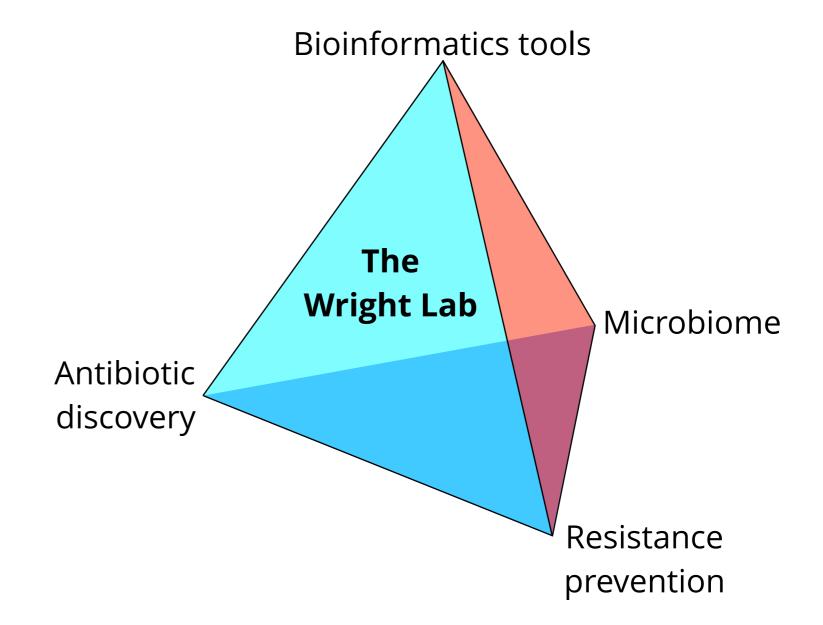


Erik S. Wright, PhD Assistant Professor

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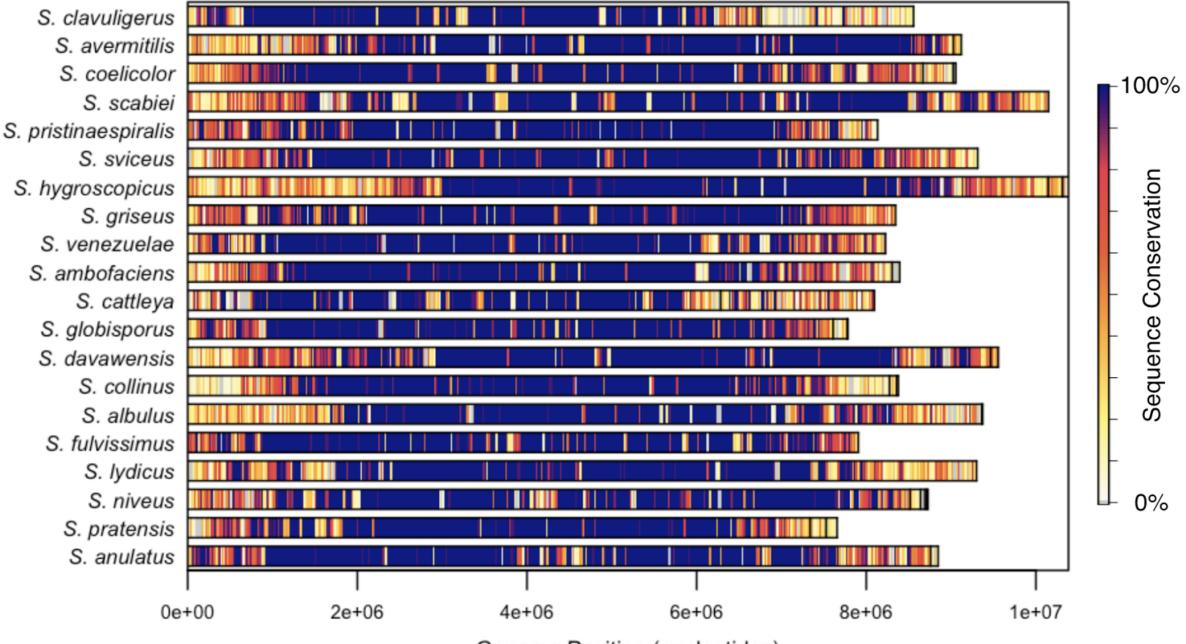






How do naturally antibiotic producing bacteria ward off resistance in their competitors?

Mining the genomes of antibiotic producing microorganisms to discover new antibiotic treatments.

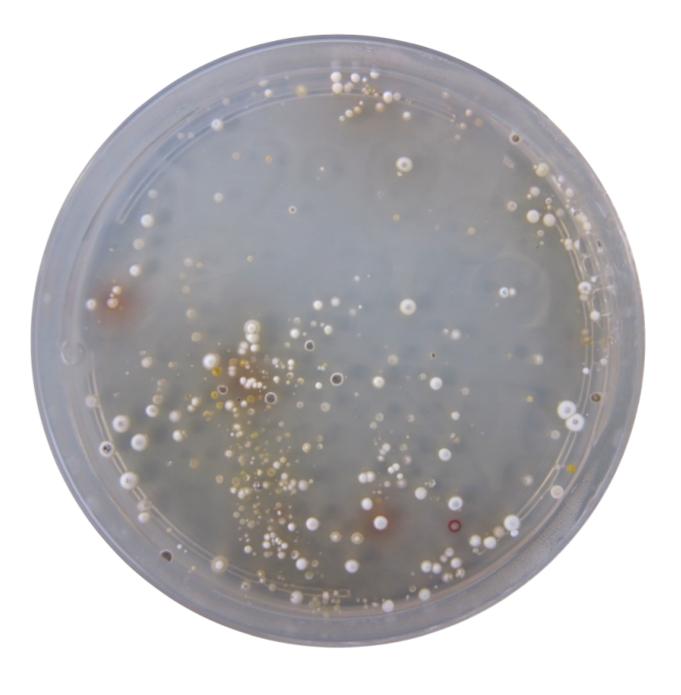


Genome Position (nucleotides)

How does the physical landscape shape the metaphorical adaptive landscape?

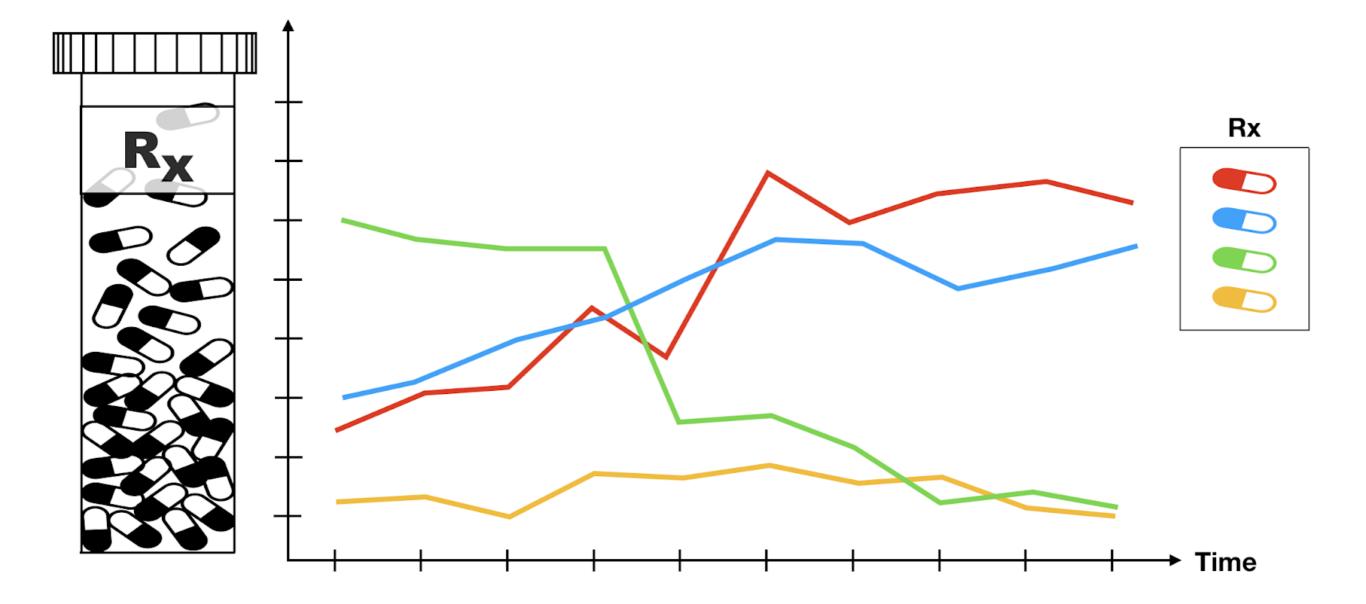
Studying the ecology and evolution of microorganisms in their natural context and in engineered 3D environments.





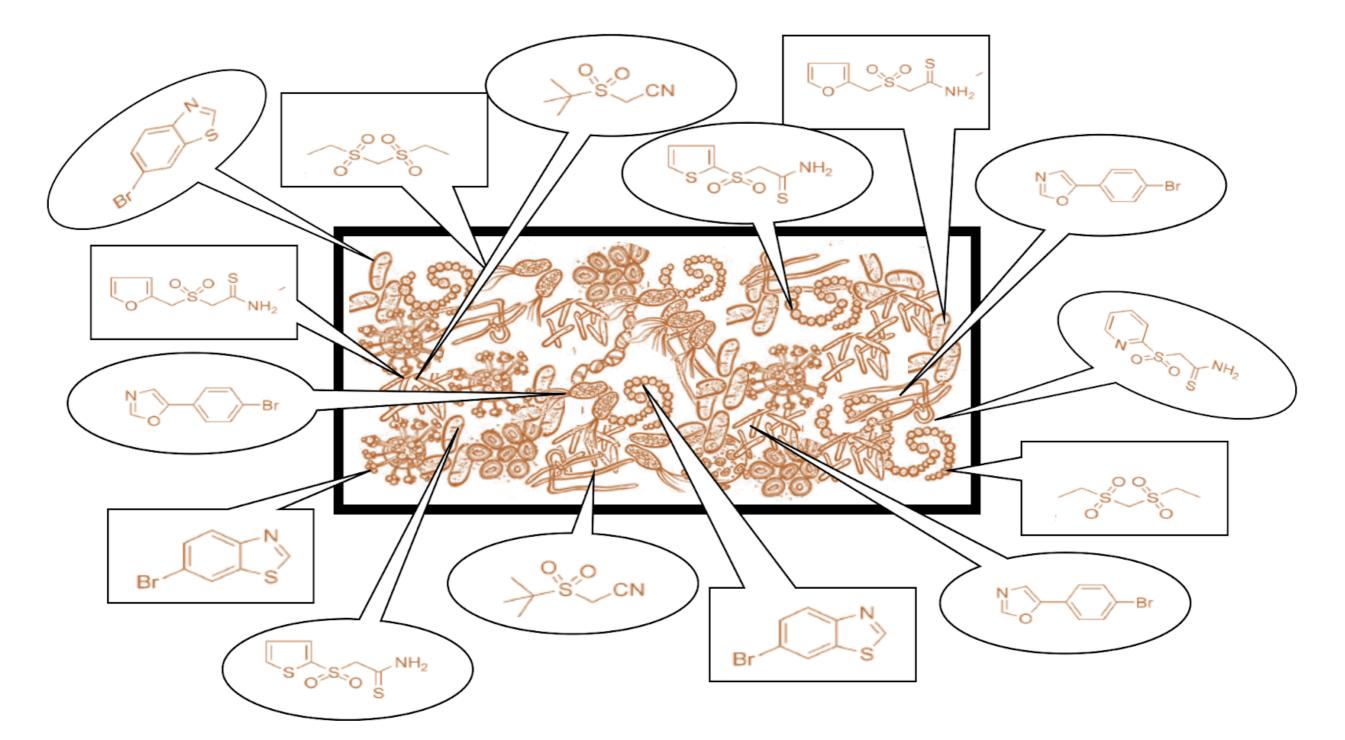
What is the optimal way to treat multi-drug resistant infections in the clinic?

Mining electronic health records for insights into how we can better conduct antimicrobial stewardship.



Can we communicate with the microbiome by learning its molecular language?

Using high-throughput mass spectrometry to decode the language of the microbiome.



What powerful insights can we draw from tens of thousands of microbial genomes?

Developing the next generation of bioinformatics tools for mining thousands of microbial genomes.

AACGCTCCGAAAGGAGCGGTAA	,TGAACGCTGGCGGCGTGCCTTACACATGCAAGTCGGATGTGTCGCAAGACACATGGCAGACGGGTGAGTAACACGTGGGAAACTTACCTCTTAGTGGGG/ ,TACCGCATGAGACCTATCGCTGGGATGCGATAGATGAAAGCTGGGGATCGTAAGACCTAGCGCTGAGAGAGA
CTGACGCAGCAACGCCGCGT	ITCAGTAGCCGGC CTG AGAGG GC GATCGGCC ACA CTGGAACT GAG ACACG GTC CAGAC TCC TACGG GAG GCAG C AGTGGGGAATCTT GCG CAATG GGC GA/ GGTGATGAAGG TCT TCGGATTGTAAAACCC TGT CGTTAGGG ACG AAGGCA TGA ATCC TAA TACGG TTC ATGT TTG ACGGTACCTAG AAA GGAAGC CCC G
GCATCTGAAACTGGAAGACTAG	ITAATACAGAG GGG GCAAGCGTTATTCGGAA TTA TTGGGCGT AAA GGGTGC GTA GGCG GT TTTTTA AGT CAGATGTGTAATCCCCCGAGCTCAACTTGGGAA AGTGCTGGAGAGGATGGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGGCCATCTGGACAGTAACTGAC
CGCCTGGGGAGTACGGTCGCA	ĊĂĂĂĊĂĠĠĂŢŢ Ă ĠĂŢĂĊĊĊŢĠĠŢĂĠŢĊĊĂĊ ĊĊ ĠŢĂĂĂĊĠĂŢ <mark>ĠĂĊĂĊŢŢ</mark> ĠĠŢĠŢŔĠŢĠĠĊĠŢŢ <mark>ĠĂĊ</mark> ĊĊĊĊ <mark>ĂĊŢ</mark> ĠŢĠĊĊĠŢĂĠĊŢĂĂĊĠĊĠĂŢĂĂĠŢĠŢ ŧĠĊŢĠĂĂĂĊŢ ĊĂĂ ĂĠĠĂĂŢŢĠĂĊĠĠĠĠĊĊĊ ĊĠĊ ĂĊĂĂĠĊĂĠĊ <mark>ĊĠĠ</mark> ŎġĊĂŢĠĊĠĠĊŢĊĂ <mark>ĂŢŢ</mark> ĊĠĊĠ ĊĂĂ ĊĠĊĠ <mark>ĂĂĠ</mark> ĂĊĊŢŢĂĊĊĂŎĠĊŢŢĠŎĊĂŢŎŢŎĊ ŧĊĊĠĊĂĂĠĠĠĊĠ ĊŢĂ ŢĂĊĂĠĠŢĠĠŢĠĊŢĊĠŢĊĂĠĊŢĊĊĠŢĠŦĊĠŢĠĂĊŎŢĠŎĠŎŢŢĨĂĠ ĠĊŢĊĊĊĊĂĊĊ ŎĂĊĊĊĊŎĂĊĊĊŢĂŢĊĂĊŢŎŎŢ
CAGGTAATGCTGGGAACTCT	ICCGCAAGGGCGCTATACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCCGGGAACGAGCGCCAACCCCCTATCACTAGTTGC IGTGAAACTGCCGTCGCAAGACGTGAGGAGGAGGAGGGGGATGATGTCAAGTCATCATGGCCTTTATGCCCTGGGGCTACACAGTGGTACAAAAGGAGGAGAAGGACAAA ICCAATCCCAAAAACCTTCTCTCAGTTCAGATTGGAGTCTGCAACTCGACTCCATGAAGCTGGAATCGCTAGTAATCGTATATCAGCAATGATACGGTGAA
	CGCCCGTCAAGCCATGGAAGCTGGGTGTACCTAAAGTCGGTAACCGAAAGGAGCCGCCTAGGGTAAAACTAGTGACTGGGGGCTAAGTCGTAACAAGGTAA
Home	
	Overview
Alignment >	DECIPHER is a software toolset that can be used for deciphering and managing
Classification	biological sequences efficiently using the R programming language. The R package
Find Chimeras	is distributed as platform independent source code under the GPL version 3 license. Some functionality of the program is accessible online through web tools.
	Some functionality of the program is accessible offline through web tools.
Oligo Design 🕨	La stalla Cara
Downloads	Installation
Tutorials	To install DECIPHER, start the latest version of R and enter:
Contact	if (!requireNamespace("BiocManager", quietly=TRUE))
	<pre>install.packages("BiocManager")</pre>