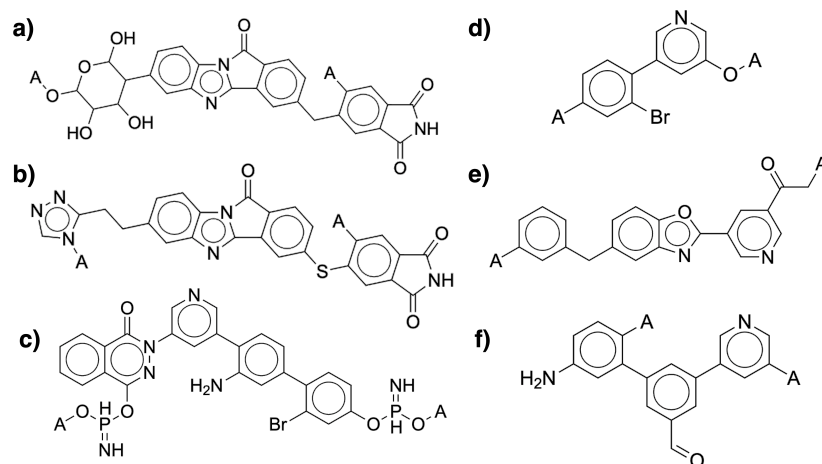


Figure 8: Example of polymer repeating units generated with the GA. "A" represents the binding sites.

241 models can successfully predict both the gas permeability and the selectivity, we used mod-
 242 els trained on the gas permeability, since these models have better predictive power than the
 243 models trained on the selectivity. After obtaining the ML models to predict the performance
 244 of any polymer membrane candidate, we implemented a data-driven inverse design algorithm
 245 to efficiently explore the polymer material space. In theory, one can use any inverse design
 246 algorithm for such a problem, but we have implemented a GA since it has been successfully
 247 used for other polymer applications. We created the gene pool using the BRICS algorithm on
 248 the experimental data and obtained 79 unique genes to initiate the GA process with 100 parent
 249 polymers that have 4 genes in their monomer unit. Fitness function is a key driving parameter
 250 in the GA, and as such, we used $P_{CO_2} \times \alpha_{CO_2/N_2} \times \alpha_{CO_2/O_2}$ to determine the fitness of the
 251 polymers. We performed crossover and mutation functions for 100 generations to create more
 252 than 16000 polymers during the GA process. Among these 16000 polymers, we were able to
 253 identify more than 20 new polymers that are above both CO_2/N_2 and CO_2/O_2 upper bounds.
 254 While validation of the new polymer structures identified in this work requires future molecular
 255 dynamics simulations and experimental measurements, this work helps identify the strengths

256 and the weaknesses of combining ML models and GAs as discussed below.

257 Three key points emerged from our analysis on comparing popular fingerprints. First,
258 hashed-based fingerprints result in lower predictive errors on the test sets than the substructure
259 keys-based fingerprints. However, hashed-based fingerprints have one main disadvantage
260 compared to the substructure keys-based fingerprints, which is not having a one-to-one correspondence
261 between the fingerprint vector and the chemical structure. This is not the case with
262 the substructure keys-based fingerprints, where each bit corresponds to a predetermined sub-
263 structure. This disadvantage does not affect our framework since we do not go back-and-forth
264 between the fingerprint and the chemical structure, and only use the fingerprinting when evaluating
265 the fitness function in the GA framework. Not performing crossover and mutation functions
266 on the fingerprints makes it possible to overcome this main disadvantage associated with
267 hashed-based fingerprints. Next, we note that the top performing polymer candidates identified
268 within this framework does not depend on which fingerprint is used in the GA. The relative
269 strength of the polymers with each other are similar with the two different fingerprints. The
270 main difference with using different fingerprints is the absolute value of the fitness function,
271 since the ML models trained on the substructure keys-based fingerprints tend to underestimate
272 the gas permeability. Finally, using the proper descriptor for a given application is still an open
273 question in the polymer informatics field, but we have shown that most often it does not affect
274 the final result. However, we emphasize that more sophisticated descriptors, like physical descriptor
275 vectors that include bulk properties of the polymer membranes, may make a difference
276 in the top performing polymers identified from the GA (57). For example, we believe the glass
277 transition temperature is a key property for polymer membranes, and including this information
278 in the fingerprint can lead to better performing polymer membranes within our framework.
279 The main bottleneck in switching from popular fingerprints to physical descriptors is gathering
280 consistent measurement data from hundreds of different experimental papers. The only way to

281 overcome this bottleneck is to create our own data sets using computational simulations so that
282 we can consistently calculate the physical properties of interest for each polymer.

283 We have demonstrated that a random forest regression model performs best when predicting
284 the gas permeability and selectivity of polymer membranes. Because there is a significant dif-
285 ference in the R^2 values and the RMSEs, we use random forest regression models in the entire
286 framework. However, random forest algorithms, like essentially all data-driven methods, are
287 intrinsically interpolative (10). They are only suited to optimize properties within the bounds
288 of the data the model was trained on. Models can still generalize, and interpolate “between
289 molecules” in some abstract design space (58), but they will not make accurate predictions
290 outside of this space. Thus, the performance of the new polymer structures identified in this
291 framework depends on the initial data set and the range of selectivity and permeability values
292 covered. One way to address this challenge is by using computer simulations combined with
293 e.g. an active learning loop to curate a polymer library will enable us to expand the number of
294 data points included in the ML framework. It is important to note that regardless of the data-
295 driven approach, ML models will always have a strong dependency on the initial data that they
296 are trained on. The only way to surpass this main limitation is to move towards active learn-
297 ing algorithms where we give the algorithm the ability to “learn” and draw inferences from its
298 experience to accelerate the evolutionary process (59, 60). New molecules generated as part of
299 the GA procedure could be screened by an uncertainty-quantifying algorithm, and when confi-
300 dence is low, new simulations can be run to acquire new ground truth data, which can then be
301 used to retrain the model. This is only possible if we use computer simulations (or a very high-
302 throughput, autonomous experiment) to curate the data since we will need to make on-the-fly
303 property estimations with an active learning framework.

304 Finally, we identify two significant points for coupling GAs with ML models to design new
305 polymer membranes. First, and most importantly, the fitness function drives the evolutionary

306 process of the GA. It is therefore of utmost importance to select the correct fitness function
307 to direct the GA towards the targeted design area. It is customary to train ML models on the
308 logarithmic permeability values since it narrows the range of the data, hence resulting in more
309 accurate models. Thus we tried the fitness function $\log(P_{CO_2}) \times \alpha_{CO_2/N_2} \times \alpha_{CO_2/O_2}$, aiming to
310 maximize both the gas permeability and selectivity throughout the evolutionary process. How-
311 ever, this fitness function was not able to push the GA towards the targeted design area. Even
312 though ML models trained on logarithmic permeability have slightly higher predictive power,
313 the small numerical value of the logarithmic permeability diminishes the importance of the per-
314 meability contribution to the fitness function. On the other hand, with a fitness function that
315 includes the absolute value of the permeability $(P_{CO_2} \times \alpha_{CO_2/N_2} \times \alpha_{CO_2/O_2})$, we were able to
316 push the evolutionary process toward the targeted design area and identified more than 20 new
317 polymers that are above both CO_2/N_2 and CO_2/O_2 upper bounds. We attribute the superior per-
318 formance of this fitness function to the fact that the absolute value of the permeability is usually
319 two orders of magnitude higher than selectivity values. This analysis also shows improving
320 the selectivity with the GA is much harder than the permeability since the fitness function be-
321 comes insensitive to the selectivity values when we include the gas permeability. In the future
322 this can be avoided by normalizing the parameters where the normalization would negate this
323 effect. Next we emphasize that, our GA was able to converge within 100 generations, since
324 running the algorithm for an additional 100 generations did not result in any superior polymer
325 membranes. With 100 generations and 4 initial building blocks in the first generation, a total
326 of 17571 new unique polymer structures were created. With 79 unique genes, the number of
327 sequences that can be generated by the GA is at least 79^4 (since longer sequences are gener-
328 ated throughout the evolutionary process). This suggests that the GA converges very fast, only
329 exploring less than 1% of the possible polymer material space. We decided to use 4 genes
330 with the initial generation because we have a relatively small gene pool. Using more building

331 blocks with the initial generation could have created more complicated structures throughout
332 the evolutionary process. This can be further explored when we have a larger gene pool.

333 Our approach demonstrates successful implementation of an ML-driven GA to design poly-
334 mer membranes for CO₂ separation, but more importantly, this framework can be used to design
335 polymer structure for any application (e.g. ion separation membranes and polymer electrolytes
336 for batteries), where there is a constrained optimization problem. The main limitation of the
337 current framework arises from its dependence on the initial experimental data. Curating the
338 data with computer simulations is a possible way to overcome this limitation. With better con-
339 trol over the initial data set we will be in a position to explore more sophisticated descriptors
340 and switch to an active learning framework where we make on-the-fly property estimations.
341 Computational ML-driven inverse design of polymer membranes is a promising platform that
342 can be further tailored to consider functions that incorporate the sustainability and synthetic vi-
343 ability of the polymers, in addition to gas selectivity and permeability, which are not yet widely
344 considered in computational studies.

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353 **Supplementary Material**

354 We provide the initial polymer library we have used to train our ML models with each polymer
355 represented as a SMILES string as well as the GA generated polymers with permeability for
356 three gasses (CO₂, N₂, and O₂).

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