Effective design principles for leakless strand displacement systems

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Artificially designed molecular systems with programmable behaviors have become a valuable tool in chemistry, biology, material science, and medicine. Although information processing in biological regulatory pathways is remarkably robust to error, it remains a challenge to design molecular systems that are similarly robust. With functionality determined entirely by secondary structure of DNA, strand displacement has emerged as a uniquely versatile building block for cell-free biochemical networks. Here, we experimentally investigate a design principle to reduce undesired triggering in the absence of input (leak), a side reaction that critically reduces sensitivity and disrupts the behavior of strand displacement cascades. Inspired by error correction methods exploiting redundancy in electrical engineering, we ensure a higher-energy penalty to leak via logical redundancy. Our design strategy is, in principle, capable of reducing leak to arbitrarily low levels, and we experimentally test two levels of leak reduction for a core “translator” component that converts a signal of one sequence into that of another. We show that the leak was not measurable in the high-redundancy scheme, even for concentrations that are up to 100 times larger than typical. Beyond a single translator, we constructed a fast and low-leak translator cascade of nine strand displacement steps and a logic OR gate circuit consisting of 10 translators, showing that our design principle can be used to effectively reduce leak in more complex chemical systems.

molecular programming | DNA strand displacement cascades | robustness | leak

N aturally evolved molecular machines are capable of conducting reliable computation from signal transduction to information storage and processing (1). The development of robust artificial molecular machinery could, in turn, enable the systematic construction of molecular computing embedded within living cells or cell-free molecular technologies.

The natural property of Watson–Crick base pairing makes DNA a powerful and unique engineering material to be rationa lly programmed and easily predicted at the nanoscale. In contrast to synthetic biology, which adapts naturally evolved molecular machines for new purposes (2), DNA nanotechnology aims to build up functionality from first principles (3). With a quantitative understanding of the kinetics and thermodynamics of DNA hybridization, the toehold-mediated strand displacement reaction (4) has emerged as a uniquely versatile building block (5). Strand displacement reactions underlie dynamics of DNA hybridization, the toehold-mediated strand displacement mechanism shown in Fig. 1A, an invader input strand displaces an output strand from an output strand through a cascade of nine strand displacement steps and a logic OR gate circuit consisting of 10 translators, showing that our design principle can be used to effectively reduce leak in more complex chemical systems.

Significance

The modern information age was enabled by encoding, transmitting, and manipulating information in a way that is robust to error. However, synthetic biology and molecular programming, fields that aim to recapitulate the successes of electronics within biochemistry, still struggle with error tolerance. The ability to create “smart” molecular systems capable of robust information processing and decision making would enable important applications in biomaterial production, biosensing, and therapeutics. Based on DNA strand displacement building blocks, we demonstrate de novo engineered molecular cascades robust to spurious interactions using an error correction scheme based on redundancy. In principle, arbitrary levels of error reduction could be attained. The information propagation cascades form a foundation for more complex, resilient, and faster programmable reaction networks.

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Desired and leak strand displacement reactions. Letter labels represent domains, which are contiguous bases that logically act as a unit. The domains

A Desired pathway: Toehold-mediated strand displacement

B Undesired pathway: Toeless strand displacement

C Short clamp domains (indicated by a darker shaded helix) help to reduce leak. The toeless displacement on the right side of the helix now requires larger fraying as shown. (Note that the clamp shown does not inhibit toeless displacement on the left side of the helix.)

Fig. 1. Desired and leak strand displacement reactions. Letter labels represent domains, which are contiguous bases that logically act as a unit. The domains with complementary sequences are labeled with asterisks. The black arrowheads show the direction of forward reactions, and the white arrowheads show the direction of backward reactions relative to the illustrated reaction pathway. Small arrowheads indicate reactions that are expected to be slow relative to other steps. Shaded background indicates molecular species that are initially present. Toehold domains are labeled by the symbol δ and a thicker strand line. (A) Intended strand displacement reactions are initiated by binding of a toehold (domain δa) followed by the displacement of the incumbent strand by the matching portion of the invader strand (domain b). The participating strands can have other domains on either side of the involved displacing region; for example, the dark blue rounded rectangle box represents the part of the released strand on the 5′ end not involved in this interaction. (B) Leak is hypothesized to be caused by toeless strand displacement reactions, which start from the fraying of the end of a DNA helix where no neighboring base pairs can help stabilize the structure. (Here, both ends of the helix could fray. The figure only shows one scenario.) After they are frayed, the opened nucleotides can be the initiation point for the undesired strand displacement. The invading strand can be a part of a larger complex, which is indicated by the yellow rounded rectangle box. (C) Short clamp domains (indicated by a darker shaded helix) help to reduce leak. The toeless displacement on the right side of the helix now requires larger fraying as shown. (Note that the clamp shown does not inhibit toeless displacement on the left side of the helix.)
to bind together to produce leaked signal. In contrast to clamping techniques that introduce an energy barrier to overall thermodynamically favorable reactions, forming such large complexes here incurs a thermodynamic (entropic) penalty, making leak unfavorable. In principle, this method could offer a systematic way to reduce leak to an arbitrarily low level by increasing $N$ and reducing concentration. In related prior experimental works, the cell surface automata by Rudchenko et al. (24) included components with effectively $N = 2$ redundancy, but leak reduction was not the aim. However, a systematic method to achieve leak reduction was still lacking before our work.

Here, we experimentally implement the previously proposed error reduction scheme (41) and demonstrate a dramatic reduction in leak. (Our scheme is compatible with the clamping technique described above. For a fair comparison with standard design methods, we use clamps throughout our design to show leak reduction beyond clamp-only schemes.) Going beyond the previous theoretical analysis (41), which required a low concentration and therefore, kinetically slow regime, here we demonstrate leak reduction for highly concentrated, fast systems. We experimentally characterize the systems from both thermodynamic and kinetic perspectives. In terms of thermodynamics, we demonstrate that it is possible to increase the free energy penalty to leak by increasing system redundancy, thus reducing the total amount of leak. We also develop a kinetic model that quantitatively captures the leak dynamics at high concentrations, including two distinct timescales of leak that we observed.

To investigate this leak reduction method, we start with the simplest nontrivial strand displacement cascade, a “translator,” which converts an input into an output of independent sequence. At the high concentrations permitted by the “leakless” design, the desired strand displacement reaction in the presence of input is very fast: the output signal reaches $>80\%$ completion within 3 min of addition of input, while by increasing redundancy, leak could be reduced to the limit of detection in our experimental setting. At $N = 3$ redundancy, no leak was observed in a 10-h experiment, even if the concentration was increased up to $10 \mu M$, which is on the order of 100 times higher than typical concentrations (50–400 nM) in strand displacement systems (9–11, 13, 16, 17, 20). In addition to showing that no measurable leak was produced in the duration of our experiment, we indirectly confirm that no significant leak would be generated even with longer incubation by measuring leak at thermodynamic equilibrium. Beyond a single translator, we also engineered a four-layer linear translator cascade consisting of 9 multistranded complexes and a three-layer digital circuit of five $OR$ gates consisting of 21 multistranded complexes. The fast (order of minutes) and low-leak (less than $5\%$ over 10 h) performance of these circuits shows that leak reduction generalizes to more complex settings.

Leakless Design
The Single-Long Domain and the Double-Long Domain Designs. To understand the leak mechanism in strand displacement systems, we begin by studying the simplest translator gate $X \rightarrow Y$, which consumes input signal strand $X$ to release output signal strand $Y$ of independent sequence to $X$. After it is released, the output strand can then react with a downstream component. The multistranded complexes are named fuels, since the net free energy of hybridization of complementary strands between signal strands and fuels drives the series of strand displacement reactions. Translators can be used to build logic $OR$ gate functionality by having multiple translators translate different input signals to the same output. Recent work demonstrated probabilistic switching circuits composed of translators, which can

Fig. 2. The typical SLD translator system. The symbol $\delta$ denotes a toehold-size subsection of a long domain (e.g., $\delta_2$ is the toehold-size $S'$ end of $\delta_2$). The faint blue background indicates the fuel and reporter species; the faint yellow background indicates the signal species. Domains that logically belong to input $X$ and output $Y$ are colored blue and red, respectively. (A) The intended pathway of the translator $X \rightarrow Y$ that translates strand $X$ to strand $Y$. Per standard practice, every fuel complex contains a clamp domain to help reduce leak. The input strand $X$ first interacts with the fuel complex $F_1$, displacing an intermediate strand $F_1$ with the toehold domain $\delta_2$ and the long domain $y_1$ exposed, which then reacts with $F_2$ releasing the output strand $Y$. The output strand $Y$ can be detected by a downstream reporter. (Inset) The sequences of $F_1$ and fuel $F_2$ used in our experiments. (B) The leak reaction of the translator in the absence of the input strand $X$. After the clamp in $F_2$ opens, the unbound domain $y_1$ in the fuel complex $F_1$ can interact with the sequestered domain $y_1'$ in $F_2$ through toehold strand displacement and then, produce the output strand $Y$. (Inset) Thermodynamic analysis suggests that there is very little energy difference between the leaked and unleaked states. Each full long domain is 15 bases, domains with the symbol $\delta$ and toehold domains are 5 bases, and clamp domains are 2 bases. The change in the number of base pairs due to the net leak reaction is equal to (toehold size) $- 2 \times$ (clamp size) $= 1$. As long as this number is small, it does not play an important role in the thermodynamics of the system. There is no difference in the number of separate components.
generate output signals with programmed concentration ratios (42). A catalytic molecular amplifier can be engineered if the output signal produced by the translator cascade is the same as the input signal. The simplicity of translator systems makes them amenable to biological applications: for example, as the molecular automata to target specific cellular surface markers (24).

Translators are also closely related to seesaw gates, which have diverse functionalities, including arbitrary Boolean and linear threshold computation (10, 11).

A typical translator gate consists of two fuel complexes (F1, F2) (Fig. 2A). In our schemes, we use four different domain types: full domains, almost full domains (with the symbol Δ), toehold domains (with the symbol δ), and clamp domains. Unless otherwise specified, full domains are 15 bases, Δ domains are 10 bases, δ domains are 5 bases, and clamp domains are 2 bases. Since we assume that domains with length longer than a toehold do not spontaneously dissociate, both the full domains and the Δ domains are called long domains. In Fig. 2A, since every fuel species is bound by one long domain, we refer to this scheme as the single-long domain (SLD) design.

The intended reaction pathway is a cascade of events in which each top strand of a fuel, after it is released, will subsequently react with a downstream fuel (or reporter) by toehold-mediated strand displacement. Critically, the toehold needed for the downstream reaction is initially sequestered within the upstream fuel complex (e.g., thick blue region of the top strand of F1 in Fig. 2), only becoming exposed and thus, active after the top strand is released. The output strand Y is initially sequestered on F2 and is expected to be released only after a cascade triggered by the input X. In our experiments, we measure the amount of Y released via a reporter complex as the downstream component. The two strands of the reporter complex are labeled by a fluorophore and a quencher. The output strand Y hybridizes with the fluorophore-labeled reporter strand, displacing its quencher-labeled binding partner and thus, separating the fluorophore and quencher. The increased fluorescence is measured by a spectrophotometer. The overall reaction results in the formation of one additionally bound toehold, which provides the thermodynamic driving force (clamps introduce slight reversibility in the desired reaction) (SI Appendix, section S1.1 has more details).

The leak pathway in the absence of input strand is thought to be caused by toehold strand displacement between the unbound long domain y1 in F1 and the bound long domain in F2 (Fig. 2B) (10). The output strand Y is thus released and can then react with a downstream component or be measured through the reporter.

To reduce leak without interfering with the desired reaction pathway, the SLD scheme can be modified to prevent the release of the output strand in the case of toehold displacement (41). As shown in Fig. 3B, the unbound domain y1 in fuel F1 can only partially displace the top strand (output strand) in fuel F2. Since the output strand remains bound by a long domain Δy2, it cannot easily dissociate. The resulting Ycomplex is then likely to quickly revert back into the two original fuel species. For leak to occur, Ycomplex must react with the downstream complex (e.g., reporter) before this reverse reaction. The intended pathway of the translator in this design is the same as that of the SLD translator: the input strand X initiates a cascade of two strand displacement reactions to produce the output strand Y (Fig. 3A). Since here, every fuel species is bound by two long domains, it is called the double-long domain (DLD) scheme.

The underlying leak reduction can be understood via a thermodynamic analysis. As simple metrics, we consider the number of base pairs and the change of the stoichiometry coefficients of reactants and products. We use “one unit of entropy” to indicate the entropic penalty due to the joining of two separate molecules. Quantitatively, one unit of entropy at concentration c M is $G_{\text{assoc}} + RT \ln(1/c) \approx 1.96 + 0.6 \ln(1/c)$ kcal/mol.

Fig. 3. The DLD translator system. The symbol Δ denotes an almost full domain, which is a 10-base subsection of a full domain. The faint yellow background indicates the signal species in the intended pathway (input X and output Y) and the species that can trigger the reporter in the leak pathway (Ycomplex). (A) The intended pathway of the translator X → Y that translates strand X to strand Y, which is similar to that of the SLD translator. (B) The proposed leak pathway of the DLD translator in the absence of the input strand X. After the clamp domain in F2 is open, the unbound domain y1 in fuel F1 displaces the y1 domain in fuel F2 through toehold strand displacement (the intermediate is shown in the pathway above the arrow), resulting in a short-lived species Ycomplex. Since the Δx1 domain is still bound, Ycomplex can quickly revert back to F1 and F2 via a unimolecular reaction (green). False-positive signal requires Ycomplex to react with the downstream reporter before dissociating. Note that Ycomplex can also isomerize to other concentrations (SI Appendix, Fig. S7). Thermodynamic analysis suggests that the leaked state has higher thermodynamic energy (one unit of entropic penalty) than the unlinked state. The change in the number of base pairs due to the leak reaction is equal to the toehold size $-2 \times \{\text{clamp size}\} = 1$. The number of separate components decreases by one after leak. Under experimental conditions, one entropy penalty is worth roughly 8 bp (in the text), and therefore, the thermodynamics is dominated by the entropic cost of leak.
at 37 °C (43). The entropic penalty is significant—at roughly 250 nM concentration and 37 °C, overcoming one unit of entropy penalty requires forming roughly 8 bp [the average free energy of forming 1 bp is 1.4 kcal/mol at 37 °C (43)]. Although the entropic penalty becomes smaller at higher concentrations, our results below demonstrate that it can still meaningfully prevent leak.

Based on these metrics, leak in the SL design is expected to be roughly thermodynamically neutral. Comparing the two states “before leak” and “after leak,” the leak reaction is driven forward by the energy of forming 1 bp, and there is no difference in the number of separate molecules (Fig. 2B). In the DLD design, leak also results in gaining the energy of binding 1 bp; however, since the output strand Y cannot be fully released in the leaked state, the after leak state has one less separate component than that of the reactants in the before leak state (Fig. 3B). Thus, compared with the SL design, the DLD design has a higher-energy penalty (one unit of entropic penalty) to leak. [Our choice of toehold and clamp lengths is typical of translator systems (10); different choices of toehold and clamp lengths would have resulted in a slightly larger gain or a slight loss of base pairs in the leak state, affecting the SLD and the DLD leak similarly.] Note that the leak reduction in the DLD design is not simply a result of the increased length of the double-stranded region of the fuels that stabilizes the complexes; DLD gives an order of magnitude greater reduction in leak. (Results and SI Appendix, section S5 have more information.)

The Triple-Long Domain Design. Beyond the DLD design, we ask if leak can be reduced further by increasing redundancy level to \( N = 3 \). The redundancy level \( N \geq 2 \) determines the number of bound long domains in fuels, the number of long domains in signal strands, the number of fuels in a single-translator system, the number of strand displacement steps in the desired reaction pathway to release the output, and most importantly, the number of fuels that must come together as a single complex before leak can occur. (Note that \( N = 1 \) is not a valid design; see SI Appendix, Fig. S11.) In the triple-long domain (TLD) scheme (Fig. 4), the sequestered output strand is bound by three long domains (\( \Delta x_3, \gamma_1, \) and \( \gamma_2 \)) in \( F3 \). All of the fuel complexes contain three bound long domains in the double-stranded region and one long domain unbound. The TLD translator contains three fuels species, and it takes three strand displacement steps to displace the output signal strand \( Y \) (Fig. 4A). Producing a leaked signal in the absence of input strand in the TLD translator system requires forming a complex with \( F1, F2 \), and \( F3 \) bound together. Leak in the TLD design is more unfavorable compared with other designs in terms of both kinetics and thermodynamics. In terms of kinetics, Fig. 4B provides a plausible leak pathway: to produce a leaked signal, \( F1 \) and \( F2 \) start by forming the four-stranded complex, which could quickly reverse to the original configuration. Then, \( F3 \) reacts with this complex, forming a six-stranded complex, which could also quickly reverse to the unreacted configuration. The downstream reporter needs to capture this six-stranded complex before the complex reverses to separate species. The leak pathway has more fast reverse steps compared with the DLD scheme, which reduces the probability of the reporter reacting with \( Y_{\text{complex}} \) even further. In terms of thermodynamics, leak results in two units of entropy penalty (and 1-bp penalty) comparing the before leak and after leak states. In principle, leak could be reduced through a systematic process to an arbitrary low level by increasing redundancy level \( N \) even further. Specifically, based on the fact that translator top strands have \( N + 1 \) long domains while bottom strands have \( N \) long domains, a counting argument shows that separating the two strands of the reporter in the absence of input (leak) requires forming a large complex of size \( 2^N \) strands (41).

While both our design and the technique of adding clamps insert additional double-stranded domains into fuel complexes,
the long domains added in our scheme can be opened via displacement rather than spontaneous dissociation as in the case of clamps. Therefore, our leakless design methodology is complementary to the technique of adding clamps, and both can be used simultaneously (as we do here). Note in particular that maximum size (toehold size) clamp schemes were recently shown to have strong thermodynamic guarantees of robustness not based on the association penalty and could in principle also lead to arbitrary leak reduction (44). However, the intended reaction in these schemes has a smaller thermodynamic driving force and necessarily does not reach full completion.

The DLD, TLD, and higher-redundancy schemes introduced in previous theoretical work (41) are motivated by the low-concentration regime in which the entropic penalty is largest and equivalently, the reverse (unimolecular) reactions along the leak pathway are much faster than the forward (bimolecular) reactions. In contrast, we demonstrate significant leak reduction with the DLD and TLD schemes even at concentrations of up to two orders of magnitude higher than the typical 50-400 nM regime.

**Results**

**Leak Reduction for a Single Translator.** To experimentally investigate the leak reduction method, we first need to generate the DNA sequences. Since the translators have the property that all domains have well-defined neighboring domains, the sequence space can be represented by one contiguous sequence (i.e., $x_1 x_2 y_1 y_2$ for the SLD and DLD designs). We generated sequence candidates randomly and eliminated the ones with sequences that could effect sequence synthesis or misfolded complexes. Because of the redundancy, it is less likely that a short truncation would result in leak in the DLD design (SI Appendix, Fig. S1).

Note that the baseline of the leak is higher in the SLD experiments. This so-called “initial leak” (13) is thought to be due to some small fraction of truncated complexes caused by imperfect sequence synthesis or misfolded complexes. Because of the redundancy, it is less likely that a short truncation would result in leak in the DLD design (SI Appendix, Fig. S2).

We would like a robust strand displacement system that is not prone to leak even at high concentration, which enables fast kinetics. Going beyond the low-concentration regime that underlies previous theoretical work (41), we increased the concentration of each fuel species to 10 μM, which is up to two orders of magnitude higher than the usual concentration...
used previously. We also increased temperatures, since higher temperature incurs a greater probability for fraying and thus, provides a more stringent test. Fig. 6A compares the leak kinetics of the SLD and the DLD translator in the absence of input strand at 37 °C. At 10 μM initial concentration of fuels, leak of the SLD translator saturates after 4 h, and it reaches one-half of the maximum within 30 min. Note that the reaction of Y with the reporter is reversible, despite being strongly biased forward, and therefore, after the initial kinetic phase of the leak, the system reaches thermodynamic equilibrium where the reporter molecules are not fully triggered. The leak fraction ([leak]/[initial fuel]) of the SLD translator after 10 h ranges from 24 to 41%, while that of the DLD translator is below 2% for all different initial fuel concentrations over all 10 h.

Our theoretical framework argues that the leak reduction of the DLD design is due to the entropy penalty manifested as unimolecular reverse reactions that undo leak intermediates rather than a result of the increased length of the double-stranded region stabilizing the fuel complexes. The results shown in SI Appendix, section S5 confirm that increasing the size of the bound domains in SLD fuel complexes to be the same as in the DLD scheme (the Long SLD scheme) does not decrease leak as much as the DLD scheme—the leak concentration after 10 h of the DLD scheme is still an order of magnitude smaller than that of the Long SLD scheme. Note that the Long SLD scheme requires longer strands than the DLD scheme, which is more expensive, especially for larger systems.

The leak kinetics of the DLD translator is compared with the TLD translator in Fig. 6B. The DLD leak shows two-phase behavior, which we discuss in Quantitative Model of Leak Reduction. As expected, the TLD translator shows an even greater degree of leak reduction, with no apparent leak even at high concentration (10 μM) for 10 h.

We further confirmed the theoretical prediction that the total amount of leak in a single-translator plus reporter system at thermodynamic equilibrium is lower in the DLD or the TLD schemes compared with the SLD scheme (Fig. 7). Leak concentration at thermodynamic equilibrium is an upper bound on the total leak that would ever be observed in the system. To reach thermodynamic equilibrium, the fuels and the reporter are slowly annealed for 18 h, and the fluorescence is subsequently measured. The annealed leak signal of the DLD design is approximately six times less than that of the SLD design. The TLD design has the least amount of total leak: when the fuel concentration is 5 μM, the TLD leak concentration is 20 times less than that of the SLD design. It is interesting that the kinetic decrease in leak seems more significant than the leak reduction at thermodynamic equilibrium.

Although the design principles demonstrated in this paper were effective in reducing leak, we did observe an undesirable property in the TLD scheme: the amount of output released was less than the amount of input provided [e.g., about 75% when fuels were initially 5 μM (SI Appendix, Fig. S9)]. A possible mechanism that could explain the decrease of the completion level, and which could only occur in designs with redundancy N ≥ 3, is presented in the SI Appendix, Fig. S10.

Quantitative Model of Leak Reduction. The thermodynamic analysis of the previous section can be quantitatively calculated by NUPACK (45) for the specific sequences that we used. The NUPACK energy model takes into account both the free energy of binding as well as the free energy of association. The predicted concentration of the leak products at equilibrium for the SLD translator is close to experimental data (SI Appendix, Fig. S3). For the DLD translator, however, NUPACK predicts an order of magnitude less leak than that experimentally observed (SI Appendix, Fig. S4). This discrepancy could be because (i) NUPACK ignores coaxial stacking and only roughly approximates the dangle energies of nucleic acids or because (ii) NUPACK disregards strand configurations with pseudoknots, which could also be stable at equilibrium.

Apart from the thermodynamic property, we studied the mechanism of the kinetic behavior. Consistent with the leak mechanism shown in Fig. 3, most of the leak involves the interaction between both of the fuels and the reporter (SI Appendix, Fig. S5). We observed that there is an unexpected two-phase kinetic behavior in the DLD translator (Fig. 6B). During the first 15 min, the leak signal quickly increases with saturating kinetics (first phase) and then continues to slowly increase at a roughly constant rate over the next 10 h (second phase). (Note that the first-phase kinetics is different from the initial leak discussed above.) To investigate the source of the second phase, we found that the leak rate of that phase does not depend on the reporter concentration (SI Appendix, Fig. S6). Considering the structure of Ycomplex, it is possible that it can reconfigure to other isomers through four-way branch migration (SI Appendix, Fig. S7), which could also be detected by the reporter. Since initiation of four-way branch migration is slow (~10−3 s−1) (46), this may be the rate-limiting step and may explain why the overall leak rate of the second phase does not depend on reporter concentration.

The kinetic model that we proposed based on this analysis (SI Appendix, section S1.6 and Table S1) fits the kinetic data well (Fig. 6B) and captures the timescales of the two-phase kinetics. In the model, the leak pathway is that the fuel species F1 and F2 react through toelss strand displacement and form Ycomplex, which can quickly dissociate back or slowly isomerize to other configurations. Both the Ycomplex and its isomers can be detected by the reporter. The quantitative model is consistent with the intuitive picture of leak reduction in the DLD scheme in that Ycomplex is much more likely to dissociate back before interacting with the reporter, even at 1 mM concentrations. Note that there may exist other leak pathways (e.g., F2 reacts with reporter first, and they form a complex; then, F1 invades, producing leak signal), and the real leak could be caused by a combination of all possible leak pathways. The model provided here shows one possible pathway and suggests that, although the species Ycomplex could quickly reverse back to the original fuel species, it can also be trapped in the leaked state through reconfiguration. Designing a leakless system with no trapped leaked state remains an open problem.

Our model of leak described in the previous section associates leak with the formation of certain large DNA complexes. Indeed,
shows the desired triggering kinetics as well as the leak reactions in the absence of input. We tested different depths of the cascade by including a different subset of fuels. In each case, the desired reaction reached half-completion at the first measured data point. In the timeframe of 100 min, the leak fraction ([leak]/[initial fuel]) is less than 4%. (Inset) Leak of the translator cascade over 10 h. The largest leak fraction is roughly 5%: [reporter] = [fuels] = 500 nM, [input] = 250 nM, 25 °C. The inputs are added no more than 3 min before measurement.

PAGE analysis (SI Appendix, Fig. S12) shows that, to produce a leaked signal, a complex with large molecular weight is formed in the DLD design of size consistent with the leak products in our model.

Cascade and OR Circuit. We applied the DLD leakless design to a translator cascade containing eight fuel species (four translators), which translates the input strand $A$ to the output strand $E$ via a sequence of intermediate output strands (Fig. 8A). Fig. 8B shows the desired triggering kinetics as well as the leak of the system. We adjusted the depth of the translator cascade by including different length portions of the cascade (e.g., $F_5$, $F_6$, $F_8$ can translate signal strand $C$ to $E$ through intermediate signal $D$, and this system has two layers of translation). The reporter reacting with the final output signal $E$ is set as a positive control. At 25 °C, for all cascade depths, the desired triggering is fast and reaches half-completion within 3 min from the time that inputs are added (Fig. 8B). Leak increases with the depth of the cascade, but after 100 min (as plotted), the leak fraction ([leak]/[initial fuel]) of even the longest cascade is less than 4%. After 10 h, the leak fraction is only 5% (Fig. 8B, Inset). To show the robustness of the system, we also conducted experiments at 37 °C with twice the initial concentration of fuel and input compared with that at 25 °C; the desired triggering signals reach half-completion at the first measured data point. While leak becomes more apparent, the leak fraction is still smaller than 9% even after 10 h (SI Appendix, Fig. S15). These results suggest that we can construct complex circuits with reduced leak and that their robustness will allow us to successfully operate at high concentrations and achieve fast kinetics.

To demonstrate the potential for reducing leak in more complex computation, we used the DLD leakless design to engineer a circuit composed of OR gates. Since one contiguous sequence could not represent the sequence space, we generated the individual signal sequences one by one (SI Appendix has more information on sequence design). A two-input logic OR gate produces output signal if at least one input signal appears. An OR gate can be constructed by putting two translators in parallel: two translators translating two independent input signals to the same output signal. Fig. 9A shows the construction of a three-layer OR circuit consisting of 10 translators (20 DLD fuel complexes) that can accept six independent input signals. The produced output signal is detected by a downstream reporter. In digital circuits, signal restoration methods are used to decide whether a logic gate outputs logic zero or one; analogously, here we cap the output signal by using a smaller concentration of the reporter than of fuels and inputs. Fig. 9B shows the kinetics of the positive triggered signals and nontriggered signal, where output value one represents fully triggering the reporter. Five of six triggered signals reach half-completion at the first data point. It takes at most 10 min for all of the triggered signals to reach 80% completion. In the 100-min timeframe, leak is less than 5% of the output signal. The same experiments with a lower concentration of the fuels and the input species were conducted (SI Appendix, Fig. S16). Even after 10 h, leak maintains a low level (less than 4%). In this timeframe, leak is mainly composed of the initial leak, and the total leak amount is around 2.8% of the concentration of fuels. These results suggest that the DLD design can be used for constructing fast, robust, and large-scale logic circuits.

Discussion
DNA strand displacement cascades have enabled the bottom-up construction of sophisticated interacting molecular machines (3–11, 13, 16–18, 20, 22–25, 47, 48). Emergent from the programed interactions of DNA complexes are functionalities, such as signal amplification, oscillation, digital and analog computation, distributed computation, control of self-assembly processes, and performing robotic tasks. However, the operation of DNA strand displacement is still hindered by system errors. In the applications of computer science and electrical communication, error correction paradigms based on redundancy include error correction codes for communication (28), Von Neumann multiplexing.
to perform accurate computation despite logic gate errors (29), and various error reduction methods based on repeated execution of probabilistic algorithms (49). Closer to our work, redundancy-based proofreading significantly reduces the error rate in algorithmic self-assembly by requiring multiple erroneous steps to occur in sequence (30).

Inspired by the error reduction methods exploiting redundancy, we have developed a systematic method capable of reducing leak to arbitrary low levels and experimentally tested the chemical error correction method. Strand displacement systems designed by the leakless method in this paper have shown remarkable behaviors combating errors: at concentrations as high as 10 μM (up to 100 times higher than the concentrations of current strand displacement systems), the leakless design could decrease leak to a level that was not apparently measurable, even at temperatures at which leak in standard designs becomes unmanageable. Moreover, the systems using the leakless design are not only kinetically robust but also, less prone to leak even after remaining inactive for as long as possible—the thermodynamic leak concentration, which is the upper bound of the system (leak reaches equilibrium), is significantly less than that of the traditional design. Beyond the simple translator system, we successfully engineered a linear translator cascade and an OR circuit with negligible leak and fast desired kinetics. The underlying leakless mechanism, which could be explained in terms of both thermodynamics and kinetics, provides an insight for the future development of the design of strand displacement systems. It is still a challenge to apply the leakless mechanism for systems other than translators, such as AND gates, which require a gate to take two signal strands simultaneously as inputs.

Apart from leak, other problems, such as imperfect DNA synthesis or the difficulty of ensuring matching stoichiometry between complementary strands, could also contribute to the lack of robustness in strand displacement systems. Errors during chemical synthesis (50) are thought to contribute to initial leak (5), and excess unpaired fuel strands are likely to cause undesired reactions with other species. Mobility-based purification protocols currently used cannot completely eliminate these issues, but more advanced purification methods (51, 52) and synthesis by enzymes (53) might improve performance. Despite these remaining challenges, which are especially important for certain applications of enzyme-free strand displacement circuits, such as the detection of minute quantities of a known target sequence by exponential feedback amplification, our solution of the leak problem already overcomes the main barrier to feedforward circuits with order of magnitude improved performance.

Specifically, our results suggest that, through this design principle, it is possible to achieve more complicated, more robust, more intelligent, and faster molecular systems with the capability of decision making or changing its state according to the outside environment. Currently, the largest strand displacement circuits were executed at 50 nM and complete on the order of 10 h (10). It is possible that the same computation could complete within a few minutes if the design of the strand displacement system is robust to leak and the reactants are safely kept at high concentration, such as 1 μM.

Recent advances in molecular programming have shown that enzyme-free strand displacement systems can be adapted to low-cost and point-of-care diagnostics, but the background noise caused by leak limits the sensitivity of nucleic acid detection (20). Our method could offer an approach for designing enzyme-free nucleic acid amplifiers for biological sequences with less background and thus, achieve a rapid and sensitive molecular detection alternative to PCR. However, the sequences that we used are short and unstructured, while biological sequences usually have significant intrinsic secondary structures, which could affect desired kinetic behavior (54) or impose sequence constraints and limit the design space. Despite these challenges, there is a body of work demonstrating strand displacement cascades with natural DNA and RNA inputs, including logic computation both in vitro (9) and in vivo (25), a molecular multigene classifier (21), regulation of cellular gene expression (26, 27), and in situ fluorescence imaging of mRNA expression (55). Destabilizing organic solvents (56) and the hybridization probe method (21) can be generally adopted to overcome secondary structure in strand displacement. We envision that, with these techniques, leakless architectures could be used to interface with biological sequences.

A variety of error correction strategies not based on redundancy have been identified in biology. For example, biological regulatory networks are usually robust to kinetic parameters, which are often attributed to feedback loops [e.g., in chemotaxis...
(57) and the circadian clock (58). Biological reactions are also often remarkably specific, with low rates of side reactions. In the kinetic proofreading model introduced by Hopfield (59), incorrect reaction products preferentially exit the reaction pathway, which increases the specificity. (Note that, in contrast to our strategy, kinetic proofreading relies on kinetics alone for error correction without affecting the thermodynamic equilibrium.) Understanding the full variety of design principles for robust molecular systems, including redundancy-based methods, provides testable hypotheses for analyzing natural regulatory networks and methods for systematically engineering complex reaction networks. It is possible to envision a near future where artificially designed molecular programs can achieve the robustness and complexity of natural systems (60).

Materials and Methods

All DNA sequences are listed in SI Appendix. DNA oligonucleotides were purchased PAGE purified from Integrated DNA Technologies. All fuel and reporter species were annealed at 40 µM in 1× TAE/Mg2+ buffer with 12.5 mM Mg2+. After annealing, the fuel species were purified using 12% PAGE. Fluorescence kinetics experiments were performed after mixing all of the species.

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1. Goodsell DS (2009) The Machinery of Life (Springer Science Business Media, New York).

2. Purnick PE, Weiss R (2009) The second wave of synthetic biology: From modules to systems. Nat Rev Mol Cell Biol 10:410–422.

3. Bath I, Turberfield AJ (2007) DNA nanomachines. Nat Nanotechnol 2:275–284.

4. Yurke B, Turberfield AJ, Mills AP, Simmel FC, Neumann JL (2000) A DNA-fuelled molecular machine made of DNA. Nature 406:605–608.

5. Zhang DY, Seelig G (2011) Dynamic DNA nanotechnology using strand-displacement reactions. Nat Nanotechnol 6:113–119.

6. Venkataraman S, Dirks RM, Rothemund PW, Winfree E, Naughton NA (2007) An autonomous polymerization motor powered by DNA hybridization. Nat Nanotechnol 2:490–494.

7. Moscati RA, Bath J, Turberfield AJ (2011) A programmable molecular robot. Nano Lett 11:982–987.

8. Thubagere AJ, et al. (2017) A cargo-sorting DNA robot. Science 357:eaan6558.

9. Seelig G, Soloveichik D, Zhang DY, Winfree E (2006) Enzyme-free nucleic acid logic circuits. Science 314:1585–1588.

10. Qian L, Winfree E (2011) Scaling up digital circuitry with DNA strand displacement cascades. Science 332:1196–1201.

11. Qian L, Winfree E, Bruck J (2011) Neural network computation with DNA strand displacement cascades. Nature 475:368–372.

12. Chen YJ, et al. (2013) Programmable chemical controllers made from DNA. Nat Nanotechnol 8:755–762.

13. Srinivas N, Parkin J, Seelig G, Winfree E, Soloveichik D (2017) Enzyme-free nucleic acid dynamical systems. Science 358:eaau2052.

14. Soloveichik D, Seelig G, Winfree E (2010) DNA as a universal substrate for chemical kinetics. Proc Natl Acad Sci USA 107:5393–5398.

15. Cardelli L (2013) Two-domain DNA strand displacement. Math Struct Comput Sci 23:247–271.

16. Zhang DY, Turberfield AJ, Yurke B, Winfree E (2007) Engineering entropy-driven reactions and networks catalyzed by DNA. Science 318:1121–1125.

17. Chen X, Briggs N, McLain JR, Ellington AD (2013) Stacking nonenzymatic circuits for high signal gain. Proc Natl Acad Sci USA 110:5386–5391.

18. Yin P, Choi HM, Calvert CR, Naughton NA (2008) Programming biomolecular self-assembly pathways. Nature 451:318–322.

19. Kotani S, Hughes WL (2017) Multi-arm junctions for dynamic DNA nanotechnology. J Am Chem Soc 139:6353–6368.

20. Li B, Ellington AD, Chen X (2011) Rational, modular adaptation of enzyme-free DNA circuits to multiple detection methods. Nucleic Acids Res 39:1110.

21. Lopez R, Wang R, Seelig G (2018) A molecular multi-genic classifier for disease diagnostics. Nat Chem 10:746–754.

22. Chen YJ, Groves B, Muscat RA, Seelig G (2015) DNA nanotechnology from the test tube to the cell. Nat Nanotechnol 10:748–760.

23. Choi HM, et al. (2010) Programmable in situ amplification for multiplexed imaging of mRNA expression. Nat Biotechnol 28:1208–1212.

24. Rudchenko M, et al. (2013) Autonomous molecular cascades for evaluation of cell surfaces. Nat Nanotechnol 8:580–586.

25. Groves B, et al. (2016) Computing in mammalian cells with nucleic acid strand exchange. Nat Nanotechnol 11:287–294.

26. Green AA, Silver PA, Collins JJ, Yin P (2014) Toehold switches: De-novo-designed regulators of gene expression. Cell 159:925–939.

27. Green AA, et al. (2017) Complex cellular logic computation using ribocomputing devices. Nature 548:117–121.

28. Zhuang Y, Bharda S, Li B, Ellington AD (2014) Mismatches improve the performance of strand-displacement nucleic acid circuits. Angew Chem 126:1876–1879.