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Queues & Bacteria:

a Tale of Modeling and Experiment

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Bacteria and RF analogies?



for their discoveries concerning genetic control of enzyme and virus synthesis

FRANÇOIS JACOB

Genetics of the bacterial cell

Nobel Lecture, December 11, 1965

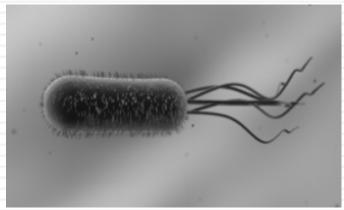
If I find myself here today, sharing with Andre Lwoff and Jacques Monod this very great honor which is being bestowed upon us, it is undoubtedly because, when I entered research in 1950, I was fortunate enough to arrive at the right place at the right time. At the right place, because there, in the attics of the Pasteur Institute, a new discipline was emerging in an atmosphere of enthusiasm, lucid criticism, nonconformism, and friendship. At the right time, because then biology was bubbling with activity, changing its ways of thinking, discovering in microorganisms a new and simple material, and drawing closer to physics and chemistry. A rare moment, in which ignorance could become a virtue.

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Bacterial Communities



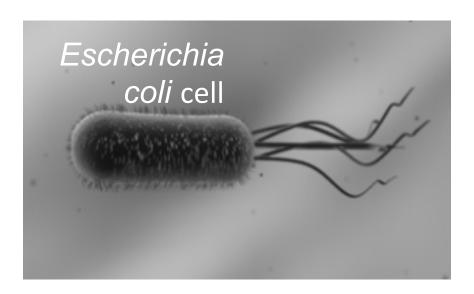


Analyze electron transport in bacterial cables
Develop models for quorum sensing

Why bacteria?

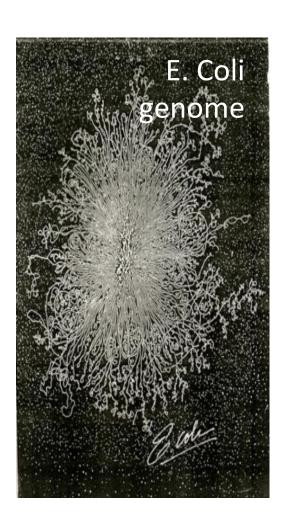


- Unicellular organisms
- One of the earliest forms of life (3-4 billion years ago)
- Aggregate biomass larger than all other plants/animals combined
- Relevant for bioremediation, plant growth, human and animal digestion, global elemental cycles including the carbon-cycle, and water treatment



Not as simple as they seem..





190 83,622 176,954 177.001 252 298 252,301 316,791 400,870 316,950 400,971 483,627 483,650 567,227 648,794 648,805 724,202 724,211 809,607 809,604 892,656 893,007 993,267 993,264 1,070,988 1.147.914 1,147,982 1,218,074 1,218,206 1,291,588 1,291,732 1,372,114 PREPARA GENERAL GENE 1,443,904 1,525,176 1,620,670 1.680.902 1,680,906 1,844,989 1,921,128 1,990,898 2,139,658 2,225,345 2,309,668 2,406,884 2,481,777 2,560,546 2,651,877 2,806,338 2.969.511 2,969,619 3,053,634 3,132,894 3,207,552 3,291,422 3,367,036 3.598.806 3,694,020 3,779,764 3.860.010 3,860,010 3,944,980 4,020,241 4.106.857 4,194,926 4,288,499 4,447,065 4,524,911 4,524,928 4,610,133

http://ecocyc.org

What is communication?



The fundamental problem of communication is that of reproducing at one point either exactly or approximately a message selected at another point.

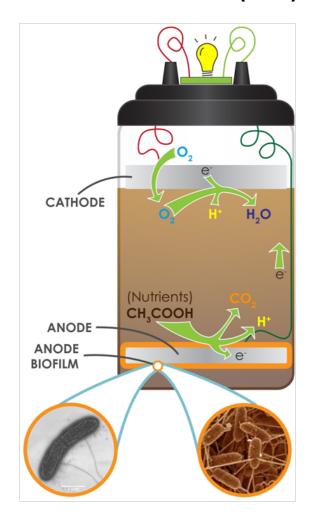
Claude Shannon, A Mathematical Theory of Communication, 1948



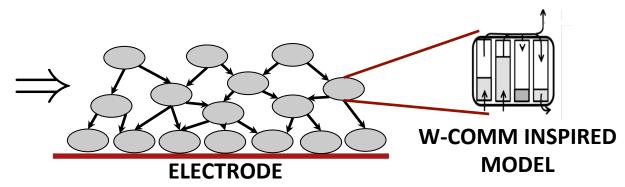
What is capacity for bacteria?



MICROBIAL FUEL CELL (MFC)



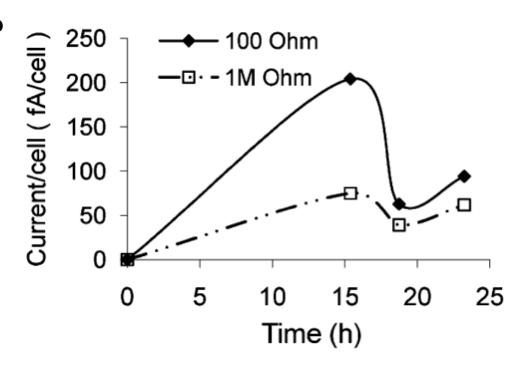
- Bacteria as "devices" that sense the environment, estimate, react
- Idea: tools from information theory and communications to model & predict bacterial networks:
 - Interactions, dynamics, formation
 - Do bacteria realize optimal control strategies?
 - *E.g.*: optimize MFC growth



How to achieve the sweet spot?



- Microbes on a 2D electrode
- Population grows as a function of time
- What happens at 15h?
- How are bacteria interacting?
- What is electron transport?

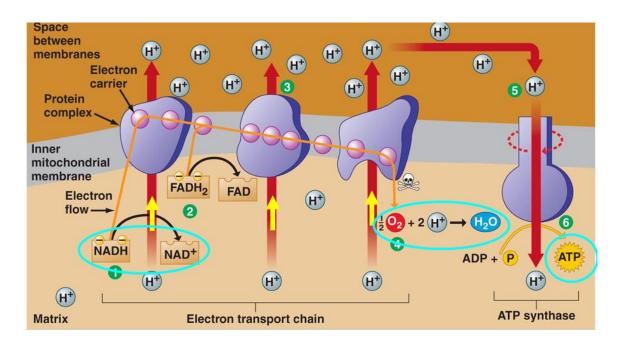


From Ken Nealson group, USC, Earth Sciences

e transport chain (ETC)



Fundamental (and well known) process in cellular respiration



- \bullet e⁻ flow creates proton gradient to pump synthesis of Adenosine triphosphate (ATP, cell's energy currency)
- Cells need a constant electron flow to produce energy (ATP)

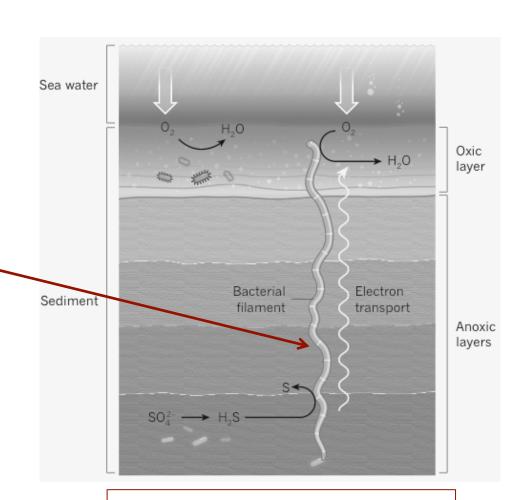
e⁻ transport



 \bullet e transport over cm-lengths

bacterial nanowires, biofilms, bacterial cables

> multi-hop communication ``network'' from e^- donor (ED) to e^- acceptor (EA)

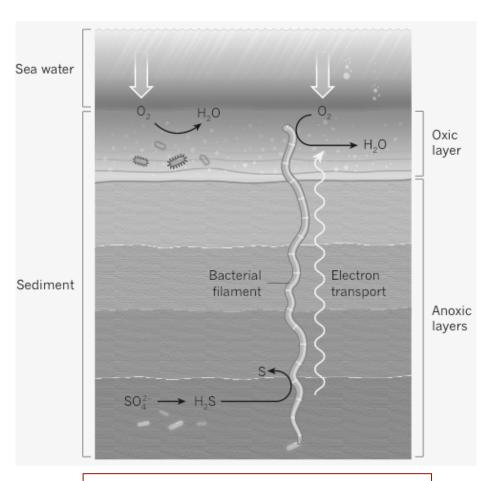


Bacterial cable (1D), Source: [Reguera, Nature'12]

e transport



- 1
- \bullet e transport over cm-lengths
 - bacterial nanowires, biofilms, bacterial cables
- □ Use communication strategies to optimize e⁻ transfer
- □ Capacity as proxy for maximal
 e⁻ transfer
- New dimension (& new models)information-energy coupling
 - Capacity ≠ bottleneck, vs wireless communications
 - Instead, local interactions & energy coupling, cells may die

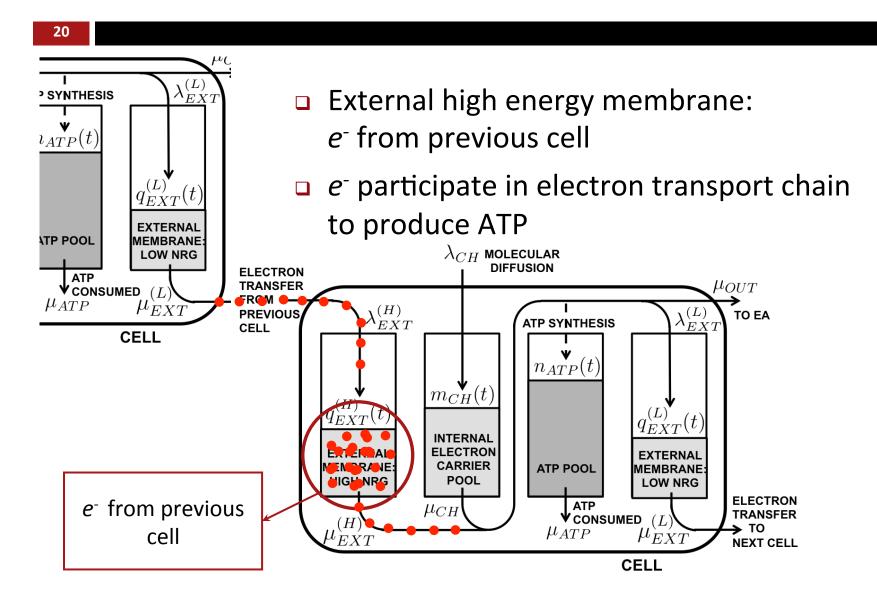


Bacterial cable (1D), Source: [Reguera, Nature'12]



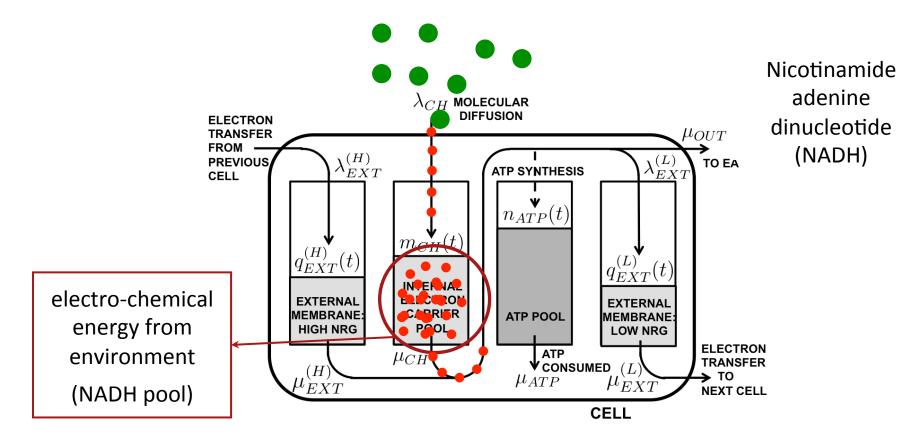
- □ **BEFORE**: modeling via deterministic ODE/PDE
 - E.g., [Klapper&Dockery,'10], [Picioreanua et al.,'07], [Marcus et al.,'07]
 - Detailed master equations & chemical reactions → huge complexity
- NOW: abstraction → stochastic queuing model inspired by W-COM
 - Chemical/electron concentrations → queues
 - Small-scale, local interactions as nuisances → stochastic model
 - Still high complexity, but tools for complexity reduction from W-COM can be exploited



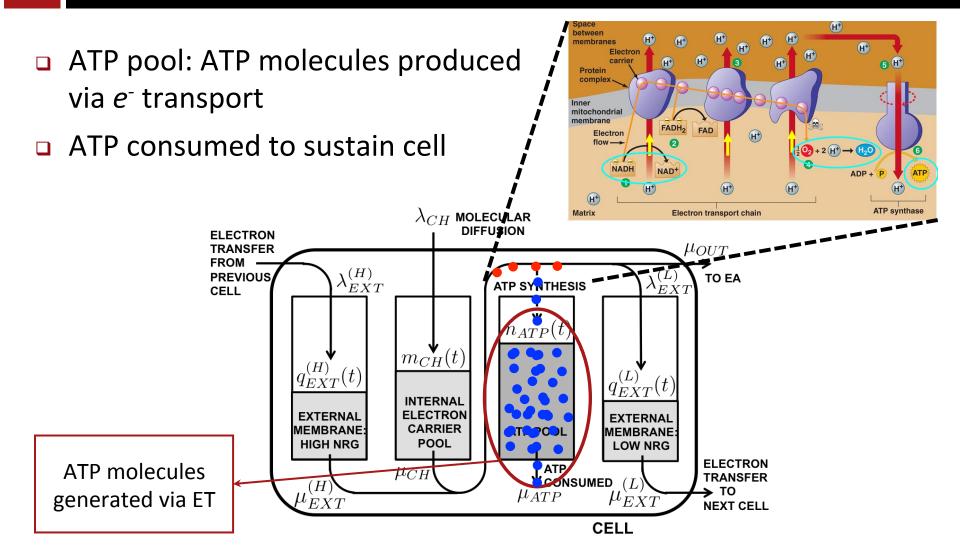




- Internal e⁻ carrier pool: e⁻ from external ED
- \bullet participate in electron transport chain to produce ATP

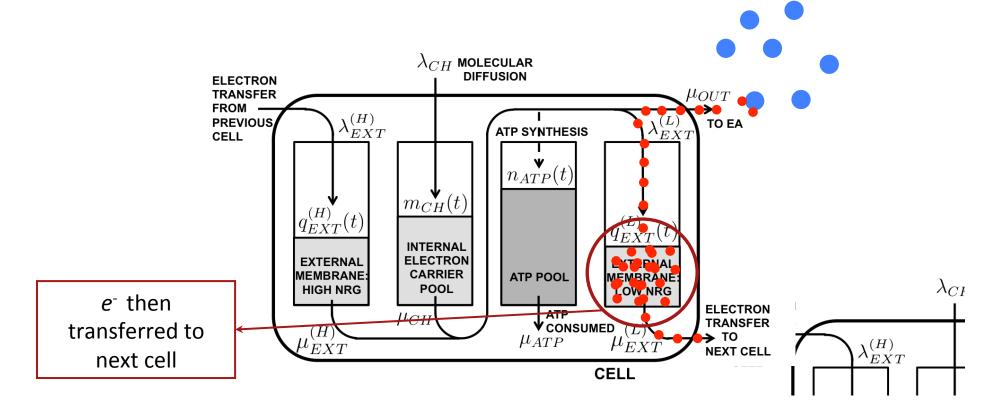






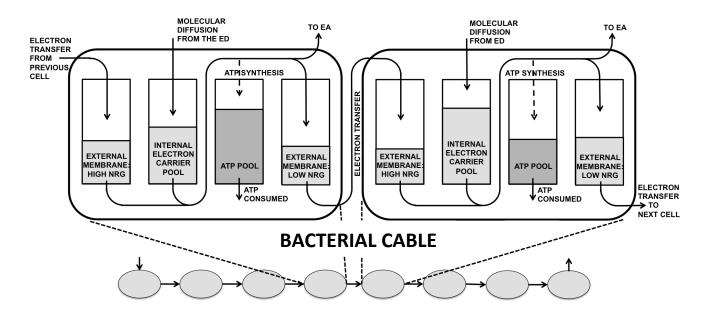


- \blacksquare External low energy membrane carries e^- after ETC. 2 paths:
 - Reduction to EA
 - e⁻ transfer to next cell or electrode





- Molecular diffusion & e⁻ transfer coexist
- ATP level = energetic state of the cell
 - ➤ Energy dimension: ATP low → cell may die
 - > Information dimension: ATP level too high → clogging



Isolated cell: experimental validation

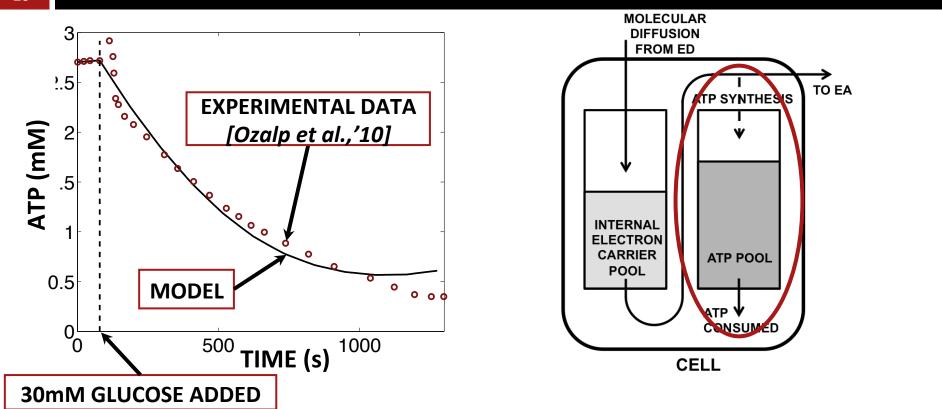


- Setup [Ozalp&al., Journal of Biological Chemistry, '10]
 - Suspension of yeast Saccharomyces cerevisiae (isolated cells)
 - ED added abruptly to starved cells
 - NADH (electron-carrier pool) and ATP levels measured
- Use experimental data to fit parameters

$$(\hat{\mathbf{x}}, \hat{\boldsymbol{\pi}}_0) = \arg\min_{\mathbf{x} \geq 0, \boldsymbol{\pi}_0 \in \mathcal{P}} \frac{1}{2} \sum_{k=0}^N \left\| \mathbf{y}_k - \boldsymbol{\pi}_0^T \prod_{j=1}^k \mathbf{P}_{\Delta}(\mathbf{x}, \mathbf{s}_{E,j-1})^{n_j - n_{j-1}} \mathbf{Z} \right\|_F^2$$
 State distribution
$$\frac{\text{Measured ATP/NADH}}{\text{(average over population)}}$$
 Fixed matrix: State indicator

Isolated cell: experimental validation



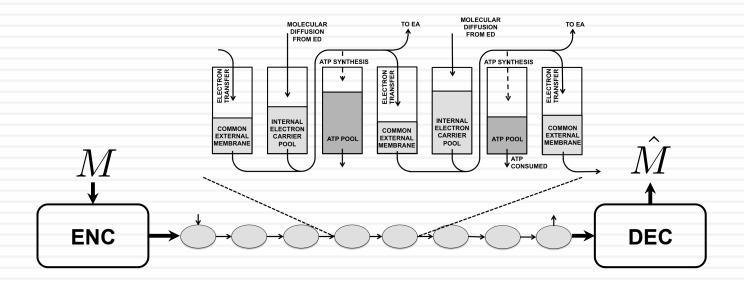


- Good fitting of experimental curve and model
- Stochastic queuing model simpler than detailed "physical" models, but captures salient features

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Information theoretic aspects



Multihop Capacity

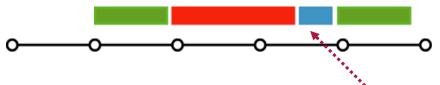


bottleneck

- Cascade of links
 - Persistently studied
- Via cut-set bounds can show that capacity is that of worst-case link

$$C = \min_{j} C_{j}$$

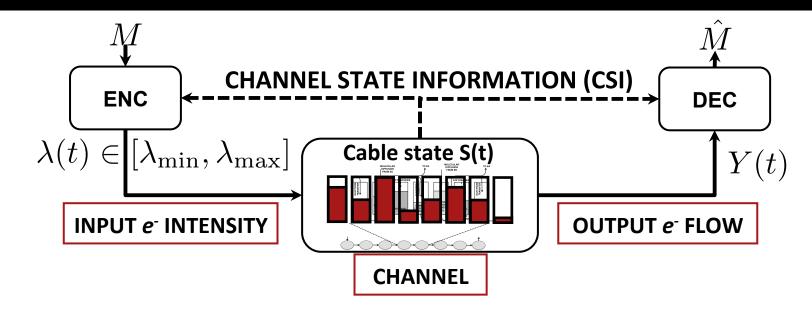
Achieved by decode-and-forward



- What happens in biological systems?
 - Communication over channels with state!
 - There is coupling between the links

Bacterial cable as communication system





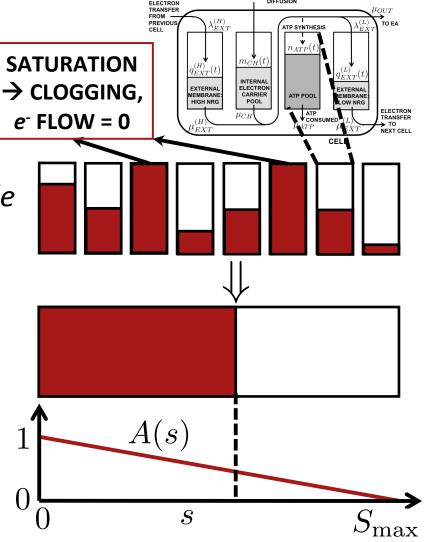
- Challenge: signal is coupled with energetic state of cells (channel state)
- ATP level = energetic state of the cell
 - ➤ Energy dimension: ATP low → cell may die
 - > Information dimension: ATP high \rightarrow clogging, e^- transfer stopped

Simplified cable model



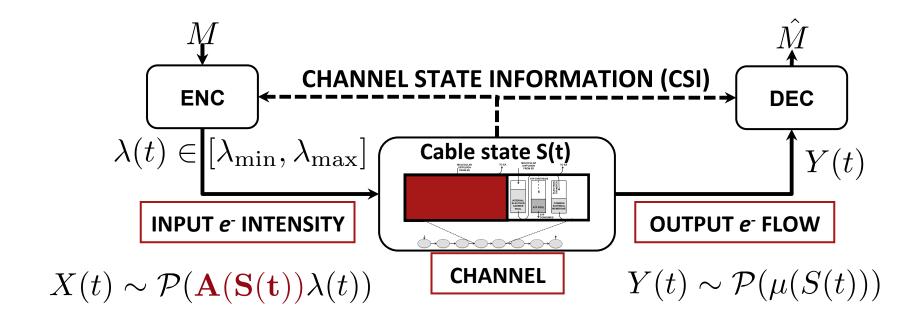
S(t)=Interconnection of all cells' states

- Simplified model: S(t)=# e⁻ in the cable
 - Local interactions averaged out over spatial dimension
 - Global effects captured by clogging state A(s)
 - S(t) small \rightarrow cells "starved"
 - S(t) large \rightarrow ATP saturation, clogging
 - A(s) = ratio of e^{-} accepted



Communication over Poisson channels with states





Prior Work

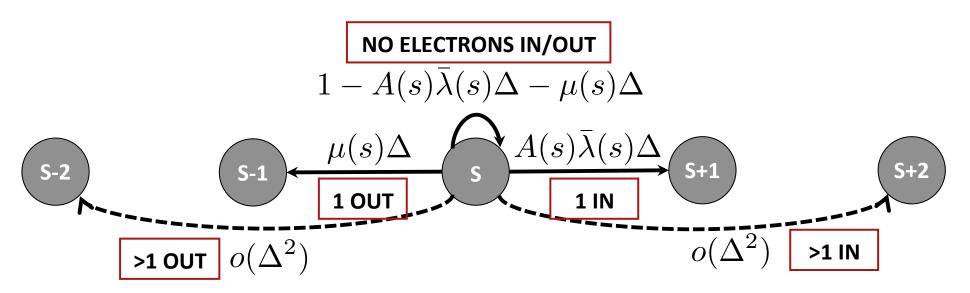


- Uncontrolled case, no CSI: [Goldsmith&Varaiya'96] iid coding
- **Uncontrolled case, partial CSIT, CSIR:** [Yuksel&Tatikonda'07]
- I.i.d. state controlled by actions, CSIT: [Weissman'10], [Choudhuri&Mitra,'12]
- **Controlled case, no CSI:** [Pfister et al.'01] i.i.d. coding; with FB: [Tatikonda&Mitter] POMDP
- Controlled case, full CSI & FB: [Chen&Berger'05] optimality of Markov coding, optimization via DP
- In our case, Markov state controlled by signal, full CSI case
- Finite-state continuous-time Markov Poisson channel
 - Static Poisson channels [Wyner'88]
 - We extend to finite-state Markov channels (**dynamic**)
 - Discrete-time: upper & lower bounds [Lapidoth&Moser'09]

Discrete time model: approximation



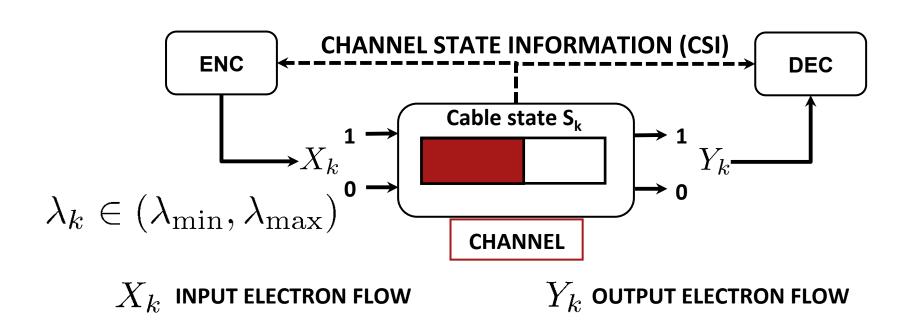
Assumption: "small" slot duration Δ [Wyner'88]



- Other events: probability $o(\Delta^2)$ -> neglected
- Only consider adjacent states

Discrete time model: approximation





- Assumption: "small" slot duration [Wyner'88]
- Channel with state (ENC controls intensity only)
- State "controlled" by input process; state-dependent output
 - Finite-state Markov [Chen&Berger'05]

Capacity of finite-state Markov channel



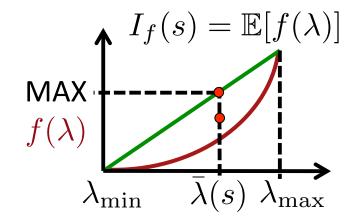
- Stationary Markov coding optimal [Chen&Berger'05]
- Capacity as dynamic program
 - Action/control: rate selection
 - Reward: $I_f^{(\Delta)}(s)$ mutual information conditioned on past state, control function
- THEOREM: capacity achieved by feedback independent inputs
 - [Chen&Berger'05] assumes feedback

Asymptotic capacity of Poisson Markov channels



 $C^* = \underbrace{\max_{\bar{\lambda}} \max_{f \in \mathcal{F}(\bar{\lambda})} \sum_{s}^{S_{\max}} \pi_{\bar{\lambda}}(s) I_f(s)}_{S_{\max}}$

- Information-Energy coupling.
 - Energy dimension:
 - Determined by $\bar{\lambda}(s)$
 - Information dimension:



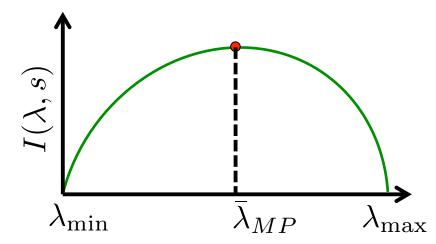
- **PROP:** Stationary distributior $\pi_f(s)$ depends only on $\ ar{\lambda}(s) = \mathbb{E}[\lambda|s]$
- *Impact:* Optimize over ENC functions f with same $ar{\lambda}(s)$
- **THEOREM:** Binary signal optimal $\lambda_k \in \{\lambda_{\min}, \lambda_{\max}\}$
 - Impact: easier to operate with a binary signal

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Myopic scheme



- $lue{}$ Myopic scheme: maximizes $I_f(s)$ in each slot
 - Can compute average rate in closed form
 - Independent of state s, no CSIT required (however, CSIR still required)
- \Box **THEOREM:** $\bar{\lambda}^*(s) \leq \bar{\lambda}_{MP}$ (otherwise, fast recharges & low rate)
 - Proof: properties of *n*-step value function

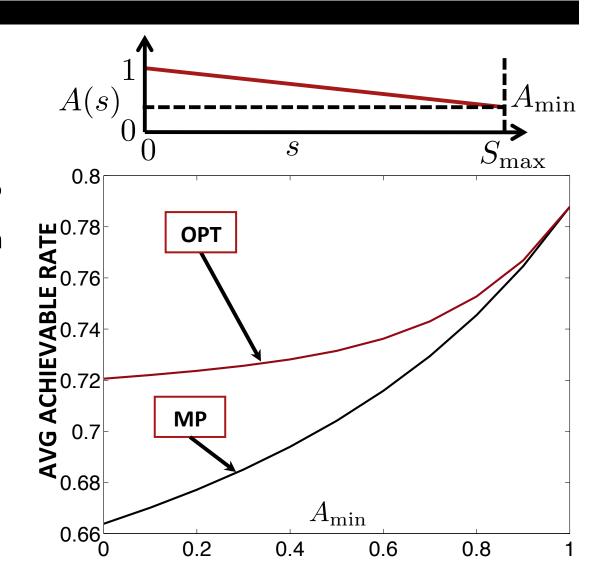


MP & OPT



Myopic scheme: greedy one step

- OPT 10% better than MP
 - MP: Greedy information transfer maximization achieves poor performance
- Information transfer
 maximization vs
 "wellness" maximization



Question

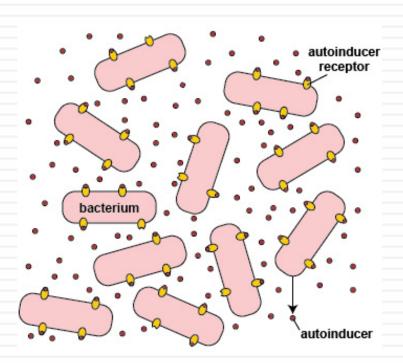


- Q: Can we apply these queueing theoretic approaches to OTHER bacterial networks?
- A: YES!
 - Quorum sensing...

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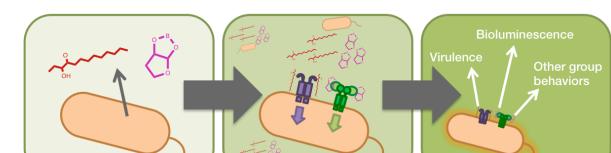
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Queuing models for Quorum Sensing



Quorum Sensing 101

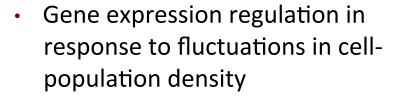




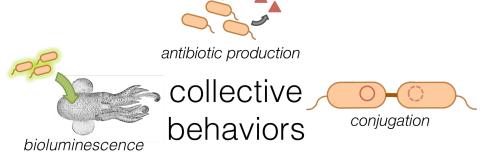
SYNTHESIS

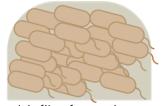
RECOGNITION

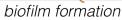
RESPONSE

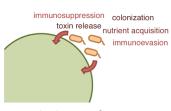


- Bacteria produce autoinducers that increase in concentration as a function of cell density
- regulates many diseases









virulence factors

http://sites.tufts.edu/quorumsensing/quorumsensing101/

Quorum Sensing



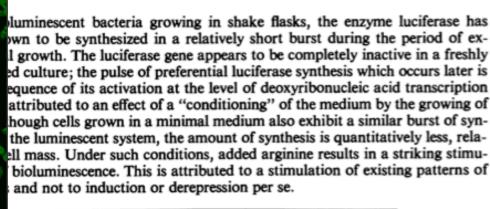
JOURNAL OF BACTERIOLOGY, October 1970, p. 313-322 Copyright ☐ 1970 American Society for Microbiology Vol. 104, No. 1 Printed in U.S.A.

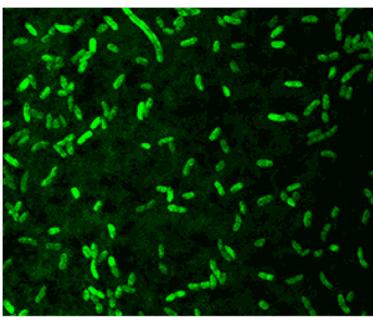
Cellular Control of the Synthesis and Activity of the Bacterial Luminescent System¹

KENNETH H. NEALSON, TERRY PLATT, AND J. WOODLAND HASTINGS

Biological Laboratories, Harvard University, Cambridge, Massachusetts, 02138 and
Marine Biological Laboratory, Woods Hole, Massachusetts 02534

Received for publication 30 April 1970





Vibrio Fischeri luminescing

Towards a model of QS



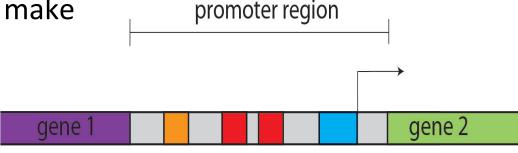
"Ingredients" of QS

- Microbial community (e.g., Pseudomonas Aeruginosa)
- 2. \rightarrow Autoinducers A(t) only global parameter, others by cell, i
 - Emitted by each cell in the environment
- 3. \blacksquare Receptors $R_i(t)$
 - They bind to autoinducers within each cell to form *complexes*
- 4. Complexes $C_i(t)$
 - 1 autoinducer bound to 1 receptor
- 5. Synthases $S_i(t)$
 - "machines" that produce autoinducers
- DNA binding sites
 - Complexes bind to them to produce *synthases*, *receptors* & *virulence factors*

Gene Expression

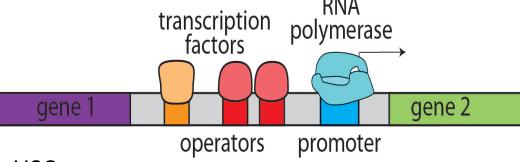


The promoter region between genes determines which proteins to make promoter region



genomic DNA

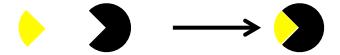
 Decision of whether or not to transcribe a gene depends on binding to operators and the promoter



Underlying processes



Autoinducers bind to receptors to create complexes



- Number of autoinducers/receptors decrease by 1
- Complexes can bind to one of three sites to create
 - Synthases (create autoinducers)

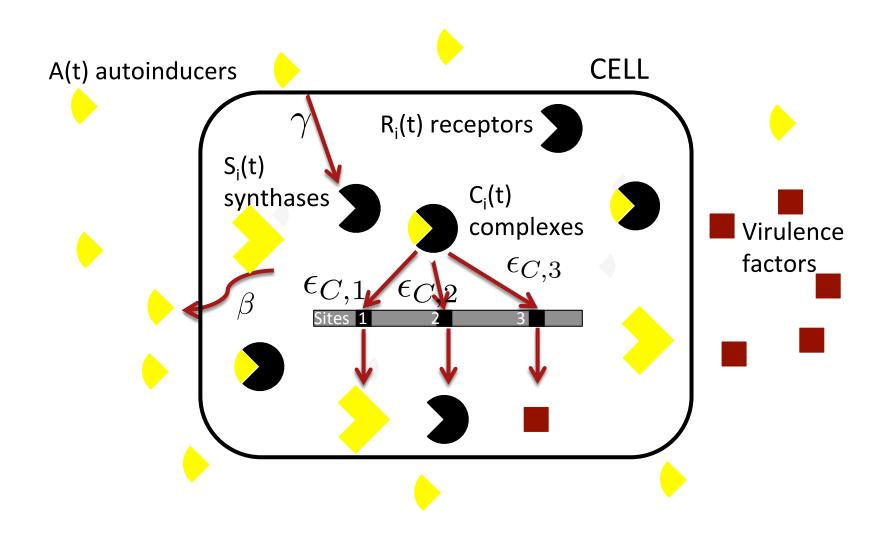




- Each have unique binding rates
- Complexes, synthases, receptors can degrade
- Cells do not die, but can duplicate

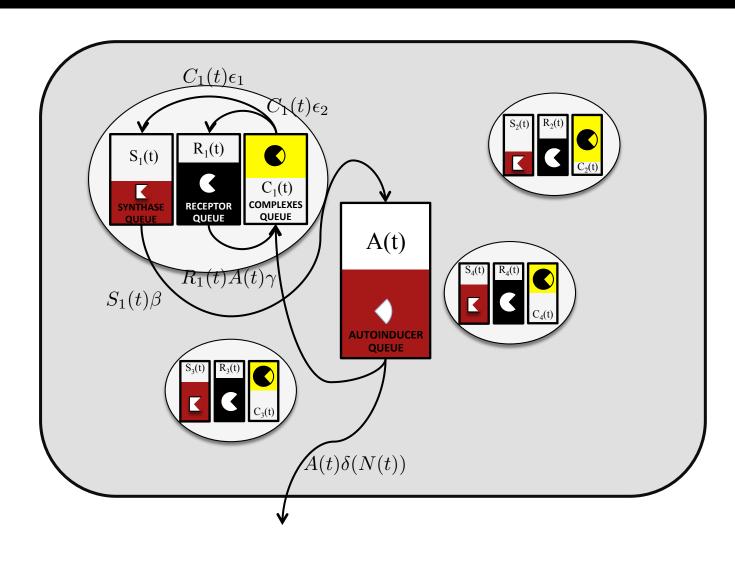
Abstraction of QS





Queuing model of QS





Compact state space representation



□ THEOREM:

 $(N(t), C_{\mathsf{TOT}}(t), R_{\mathsf{TOT}}(t), S_{\mathsf{TOT}}(t))$

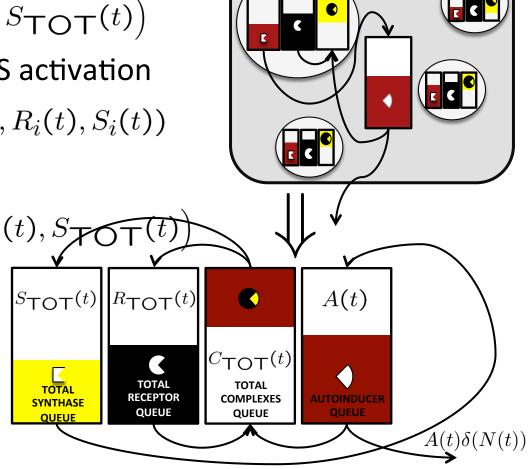
is a sufficient statistic for QS activation

□ Don't need to track $(C_i(t), R_i(t), S_i(t))$

for each cell,

track $(C_{TOT}(t), R_{TOT}(t), S_{TOT}(t), S_{TOT}(t$

Lower complexity!



Simulations

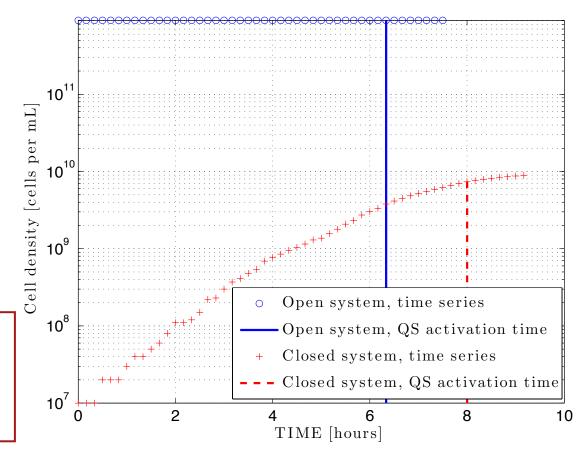


Simulation tools based on queuing model

- Cell density is higher in open system
 - Larger concentration of autoinducers
 - Faster activation time

OPEN SYSTEM: cells grow in open space (no boundaries → leakage of autoinducers)

CLOSED SYSTEM: cells grow in finite box (boundaries→ no leakage)



Simulations

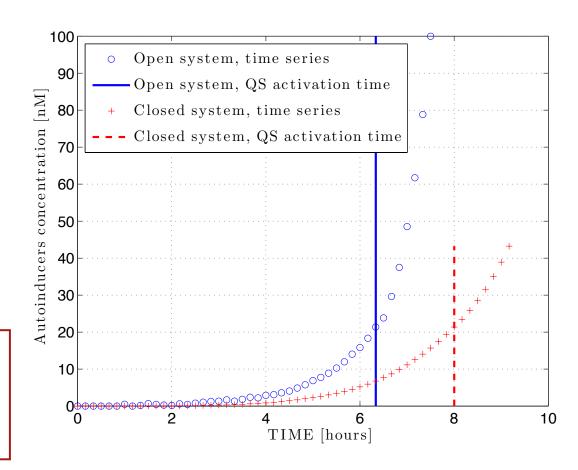


Simulation tools based on queuing model

- Model allows realistic performance evaluation in short time
- Use of complexity reduction tools from wireless comm

OPEN SYSTEM: cells grow in open space (no boundaries→leakage of autoinducers)

CLOSED SYSTEM: cells grow in finite box (boundaries → no leakage)

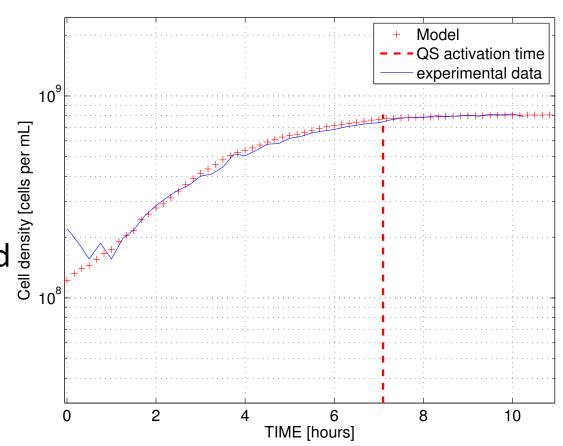


Experimental results



- Closed system
- □ Escherichia coli cells grown in LB media at
- grown in LB media at 37C

 Green Fluorescence protein (GFP) monitored protein (GFP) monitored (~ gene expression □ Green Fluorescence (~ gene expression activity)

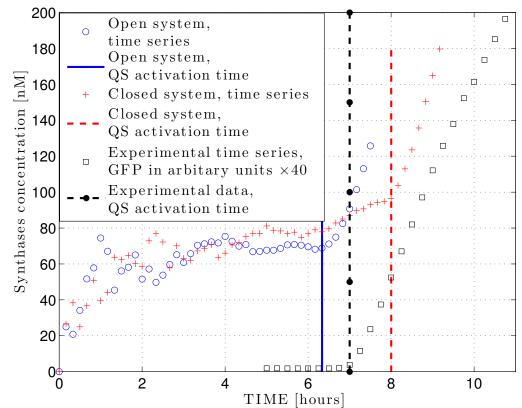


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Experimental results



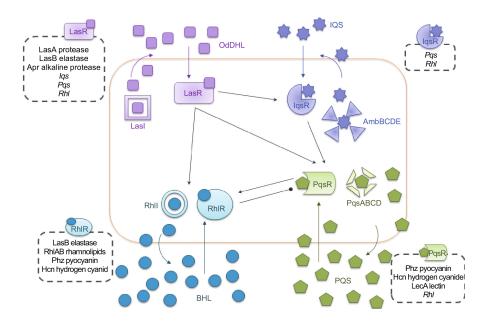
- Closed system
- Escherichia coli cells grown in LB media at 37C
- Green Fluorescence protein (GFP) monitored (~ gene expression activity)
- Model & experiments:
 - Similar qualitatively
 - But GFP=0 before QS activation (low basal expression rate) → further investigation needed



It is much more complicated...



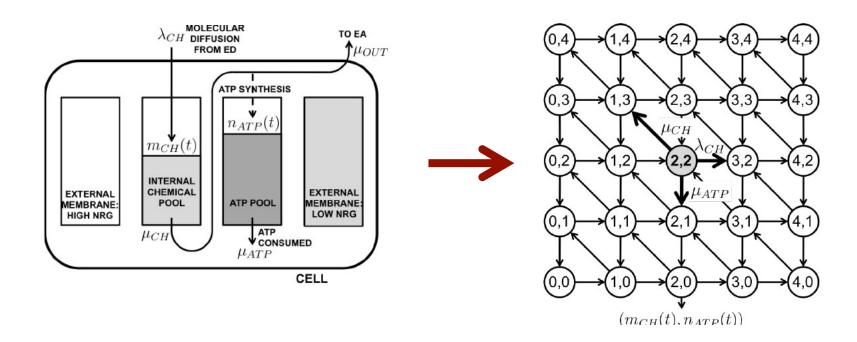
- □ The hierarchy quorum sensing network in Pseudomonas aeruginosa, Lee & Zhang, Protein&Cell 2015, 6(1):26–41
- Both stimulatory and suppressive interactions



Schematic representation of the four QS signaling networks in **P**. **aeruginosa** and their respective regulons

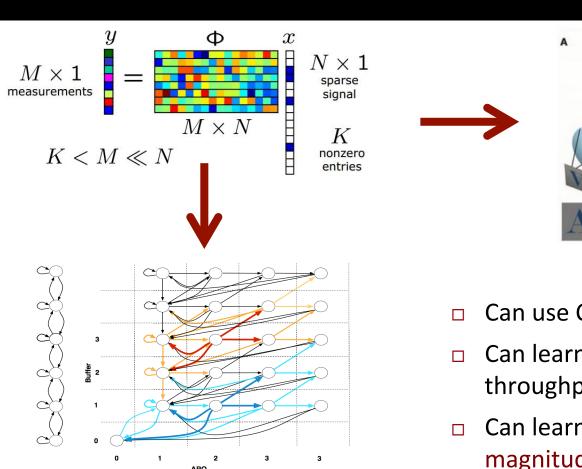
Bacterial Models





Large Scale Networks

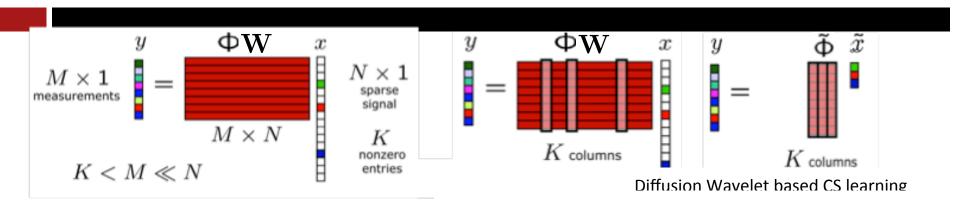




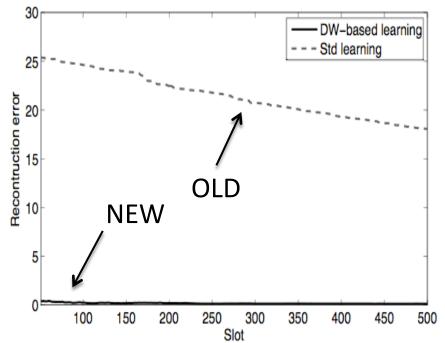
- Can use CS on graphs
- □ Can learn cost functions (e.g. throughput, SINR, BER, etc.)
- Can learn with two orders magnitude fewer samples

Use your favorite CS method





- Using Least Squares Residual Compressed sensing handles instability
 - Vaswani, IEEE Trans on SP 8/2010



Levorato, M & Goldsmith, EURASIP Wireless Comm & Net, 8/12

Summary



- Stochastic queuing theoretic model
 - Captures salient features, amenable to complexity reduction using W-COM tools (vs detailed physical models)
- □ IT aspects, coupling between
 - Coupling between wellness & information transfer
 - Impact: state estimation to adapt signal and optimize this tradeoff
- Quorum sensing modeling
 - Need to consider multiple signaling mechanisms
 - Experimental data analysis
 - Optimization to mitigate virulence factors

Thanks to...







Mohammed El-Naggar



PUBLICATONS

N. Michelusi, S. Pirbadian, M.Y. El-Naggar, U. Mitra, "A Stochastic Model for Electron Transfer in Bacterial Cables", IEEE JSAC- Series on Molecular, Biological, and Multi-Scale Communications 32 (12), , pp.2402-2416, Dec. 2014

N. Michelusi, U. Mitra, "Capacity of electronbased communication over bacterial cables: the full-CSI case", IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 1(1), pp. 62-75, March 2015.

N. Michelusi, J. Boedicker, M. El-Naggar, U. Mitra, ``Queuing models for abstracting interactions in Bacterial communities," IEEE JSAC Issue on Emerging Technologies, to appear.

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principles, design, and analysis of signaling and information systems beyond conventional electromagnetism, small-scale and multi-scale applications. molecular, quantum, chemical and biological techniques

