Self-adaptive biosystems through tunable genetic parts and circuits

Vittorio Bartoli¹, Mario di Berrnardo^{1,2,3} and Thomas E. Gorochowski^{2,4,*}

- ¹ Department of Engineering Mathematics, University of Bristol, Woodland Road, Bristol, UK
- ² BrisSynBio, University of Bristol, Life Sciences Building, Tyndall Avenue, Bristol, UK
- ³ Department of Electrical Engineering and Information Technology, University of Naples Federico II, Via Claudio 21, Napoli, Italy
- ⁴ School of Biological Sciences, University of Bristol, Life Sciences Building, Tyndall Avenue, Bristol, UK
- * Correspondence should be addressed to T.E.G. (thomas.gorochowski@bristol.ac.uk)

Keywords: tunable; genetic part; control; adaptation; cybergenetics; synthetic biology; systems biology.

(c) (i)

1 Abstract

2 Biological systems often need to operate in complex environments where conditions can rapidly change. This is possible due to their inherent ability to sense changes and adapt their 3 behavior in response. Here, we detail recent advances in the creation of synthetic genetic 4 parts and circuits whose behaviors can be dynamically tuned through a variety of intra- and 5 extra-cellular signals. We show how this capability lays the foundation for implementing control 6 engineering schemes in living cells and allows for the creation of biological systems that are 7 able to self-adapt, ensuring their functionality is maintained in the face of varying 8 environmental and physiological conditions. We end by discussing some of the broader 9 implications of this technology for the safe deployment of synthetic biology. 10

11

12 Highlights

- Tunable genetic parts allow for their input-output relationship to be dynamically varied in
 response to intra- and extra-cellular signals.
- Self-adaptive biological systems can be built using a combination of control engineering
 principles and tunable genetic parts and circuits.
- An ability to engineer self-adaptive systems will be crucial in deploying synthetic biology
 into complex and changeable real-world environments.

19 Introduction

A key characteristic of all living organisms is their ability to adapt. From altering metabolism to best utilize a shift in nutrients, to regulating ion transport to maintain cellular homeostasis, adaptive responses are crucial to many aspects of life. To enable such adaptive processes, cells have evolved a wide array of sensors able to capture information about their local environment as well as their internal state. These sensors are connected to cellular circuits that both monitor and modify internal processes with the goal of maintaining a desired functionality (e.g. homeostasis) no matter the perturbations experienced by the cell.

Unlike in Nature, engineered biological systems often lack the ability to adapt to 27 changing conditions, making them fragile and causing them to break easily [1–6]. This stems 28 historically from an absence of genetic parts that can be used to dynamically tune the 29 response of a system and the additional burden of implementing control processes on top of 30 a basic functioning system. This view is, however, beginning to change [7-9]. Recent 31 developments in synthetic biology have led to a wide variety of biological parts able to 32 precisely regulate the transcription [10–14] and translation [15–19] of genes in response to 33 diverse intra- and extra-cellular signals [20]. Furthermore, the benefits of exploiting control 34 engineering principles to create robust biosystems is also becoming recognized [7–9,21,22]. 35 This stems from a growing need in many applications for reliable and guaranteed 36 functionalities no matter the strain of cell used, or the environment deployed to [23]. 37

In this work, we discuss some of the recent advances towards engineering selfadaptive biological systems. We begin by providing an overview of the wide variety of parts now available for sensing and tuning cellular behaviors and show some of the ways these can be used to create adaptive genetic circuits. We than discuss recent steps towards using these circuits to implement closed-loop feedback control within living cells to create self-adaptive systems and end by outlining some of the future applications that such capabilities could support.

45

46 **Tunable genetic parts**

47 To develop an adaptive system, it is necessary to be able to dynamically alter/tune the inputoutput relationship of parts within the system. These 'tunable' components come in many 48 different forms, however, conceptually have a common structure (Figure 1a). Each tunable 49 element consists of an input and output, and a further tuner input that is able to alter the input-50 output relationship in a useful way [24]. Input, output and tuner signals can take many forms, 51 from gene expression rate to protein phosphorylation state. However, one of the most 52 commonly used is transcriptional activity [3,6,25]. This is captured by the RNA polymerase 53 (RNAP) flux along DNA and can be directed to particular points by positioning 54

promoters that control the transcriptional initiation of RNAP. This makes it simpler to connect
 individual parts by making the output promoter of one the input promoter of another [10,26].

57 While there are many ways that the behavior of biological parts can be tuned, the most 58 widespread and easiest to apply is through the control of gene expression. By incorporating 59 additional regulatory parts to modify the rate of transcription and/or translation of an output 60 gene it is possible to create a tunable expression system (TES) that can vary the amount of 61 output protein produced for a given input transcriptional activity [24]. As gene expression 62 underlies many core cellular behaviors this approach is a flexible means to control a variety 63 of biological functionalities in a dynamic and tunable way.

The core structure of a TES comprises of promoters acting as signals for the input and 64 tuner, a gene that is expressed as output, and internal regulators that allow the input and tuner 65 promoters to dynamically alter output protein expression rate (Figure 1a). For the input and 66 tuner promoters, a variety of sensors with transcriptional outputs now exist to sense 67 environmental conditions such as chemical concentrations [27] and light [28,29], as well as 68 internal cellular states (e.g. stress responses) [9] and population level features like cell density 69 through quorum sensing [30]. Similarly, many output genes exist that enable control of cellular 70 71 behaviors from modifying their metabolic state [31-33] to cell movement [34] and even cellto-cell communications [30]. The final component in the TES is the internal regulator used to 72 modulate how transcriptional activity of the input promoter is transformed into a protein 73 expression rate. To make this relationship a function of the transcriptional activity of the tuner 74 promoter, numerous types of transcriptional and translational regulators can be used (Figure 75 **1b**). These include: 1. toehold switches (THSs) where translation rate is controlled through 76 expression of a trigger RNA that is able to disrupt secondary structures around the RBS of the 77 output gene [15,16,24]; 2. small transcription activating RNAs (STARS) which interact with 78 transcriptional terminators that are placed in the 5' untranslated region (UTR) of a gene and 79 regulate premature RNAP termination [11,12,35]; 3. small RNAs (sRNAs) that can be 80 designed to bind the ribosome binding site for a gene of interest and suppress translation 81 initiation [18]; 4. σ /anti- σ pairs where the anti- σ protein is expressed by the tuner promoter to 82 reduce the expression rate of input promoters driven by the cognate σ -factor [36,37]; 5. split 83 T7 RNAPs where the input and tuner promoters express different halves and the gene of 84 interest is connected to the cognate promoter of the RNAP [38]; and 6. other programmable 85 transcription factors like CRISPRi/a [14], transcription activator-like effector nucleases 86 (TALENs) [39] and zinc fingers (ZFs) [40] that can be expressed by the tuner promoter and 87 interfere or enhance transcription initiation or elongation from the input promoter. 88

Although it is more common for the input and tuner promoters to be different, recently it has been shown that by using identical promoters to control both regulatory inputs in unison, more stringent control of a protein expression can be achieved as well as sharp digital-like

transitions between OFF and ON states [35,41] (Greco et al. bioRxiv doi:
 10.1101/2020.07.04.187500).

It should also be noted that other approaches to tuning gene expression have been developed. For example, two-component systems where phosphorylation rates can be modified by the concentration of specific kinases [42] and CRISPRi systems where the strength of repression is controlled by base mismatches in the guide RNA (gRNA) [9]. However, in most cases tuning of such systems requires the physical modification of the encoding DNA making it impossible to dynamically regulate behavior.

100

101 Adaptive genetic circuitry

To implement more complex functionalities, it is often necessary to connect together many 102 genetic parts into a circuit [6]. In other engineering fields such as electronics, specifying the 103 connections between components would generally be sufficient to create a working system. 104 This is due to electronic components having standardized operating ranges to ensure 105 compatibility and reliable functionalities no matter the context they are used in. For example, 106 complementary metal-oxide-semiconductor (CMOS) electronic logic gates expect inputs of 0-107 1.5 V for an OFF state and 3.5–5 V for an ON state. In biology, such standardization is difficult 108 due to the diversity of biochemical components used and challenges in engineering them to 109 ensure a common level of response [26,43]. Therefore, rather than imposing constraints on 110 biology that are near impossible to implement, it is instead necessary to work with the diversity 111 present and ensure that components connected have inputs and outputs that are 'matched' 112 to guarantee signals propagate correctly [6,20,44]. Many of the advances in automated 113 genetic circuit design have revolved around ensuring parts perform consistently when used in 114 different ways (e.g. insulating their function from varying genetic context [45,46]) and 115 automating the selection of combinations of parts within a circuit such that their inputs and 116 outputs are optimally matched [6,26,43]. 117

Tunable genetic parts can greatly simplify this process by removing the need to 118 reassemble a circuit if two parts are found to be mismatched when connected. At the cost of 119 additional tuning inputs to a circuit, tunable genetic parts can have their response function 120 dynamically varied after circuit assembly (Figure 2a). This allows parts to be dynamically 121 matched and opens up the possibility of rapidly optimizing overall circuit function without the 122 need to reassemble underlying DNA (Figure 2b). In addition to simplifying the creation of 123 optimized circuits, the ability to dynamically vary the response dynamics of individual parts is 124 also valuable for systems that must function in highly changeable environments, where shifts 125 might cause physiological changes that impact some or all parts in a circuit [4,5,47]. 126

Beyond the tuning of steady-state response functions, circuits capable of exhibiting 127 dynamic behaviors such as oscillations have also been developed, where characteristics such 128 as period and amplitude can be varied through diverse inputs to the system. In one such 129 oscillator for Escherichia coli cells, positive and negative feedback loops are implemented 130 using the P_{BAD} (positive) and P_{tac} (negative) systems which can be further regulated using 131 arabinose and isopropyl β-D-1-thiogalactopyranoside (IPTG), respectively [48]. It was found 132 that increasing the concentration of Arabinose caused a lengthening of the oscillatory period, 133 while increasing an IPTG concentration or temperature led to a shortening of the oscillatory 134 period. Other tunable oscillator circuits have also been developed to allow for control via light 135 [49], to synchronize behaviors across a population of cells [50] and to function in mammalian 136 cells [51]. Furthermore, they've been modelled to demonstrate regulatory motifs capable of 137 having their oscillatory amplitude and frequency tuned independently [52]. 138

139

Towards self-adaptive systems

A limitation of using tunable genetic parts and circuits is the need for external inputs to be continually provided. A solution to this is to connect the output of a cellular process to the tuner input of the circuit, creating a closed-loop self-adaptive system. There has been growing interest in the application of closed-loop feedback control in biology and the role that control engineering principles might play in creating robust biosystems [8,21,22,53].

Some simple feedback control schemes have already been implemented in living cells. 146 Many of these focus on the development of dynamic regulatory schemes for metabolism to 147 maximize the yield of desired products [33,54,55]. Feedback is created by either using 148 endogenous transcription factors that respond to intermediate metabolites of interest [31,56], 149 or by the design of RNA aptamers able to sense and then actuate gene expression or shifts 150 in metabolic fluxes in response to changes in metabolite concentrations (Glasscock et al. 151 bioRxiv doi: 10.1101/529180). Related to this, general cellular stress responses have also 152 been used as triggers for feedback control. Specifically, the σ^{32} heat-shock response of *E. coli* 153 was found to be rapidly activated when cells were burdened by excessive protein expression 154 [57]. By connecting the endogenous $P_{htpG1} \sigma^{32}$ -promoter to a CRISPRi based feedback control 155 system (Figure 3a), it was shown that protein expression of burdensome synthetic genetic 156 constructs could be dynamically regulated to reduce cellular burden [9]. This both increased 157 overall protein yield, as there was less impact of cellular growth, and the evolutionary stability 158 of the synthetic genetic constructs as there was less selective pressure for mutations. Similar 159 approaches have been implemented using repressor proteins for negative feedback regulation 160 and the $P_{ibpAB} \sigma^{32}$ -promoter as a sensor of burden [58]. Dynamic regulation of protein 161 expression has also been performed in mammalian cells using translation-based negative 162

feedback control [59] and general-purpose gene expression controllers based on quorum sensing [32].

More general feedback control schemes in living cells include the antithetic integral controller motif that uses sequestration mechanisms such as molecular titration to implement an embedded feedback controller [8]. This motif guarantees perfect adaptation, rejecting constant disturbances so that the output of the genetic system of interest initially responds to an external input but then returns to basal levels while the input persists [21].

Molecular titration has also been shown to be an effective mechanism to implement 170 'comparator' devices able to produce an output function of the mismatch between the levels 171 of two different inputs, an essential component of any biomolecular controller [36,60]. 172 Implementations of more sophisticated control strategies have also been recently presented, 173 such as the biomolecular PID controller presented in [61]. As the complexity of biomolecular 174 control designs increases, to successfully implement the control function, the parts needed to 175 construct the control strategy must be finely tuned to guarantee the right balance between the 176 sensing and actuating parts of a circuit [62]. The use of tunable parts could open the way to 177 the development of adaptive biomolecular controllers able to self-tune themselves in order to 178 guarantee the robust execution of the control task they are assigned to perform even in the 179 presence of perturbations, cell-to-cell variability, etc. This might be even more crucial when 180 the control functions are spread among different populations in a microbial consortium as 181 recently suggested in [63]. 182

Beyond simple feedback motifs, it can be difficult to implement complex control 183 algorithms using biochemical components because the feedback strengths and dynamics 184 required may be difficult to match to available parts. Therefore, an intermediate step is 185 sometimes taken whereby a computer is used to implement controller logic within the 186 feedback loop and create what is termed a cybergenetic system [22] (Figure 3b). 187 Cybergenetic systems often rely on single-cell microcopy platforms and microfluidics to image 188 engineered cells whose current state is displayed via fluorescent reporter proteins and use 189 chemical inducers [64,65] or light [28,29,66,67] as inputs to perturb the cells states in a pre-190 defined way (i.e. the cells are engineered to sense and update their state in response to a 191 stimulus). The computer-based controller runs in real-time analyzing microscopy images to 192 extract the current states of cells and then immediately computes a control action, which is 193 then administered by varying chemicals concentrations or light that the cells are exposed to. 194 Such systems have been shown capable of controlling both population [8,64,66,68] and 195 single-cell behaviors [67]. Moreover, toolkits have emerged to simplify their creation by 196 handling image analysis, tracking and calculation of control actions (Pedone et al. bioRxiv doi: 197 10.1101/2020.06.25.171751). The major advantage of this hybrid approach is that the 198

computer controllers are cell-agnostic, allowing them to be used with any biosystem that hasthe same types of control inputs and observable outputs.

201

202 Conclusions

The creation of self-adaptive biosystems that can function in the face of varying and uncertain 203 environments will be a crucial step for the safe deployment of synthetic biology into everyday 204 life. Recent advances in biological control engineering provide the theoretical foundations 205 necessary to design such systems and, as we have shown, tunable genetic parts and circuits 206 can support their physical implementation [24]. While the self-adaptive systems built to date 207 have mostly been small-scale proof-of concepts, it is clear that the ability to synthesize and 208 assemble entire genomes is in reach [69,70]. Demonstrating the value of integrating tunable 209 parts and circuits within these cellular systems will be crucial to moving beyond the mere 210 recoding of existing genomic information and towards the creation of synthetic cells built from 211 the ground up to reliably implement novel functionalities. Furthermore, they will support the 212 scale-up of these systems by enabling us to move beyond single-cells and towards the 213 engineering of collective behaviors of vast populations of cells [71] or even entire synthetic 214 ecologies [72]. 215

216

217 Acknowledgements

This work was supported by BrisSynBio, a BBSRC/EPSRC Synthetic Biology Research Centre grant BB/L01386X/1 (M.d.B., T.E.G.), EPSRC/BBSRC Centre for Doctoral Training in Synthetic Biology grant EP/L016494/1 (V.B.), the EU Horizon 2020 research project COSY-BIO grant 766840 (M.d.B), and a Royal Society University Research Fellowship grant UF160357 (T.E.G.) This study did not involve any underlying data.

223

Author Contributions

All authors contributed to the writing and editing. T.E.G. and V.B. produced the figures.

226

227 Declaration of Interest

None.

229	References	
230	• (of special interest
231	•• (of outstanding interest
232		
233	1.	Fernandez-Rodriguez J, Yang L, Gorochowski TE, Gordon DB, Voigt CA: Memory and
234		Combinatorial Logic Based on DNA Inversions: Dynamics and Evolutionary
235		Stability. ACS Synth Biol 2015, 4:1361–1372.
236	2.	Sleight SC, Bartley BA, Lieviant JA, Sauro HM: Designing and engineering
237		evolutionary robust genetic circuits. J Biol Eng 2010, 4:12.
238	3.	Gorochowski TE, Espah Borujeni A, Park Y, Nielsen AA, Zhang J, Der BS, Gordon DB,
239		Voigt CA: Genetic circuit characterization and debugging using RNA-seq. Mol Syst
240		<i>Biol</i> 2017, 13 :952.
241	4.	Gorochowski TE, van den Berg E, Kerkman R, Roubos JA, Bovenberg RAL: Using
242		Synthetic Biological Parts and Microbioreactors to Explore the Protein
243		Expression Characteristics of Escherichia coli. ACS Synth Biol 2014, 3:129–139.
244	5.	Moser F, Broers NJ, Hartmans S, Tamsir A, Kerkman R, Roubos JA, Bovenberg R,
245		Voigt CA: Genetic Circuit Performance under Conditions Relevant for Industrial
246		Bioreactors. ACS Synth Biol 2012, 1:555–564.
247	6.	Brophy JAN, Voigt CA: Principles of genetic circuit design. Nat Methods 2014,
248		11 :508.
249	7.	Segall-Shapiro TH, Sontag ED, Voigt CA: Engineered promoters enable constant
250		gene expression at any copy number in bacteria. Nat Biotechnol 2018, 36:352.
251	8.	Aoki SK, Lillacci G, Gupta A, Baumschlager A, Schweingruber D, Khammash M: A
252		universal biomolecular integral feedback controller for robust perfect adaptation.
253		<i>Nature</i> 2019, 570 :533–537.
254		•• Details the discovery of a universal biochemical controller topology for achieving
255		integral feedback and perfect adaptation. This regulatory motif is further implemented
256		using σ /anti- σ pairs and used to robustly control the growth rate of Escherichia coli
257		cells. Other tunable parts that rely on sequestering of molecular species could offer
258		additional means to implement similar control systems.

259	9.	Ceroni F, Boo A, Furini S, Gorochowski TE, Borkowski O, Ladak YN, Awan AR, Gilbert
260		C, Stan G-B, Ellis T: Burden-driven feedback control of gene expression. Nat
261		Methods 2018, 15 :387–393.
262		•• Details the development of a feedback control system to automatically regulate the
263		burden experienced by cells expressing a synthetic genetic construct. The major
264		contribution is the detailed analysis of endogenous cellular responses to find a suitable
265		burden-responsive promoter and the use of a tunable CRISPRi feedback regulatory
266		mechanism that enables any synthetic construct to be targeted. It is shown that this
267		system can significantly improve the yield of protein products, as well as the
268		evolutionary stability of genetic constructs.
269	10.	Stanton BC, Nielsen AAK, Tamsir A, Clancy K, Peterson T, Voigt CA: Genomic
270		mining of prokaryotic repressors for orthogonal logic gates. Nat Chem Biol 2014,
271		10 :99–105.
272	11.	Chappell J, Westbrook A, Verosloff M, Lucks JB: Computational design of small
273		transcription activating RNAs for versatile and dynamic gene regulation. <i>Nat</i>
274		<i>Commun</i> 2017, 8 :1051.
275	12.	Chappell J, Takahashi MK, Lucks JB: Creating small transcription activating RNAs.
276		<i>Nat Chem Biol</i> 2015, 11 :214–220.
277	13.	Kim H, Bojar D, Fussenegger M: A CRISPR/Cas9-based central processing unit to
278		program complex logic computation in human cells. Proc Natl Acad Sci 2019,
279		116 :7214.
280	14.	Gilbert LA, Horlbeck MA, Adamson B, Villalta JE, Chen Y, Whitehead EH, Guimaraes
281		C, Panning B, Ploegh HL, Bassik MC, et al.: Genome-Scale CRISPR-Mediated
282		Control of Gene Repression and Activation. Cell 2014, 159:647-661.
283	15.	Green AA, Silver PA, Collins JJ, Yin P: Toehold Switches: De-Novo-Designed
284		Regulators of Gene Expression. Cell 2014, 159:925–939.
285	16.	Green AA, Kim J, Ma D, Silver PA, Collins JJ, Yin P: Complex cellular logic
286		computation using ribocomputing devices. Nature 2017, 548:117.
287	17.	Gorochowski TE, Chelysheva I, Eriksen M, Nair P, Pedersen S, Ignatova Z: Absolute
288		quantification of translational regulation and burden using combined sequencing
289		approaches. Mol Syst Biol 2019, 15:e8719.

290	18.	Kelly CL, Harris AWK, Steel H, Hancock EJ, Heap JT, Papachristodoulou A: Synthetic
291		negative feedback circuits using engineered small RNAs. Nucleic Acids Res 2018,
292		46 :9875–9889.
293	19.	Soper T, Mandin P, Majdalani N, Gottesman S, Woodson SA: Positive regulation by
294		small RNAs and the role of Hfq. Proc Natl Acad Sci 2010, 107:9602.
295	20.	Greco FV, Tarnowski MJ, Gorochowski TE: Living computers powered by
296		biochemistry. The Biochemist 2019, 41 :14–18.
	04	Driet C. Curste A. Khammach M. Antithetic Internel Fredheck Fredman Debugt
297	21.	
298		Perfect Adaptation in Noisy Biomolecular Networks. Cell Syst 2016, 2:15–26.
299	22.	M. Khammash, M. Di Bernardo, D. Di Bernardo: Cybergenetics: Theory and
300		Methods for Genetic Control System. In 2019 IEEE 58th Conference on Decision
301		and Control (CDC) 2019:916–926.
302		• A clear introduction to the emerging field of cybernetics covering the key theory and
303		experimental methods that make these types of system possible.
004	22	Heringe C. Teng W. Wang C. Deehmulth AT. von Winden MA. Chu, L. von Culik MM
304	23.	Haringa C, Tang W, Wang G, Deshmukh AT, van Winden WA, Chu J, van Gulik WM,
305		Heijnen JJ, Mudde RF, Noorman HJ: Computational fluid dynamics simulation of
306		an industrial P. chrysogenum fermentation with a coupled 9-pool metabolic
307		model: Towards rational scale-down and design optimization. Chem Eng Sci
308		2018, 175 :12–24.
309	24.	Bartoli V, Meaker GA, di Bernardo M, Gorochowski TE: Tunable genetic devices
310		through simultaneous control of transcription and translation. Nat Commun 2020,
311		11:2095.
312		•• The first time a generalized tunable expression system (TES) is developed. The TES
313		is used to create tunable logic gates (NOT and NOR) that are more compatible than
314		existing parts, and some key biomolecular design constraints are explored for future
315		development of tunable part and systems.
316	25.	Canton B, Labno A, Endy D: Refinement and standardization of synthetic
317		biological parts and devices. Nat Biotechnol 2008, 26:787.
	• -	
318	26.	Nielsen AAK, Der BS, Shin J, Vaidyanathan P, Paralanov V, Strychalski EA, Ross D,
319		Densmore D, Voigt CA: Genetic circuit design automation. Science 2016,
320		352 :aac7341.

321 322 323	27.	Meyer AJ, Segall-Shapiro TH, Glassey E, Zhang J, Voigt CA: Escherichia coli "Marionette" strains with 12 highly optimized small-molecule sensors. <i>Nat Chem</i> <i>Biol</i> 2019, 15 :196–204.
324 325 326	28.	Baumschlager A, Aoki SK, Khammash M: Dynamic Blue Light-Inducible T7 RNA Polymerases (Opto-T7RNAPs) for Precise Spatiotemporal Gene Expression Control. ACS Synth Biol 2017, 6:2157–2167.
327 328	29.	Castillo-Hair SM, Baerman EA, Fujita M, Igoshin OA, Tabor JJ: Optogenetic control of Bacillus subtilis gene expression. <i>Nat Commun</i> 2019, 10 :3099.
329 330	30.	Scott SR, Hasty J: Quorum Sensing Communication Modules for Microbial Consortia. ACS Synth Biol 2016, 5:969–977.
331 332 333 334 335 336 337	31.	 Doong SJ, Gupta A, Prather KLJ: Layered dynamic regulation for improving metabolic pathway productivity in Escherichia coli. Proc Natl Acad Sci 2018, 115:2964. Employs the novel use of two orthogonal and tunable regulators to dynamically control and optimize several aspects of cellular metabolism for D-glucaric acid production. Highlights the value of tunable regulation for metabolic applications and the highest reported titers of glucaric acid in <i>Escherichia coli</i> cells.
338 339 340	32.	Gupta A, Reizman IMB, Reisch CR, Prather KLJ: Dynamic regulation of metabolic flux in engineered bacteria using a pathway-independent quorum-sensing circuit. <i>Nat Biotechnol</i> 2017, 35 :273.
341 342 343	33.	Moser F, Espah Borujeni A, Ghodasara AN, Cameron E, Park Y, Voigt CA: Dynamic control of endogenous metabolism with combinatorial logic circuits . <i>Mol Syst Biol</i> 2018, 14 :e8605.
344 345	34.	Blair KM, Turner L, Winkelman JT, Berg HC, Kearns DB: A Molecular Clutch Disables Flagella in the Bacillus subtilis Biofilm. <i>Science</i> 2008, 320 :1636–1638.
346 347 348	35.	Westbrook AM, Lucks JB: Achieving large dynamic range control of gene expression with a compact RNA transcription–translation regulator. <i>Nucleic Acids Res</i> 2017, 45 :5614–5624.
349 350 351	36.	Annunziata F, Matyjaszkiewicz A, Fiore G, Grierson CS, Marucci L, di Bernardo M, Savery NJ: An Orthogonal Multi-input Integration System to Control Gene Expression in Escherichia coli . <i>ACS Synth Biol</i> 2017, 6 :1816–1824.

352 353 354 355	37.	Rhodius VA, Segall-Shapiro TH, Sharon BD, Ghodasara A, Orlova E, Tabakh H, Burkhardt DH, Clancy K, Peterson TC, Gross CA, et al.: Design of orthogonal genetic switches based on a crosstalk map of σs, anti-σs, and promoters . <i>Mol</i> <i>Syst Biol</i> 2013, 9 :702.
356 357 358	38.	Segall-Shapiro TH, Meyer AJ, Ellington AD, Sontag ED, Voigt CA: A 'resource allocator' for transcription based on a highly fragmented T7 RNA polymerase . <i>Mol Syst Biol</i> 2014, 10 :742.
359 360	39.	Moore R, Chandrahas A, Bleris L: Transcription Activator-like Effectors: A Toolkit for Synthetic Biology. ACS Synth Biol 2014, 3 :708–716.
361 362 363	40.	Khalil AS, Lu TK, Bashor CJ, Ramirez CL, Pyenson NC, Joung JK, Collins JJ: A Synthetic Biology Framework for Programming Eukaryotic Transcription Functions. <i>Cell</i> 2012, 150 :647–658.
364 365 366	41.	Calles B, Goñi-Moreno Á, de Lorenzo V: Digitalizing heterologous gene expression in Gram-negative bacteria with a portable ON/OFF module . <i>Mol Syst Biol</i> 2019, 15 :e8777.
367 368 369	42.	Schmidl SR, Sheth RU, Wu A, Tabor JJ: Refactoring and Optimization of Light- Switchable Escherichia coli Two-Component Systems . <i>ACS Synth Biol</i> 2014, 3 :820–831.
370 371	43.	P. Vaidyanathan, B. S. Der, S. Bhatia, N. Roehner, R. Silva, C. A. Voigt, D. Densmore: A Framework for Genetic Logic Synthesis . <i>Proc IEEE</i> 2015, 103 :2196–2207.
372 373 374	44.	Grozinger L, Amos M, Gorochowski TE, Carbonell P, Oyarzún DA, Stoof R, Fellermann H, Zuliani P, Tas H, Goñi-Moreno A: Pathways to cellular supremacy in biocomputing . <i>Nat Commun</i> 2019, 10 :5250.
375 376	45.	Qi L, Haurwitz RE, Shao W, Doudna JA, Arkin AP: RNA processing enables predictable programming of gene expression. <i>Nat Biotechnol</i> 2012, 30 :1002.
377 378	46.	Lou C, Stanton B, Chen Y-J, Munsky B, Voigt CA: Ribozyme-based insulator parts buffer synthetic circuits from genetic context . <i>Nat Biotechnol</i> 2012, 30 :1137.
379 380 381	47.	Wohlgemuth SE, Gorochowski TE, Roubos JA: Translational sensitivity of the Escherichia coli genome to fluctuating tRNA availability . <i>Nucleic Acids Res</i> 2013, 41 :8021–8033.

382 383	48.	Stricker J, Cookson S, Bennett MR, Mather WH, Tsimring LS, Hasty J: A fast, robust and tunable synthetic gene oscillator. <i>Nature</i> 2008, 456 :516.
384 385	49.	Mahajan T, Rai K: A novel optogenetically tunable frequency modulating oscillator. <i>PLOS ONE</i> 2018, 13 :e0183242.
386	50.	
387 388		Santos VA, van Passel MW, Hugenholtz F: Design and analysis of a tunable synchronized oscillator. <i>J Biol Eng</i> 2013, 7 :26.
389 390	51.	Tigges M, Marquez-Lago TT, Stelling J, Fussenegger M: A tunable synthetic mammalian oscillator. <i>Nature</i> 2009, 457 :309–312.
391	52.	Tomazou M, Barahona M, Polizzi KM, Stan G-B: Computational Re-design of
392		Synthetic Genetic Oscillators for Independent Amplitude and Frequency
393		Modulation. <i>Cell Syst</i> 2018, 6 :508-520.e5.
394		Theoretical study demonstrating how genetic oscillators can be redesigned to enable
395		the independent tuning of amplitude and frequency. The major contribution is the
396		discovery of the important role that enzymatic degradation can play in allowing a
397		decoupling of internal processes, and thus tuning of system dynamics.
398	53.	Del Vecchio D, Dy AJ, Qian Y: Control theory meets synthetic biology. J R Soc
399		Interface 2016, 13 :20160380.
400	54.	Zhang J, Jensen MK, Keasling JD: Development of biosensors and their
401		application in metabolic engineering. Synth Biol • Synth Biomol 2015, 28:1-8.
402	55.	Tan SZ, Prather KL: Dynamic pathway regulation: recent advances and methods
403		of construction. Mech Biol Energy 2017, 41:28–35.
404	56.	Chou HH, Keasling JD: Programming adaptive control to evolve increased
405		metabolite production. Nat Commun 2013, 4:2595.
406	57.	Ceroni F, Algar R, Stan G-B, Ellis T: Quantifying cellular capacity identifies gene
407		expression designs with reduced burden. Nat Methods 2015, 12:415–418.
408	58.	Dragosits M, Nicklas D, Tagkopoulos I: A synthetic biology approach to self-
409		regulatory recombinant protein production in Escherichia coli. J Biol Eng 2012,
410		6 :2.

411 412 413	59.	Stapleton JA, Endo K, Fujita Y, Hayashi K, Takinoue M, Saito H, Inoue T: Feedback Control of Protein Expression in Mammalian Cells by Tunable Synthetic Translational Inhibition . <i>ACS Synth Biol</i> 2012, 1 :83–88.
414 415 416	60.	Cuba Samaniego C, Giordano G, Kim J, Blanchini F, Franco E: Molecular Titration Promotes Oscillations and Bistability in Minimal Network Models with Monomeric Regulators . <i>ACS Synth Biol</i> 2016, 5 :321–333.
417 418 419	61.	Chevalier M, Gómez-Schiavon M, Ng AH, El-Samad H: Design and Analysis of a Proportional-Integral-Derivative Controller with Biological Molecules . <i>Cell Syst</i> 2019, 9 :338-353.e10.
420 421 422	62.	M. Filo, M. Khammash: Optimal Parameter Tuning of Feedback Controllers with Application to Biomolecular Antithetic Integral Control . In 2019 IEEE 58th Conference on Decision and Control (CDC) 2019:951–957.
423 424 425 426	63.	Fiore G, Matyjaszkiewicz A, Annunziata F, Grierson C, Savery NJ, Marucci L, di Bernardo M: In-Silico Analysis and Implementation of a Multicellular Feedback Control Strategy in a Synthetic Bacterial Consortium. <i>ACS Synth Biol</i> 2017, 6 :507– 517.
427 428 429 430 431 432 433	64.	 Fiore G, Perrino G, di Bernardo M, di Bernardo D: In Vivo Real-Time Control of Gene Expression: A Comparative Analysis of Feedback Control Strategies in Yeast. <i>ACS Synth Biol</i> 2016, 5:154–162. Demonstration of the ability to combine single-cell imaging of yeast cells in microfluidics with real-time feedback control of chemical inducers to robustly regulate gene expression. A number of control algorithms are tested, with the performance of each varying for different tasks.
434 435 436 437	65.	Postiglione L, Napolitano S, Pedone E, Rocca DL, Aulicino F, Santorelli M, Tumaini B, Marucci L, di Bernardo D: Regulation of Gene Expression and Signaling Pathway Activity in Mammalian Cells by Automated Microfluidics Feedback Control . <i>ACS</i> <i>Synth Biol</i> 2018, 7 :2558–2565.
438 439 440 441 442	66.	 Milias-Argeitis A, Rullan M, Aoki SK, Buchmann P, Khammash M: Automated optogenetic feedback control for precise and robust regulation of gene expression and cell growth. <i>Nat Commun</i> 2016, 7:12546. Describes the development of an automated system to allow for reliable long-term optogenetic control-based experiments. Combines tunable expression systems based

doi:10.20944/preprints202007.0751.v2

443

automated sampling and analysis. Demonstrates the value of fully integrated and self-444 adaptive systems. 445 67. Rullan M, Benzinger D, Schmidt GW, Milias-Argeitis A, Khammash M: An Optogenetic 446 Platform for Real-Time, Single-Cell Interrogation of Stochastic Transcriptional 447 Regulation. Mol Cell 2018, 70:745-756.e6. 448 68. Pedone E, Postiglione L, Aulicino F, Rocca DL, Montes-Olivas S, Khazim M, di 449 Bernardo D, Pia Cosma M, Marucci L: A tunable dual-input system for on-demand 450 dynamic gene expression regulation. Nat Commun 2019, 10:4481. 451 • Describes a new multi-level system for controlling gene expression in mammalian 452 cells. By combining transcriptional control with post-translational destabilization, it is 453 possible to rapidly modulate protein expression level. The benefits of these properties 454 for control applications are also shown. 455 69. Fredens J, Wang K, de la Torre D, Funke LFH, Robertson WE, Christova Y, Chia T, 456 Schmied WH, Dunkelmann DL, Beránek V, et al.: Total synthesis of Escherichia coli 457 with a recoded genome. Nature 2019, 569:514-518. 458 70. Richardson SM, Mitchell LA, Stracquadanio G, Yang K, Dymond JS, DiCarlo JE, Lee 459 D, Huang CLV, Chandrasegaran S, Cai Y, et al.: Design of a synthetic yeast 460 genome. Science 2017, 355:1040. 461 71. Karkaria BD, Treloar NJ, Barnes CP, Fedorec AJH: From Microbial Communities to 462 Distributed Computing Systems. Front Bioeng Biotechnol 2020, 8:834. 463 72. Gorochowski TE, Hauert S, Kreft J-U, Marucci L, Stillman NR, Tang T-YD, Bandiera L, 464 Bartoli V, Dixon DOR, Fedorec AJH, et al.: Toward engineering biosystems with 465 emergent collective functions. Front Bioeng Biotechnol 2020, 8:705. 466 73. Beal J, Nguyen T, Gorochowski TE, Goñi-Moreno A, Scott-Brown J, McLaughlin JA, 467 Madsen C, Aleritsch B, Bartley B, Bhakta S, et al.: Communicating Structure and 468 Function in Synthetic Biology Diagrams. ACS Synth Biol 2019, 8:1818–1825. 469

on two-component light sensors and supporting hardware for continuous culture,



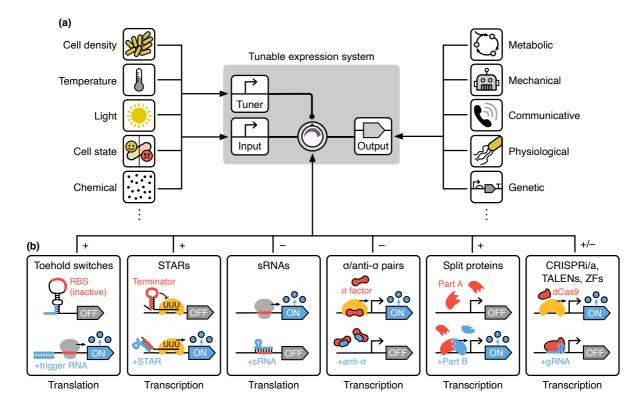


Figure 1: Tunable genetic parts. (a) Schematic of a tunable expression system (TES) where 472 a variety of different inputs and output can be selected. Typically, inputs are transcriptional 473 signals related to environmental or cellular states and the output is the expression of a gene 474 that influences cellular behavior or acts as an input to another part of a larger circuit. (b) Major 475 regulatory mechanisms that can be used to tune gene expression in a TES. Both active and 476 inactive states shown in addition to whether the tuner will cause activation (+) or repression 477 (-) of the output. The stage in gene expression (i.e. transcription or translation) where 478 regulation takes place is shown below the box for each mechanism. Ribosomes and RNA 479 polymerase (RNAP) shown by light grey and orange shapes without an outline, respectively. 480 For the CRISPRi/a, TALENs and ZFs box a repressive CRISPRi system is shown. This can 481 be modified to be an activator by fusing dCas9 to an activator domain to recruit RNAP to the 482 promoter. In general, the additional blue element would be expressed by the tuner input to 483 modulate expression of the output. RBS, ribosome binding site; sRNA, small RNA; STAR, 484 small transcription activating RNAs; siRNA, small interfering RNA; CRISPRi/a, clustered 485 regularly interspaced short palindromic repeats interference/activation; TALEN, transcription 486 activator-like effector neclease; ZF, zinc finger; gRNA, guide RNA. 487

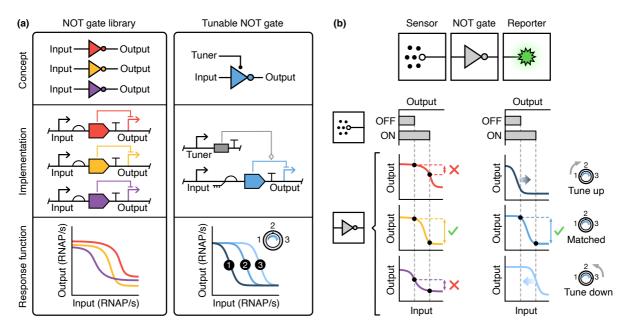


Figure 2: Tunable genetic parts enable the construction of adaptive circuits. (a) Libraries 489 of genetic parts (e.g. NOT gates) are commonly created that cover a range of different 490 behaviors (left box). These differences are shown by the specific response function of each 491 part, which captures the steady-state input-output relationship. For most genetic parts the 492 response function is fixed, and so physical replacement is necessary if a part is not compatible 493 when used in a system. In contrast, tunable genetic parts (right box) have additional tuner 494 inputs that allow the shape and position of the response function to be dynamically varied as 495 required. (b) Schematic of a simple genetic circuit where a sensor input is inverted to give a 496 desire output reporter (e.g. green fluorescence). For the sensor and NOT gate to parts to work 497 effectively, the output of the sensor must 'match' the response function of the NOT gate (dotted 498 grey lines). If the parts are matching, then a large change in the NOT gate output will occur 499 when the sensor switches between OFF and ON states. For standard NOT gates (left column) 500 entire libraries need to be assembled and screened to find a working combination. 501 Furthermore, if the environment changes then so too might the behavior of the parts making 502 reassembly necessary. For a tunable NOT gate (right column), the tuner input can be varied 503 until the gate perfectly matches the sensor's outputs. No reassembly is required, allowing the 504 circuit to be dynamically tuned to changing conditions. Genetic circuits shown using Synthetic 505 Biology Open Language (SBOL) Visual notation [73]. RNAP, RNA polymerase. 506

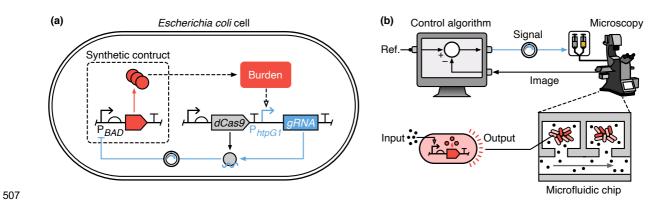


Figure 3: Self-adaptive systems. (a) Embedding burden-based controller. A synthetic 508 construct expresses a burdensome protein. Endogenous cellular processes (dashed arrows) 509 lead to the activation of the P_{htpG1} promoter under high levels of protein expression burden 510 causing expression of a guide RNA (gRNA). This gRNA forms a complex with a constitutively 511 expressed dCas9 protein that then targets the promoter of the synthetic construct, down 512 regulating its expression. The strength of this negative feedback loop is dynamically 'tuned' 513 by the endogenous burden signal as well as mismatches in the gRNA to the target promoter 514 that reduce the binding affinity of the dCas9:gRNA complex. Panel adapted from [9]. (b) 515 Schematic of an external in silico control system. Living cells grow in a microfluidic chip that 516 is continually imaged by a microscope. These images are set to a computer, analyzed and an 517 output signal from the cells (e.g. fluorescence) compared to a desired reference value. A 518 control algorithm assesses this difference and emits a control signal, which actuates syringes 519 and changes the concentration of a signaling molecule provided to the cells. The cells sense 520 this change and alter their gene expression in response. The strength of feedback in this 521 system can be tuned by modulating the control signals produced. Grey arrow in the 522 microfluidic chip represents the flow of nutrients and signaling molecules. gRNA, guide RNA. 523