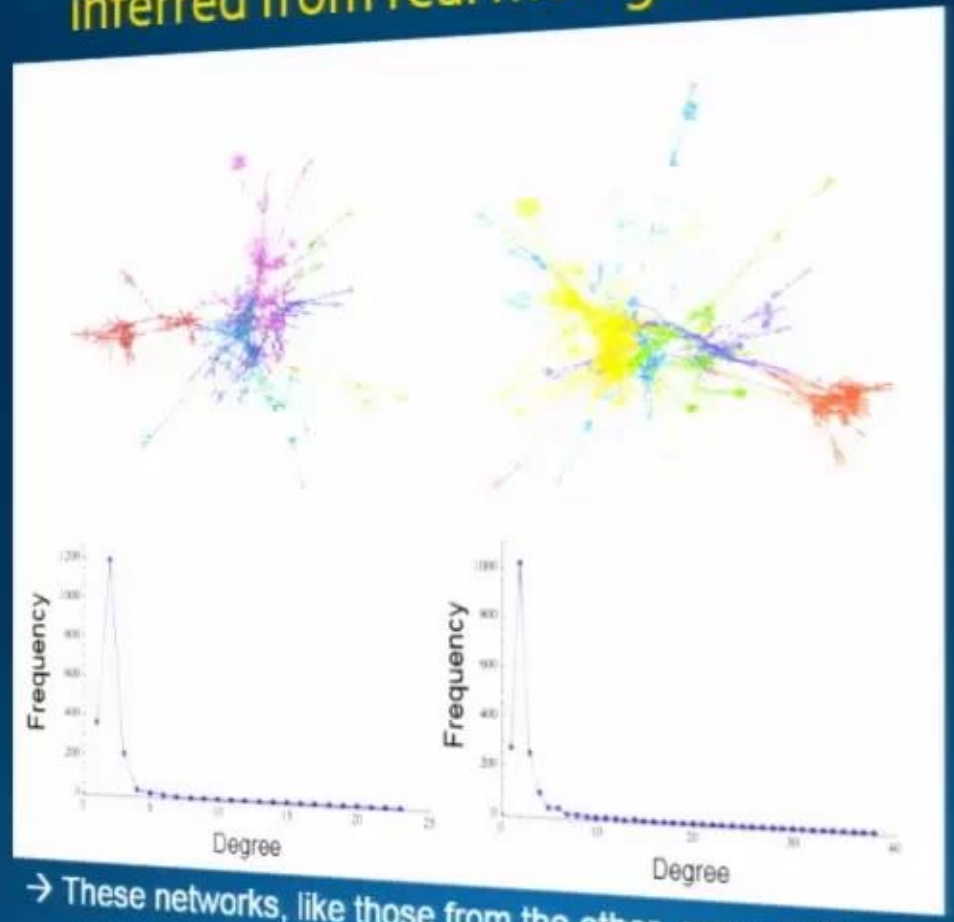
Topological analysis of metabolic networks inferred from real metagenomes



→ These networks, like those from the other communities analyzed (not shown), are scale-free

1
00:00:11,680 --> 00:00:10,330
yeah okay so i'm harrison and i'll be

2
00:00:13,650 --> 00:00:11,690
talking about the evolution about about

3
00:00:16,180 --> 00:00:13,660
communities I'm at Arizona State and

4
00:00:18,070 --> 00:00:16,190
working with a hundred Kim who's a

5
00:00:22,179 --> 00:00:18,080
postdoc in my lab Jason Raymond Sarah

6
00:00:23,589 --> 00:00:22,189
Walker two advisors of mine okay so just

7
00:00:25,089 --> 00:00:23,599
a quick outline I'm going to talk about

8
00:00:28,269 --> 00:00:25,099
some research questions i'm interested

9
00:00:30,220 --> 00:00:28,279
in the motivation behind my work some of

10
00:00:31,720 --> 00:00:30,230
the basics because i think some of the

11
00:00:33,850 --> 00:00:31,730
stuff i'll be talking about a lot of

12
00:00:34,750 --> 00:00:33,860
people won't be really familiar with and

13
00:00:36,520 --> 00:00:34,760

then i'll give you a little bit more

14
00:00:38,080 --> 00:00:36,530
detail approach of the work that i'm

15
00:00:39,310 --> 00:00:38,090
doing in terms of the network analysis

16
00:00:41,410 --> 00:00:39,320
on the yellowstone communities and

17
00:00:45,160 --> 00:00:41,420
computational simulations and some

18
00:00:47,979 --> 00:00:45,170
working conclusions ok so the research

19
00:00:50,020 --> 00:00:47,989
questions that i want you guys to think

20
00:00:53,799 --> 00:00:50,030
about and that i'm kind of focused on

21
00:00:56,830 --> 00:00:53,809
for this particular talk and in general

22
00:00:58,720 --> 00:00:56,840
overall with my work how is the

23
00:01:00,340 --> 00:00:58,730
functional and taxonomic diversity of

24
00:01:02,170 --> 00:01:00,350
microbial community reflected in the

25
00:01:03,819 --> 00:01:02,180
topological properties of the metabolic

26
00:01:05,920 --> 00:01:03,829
network are there any interesting

27
00:01:08,590 --> 00:01:05,930
patterns that's probably overwhelming

28
00:01:10,380 --> 00:01:08,600
and I haven't really defined a lot of

29
00:01:12,899 --> 00:01:10,390
these things like topological properties

30
00:01:14,920 --> 00:01:12,909
and I'll do that in a couple minutes

31
00:01:17,499 --> 00:01:14,930
keep that in mind a little bit but I'll

32
00:01:19,570 --> 00:01:17,509
kind of get more high-level here so what

33
00:01:20,740 --> 00:01:19,580
others is what changes do microbial

34
00:01:22,120 --> 00:01:20,750
communities undergo while they're

35
00:01:23,859 --> 00:01:22,130
evolving alongside a changing

36
00:01:28,990 --> 00:01:23,869
environment and kind of what I'm getting

37
00:01:30,819 --> 00:01:29,000
at here is trying to figure out how wife

38
00:01:32,080 --> 00:01:30,829

and its environment co-evolved I think

39
00:01:34,690 --> 00:01:32,090
that's really important question that a

40
00:01:36,280 --> 00:01:34,700
lot of people overlook oftentimes people

41
00:01:37,749 --> 00:01:36,290
talk about life as adapting to its

42
00:01:43,810 --> 00:01:37,759
environment but not necessarily is the

43
00:01:46,420 --> 00:01:43,820
environment adapting to life okay so why

44
00:01:49,569 --> 00:01:46,430
do we all care a lot of times with

45
00:01:50,740 --> 00:01:49,579
biology traditionally people are very

46
00:01:52,810 --> 00:01:50,750
reductionist and how they think about

47
00:01:54,700 --> 00:01:52,820
things and kind of this whole idea with

48
00:01:57,219 --> 00:01:54,710
you know like the Human Genome Project

49
00:01:59,469 --> 00:01:57,229
and trying to understand you know maybe

50
00:02:01,270 --> 00:01:59,479
if we understand exactly how the genome

51
00:02:03,310 --> 00:02:01,280
works and exactly what every single gene

52
00:02:05,529 --> 00:02:03,320
does we'll know exactly how biology does

53
00:02:07,240 --> 00:02:05,539
everything recently people have kind of

54
00:02:10,420 --> 00:02:07,250
pulled away from that and instead of

55
00:02:11,710 --> 00:02:10,430
going top down and they're trying to

56
00:02:13,120 --> 00:02:11,720
work from the bottom up where if you

57
00:02:14,970 --> 00:02:13,130
understand genes then you'll understand

58
00:02:17,290 --> 00:02:14,980
organisms you know understand societies

59
00:02:19,360 --> 00:02:17,300
it's kind of more of a complex problem

60
00:02:20,740 --> 00:02:19,370
and so it's more of a complex

61
00:02:23,530 --> 00:02:20,750
Systems problem where there's a lot of

62
00:02:25,899 --> 00:02:23,540
interesting interactions between life

63
00:02:27,940 --> 00:02:25,909

and the different aspects of life in

64
00:02:30,130 --> 00:02:27,950
terms of at the organismal level and at

65
00:02:32,080 --> 00:02:30,140
the enzymatic level and also between

66
00:02:35,410 --> 00:02:32,090
organisms and between organisms and

67
00:02:39,100 --> 00:02:35,420
their environments and some kind of the

68
00:02:40,750 --> 00:02:39,110
broader implications of work of trying

69
00:02:43,390 --> 00:02:40,760
to understand how life and its

70
00:02:45,610 --> 00:02:43,400
environment interact climate ologies a

71
00:02:47,440 --> 00:02:45,620
big example so how are humans affecting

72
00:02:49,899 --> 00:02:47,450
the climate how's the climate affecting

73
00:02:52,660 --> 00:02:49,909
humans has a lot of implications for a

74
00:02:54,400 --> 00:02:52,670
life going forward on earth biomedicine

75
00:02:55,809 --> 00:02:54,410
a big thing right now is understanding

76
00:02:57,009 --> 00:02:55,819
the human microbiome there's a lot of

77
00:02:58,720 --> 00:02:57,019
money being funneled into that and

78
00:03:01,270 --> 00:02:58,730
that's kind of like how does your gut

79
00:03:04,140 --> 00:03:01,280
microbiome reflect your health and how

80
00:03:07,809 --> 00:03:04,150
can we kind of utilize that in order to

81
00:03:09,580 --> 00:03:07,819
understand diagnose people and also

82
00:03:11,830 --> 00:03:09,590
understand how to treat them different

83
00:03:14,619 --> 00:03:11,840
diseases planetary science is probably

84
00:03:16,930 --> 00:03:14,629
most obvious one for this crowd and so

85
00:03:18,460 --> 00:03:16,940
what effect does emerging life have on

86
00:03:22,149 --> 00:03:18,470
its environment so that's kind of like

87
00:03:23,800 --> 00:03:22,159
bio signatures and also how does the

88
00:03:27,970 --> 00:03:23,810

environment affect what kind of life is

89
00:03:29,559 --> 00:03:27,980
as possible to evolve okay so the

90
00:03:32,199 --> 00:03:29,569
approach that I'm going to be looking at

91
00:03:34,720 --> 00:03:32,209
for looking at how the cove alleged

92
00:03:36,550 --> 00:03:34,730
coevolution of life in its environment I

93
00:03:37,960 --> 00:03:36,560
work from two aspects I do some

94
00:03:39,940 --> 00:03:37,970
computational modeling so I try to

95
00:03:42,309 --> 00:03:39,950
simulate microbial communities and

96
00:03:44,379 --> 00:03:42,319
evolution of microbial communities and

97
00:03:47,650 --> 00:03:44,389
I'm also doing some data analysis from

98
00:03:50,349 --> 00:03:47,660
actual real hard field data so we have

99
00:03:51,490 --> 00:03:50,359
some Yellowstone field data and I'll be

100
00:03:53,619 --> 00:03:51,500
talking to you a little bit about that

101
00:03:55,059 --> 00:03:53,629
and then kind of how these two things

102
00:03:57,550 --> 00:03:55,069
get tied together is this idea of

103
00:04:01,119 --> 00:03:57,560
network analysis so you can construct

104
00:04:03,520 --> 00:04:01,129
networks from the metabolisms of both

105
00:04:05,619 --> 00:04:03,530
the simulated work that I'm doing and

106
00:04:07,030 --> 00:04:05,629
also from the metabolisms that we infer

107
00:04:09,009 --> 00:04:07,040
in these communities that we go out and

108
00:04:10,839 --> 00:04:09,019
sample and you can represent them as

109
00:04:12,280 --> 00:04:10,849
networks and then you can measure these

110
00:04:14,379 --> 00:04:12,290
different properties and networks and

111
00:04:15,909 --> 00:04:14,389
use that to compare them and we hope to

112
00:04:17,529 --> 00:04:15,919
infer the evolutionary history of

113
00:04:19,120 --> 00:04:17,539

accident microbial communities through

114
00:04:22,750 --> 00:04:19,130
these models which is constrained by the

115
00:04:24,339 --> 00:04:22,760
field data okay so just really basics a

116
00:04:26,770 --> 00:04:24,349
lot of people probably know this but

117
00:04:29,380 --> 00:04:26,780
just for any people who are more

118
00:04:30,790 --> 00:04:29,390
ingrained in astronomy metabolism is

119
00:04:33,170 --> 00:04:30,800
just the chemical processes that occur

120
00:04:35,270 --> 00:04:33,180
that keep life living

121
00:04:37,279 --> 00:04:35,280
metabolic pathways just a sequence of

122
00:04:39,890 --> 00:04:37,289
those processes in metabolic network is

123
00:04:41,779 --> 00:04:39,900
just interconnected pathways so just on

124
00:04:43,760 --> 00:04:41,789
the right here I just this is a

125
00:04:45,469 --> 00:04:43,770
metabolic network example so this is

126
00:04:49,879 --> 00:04:45,479
amino acid a bunch of amino acid

127
00:04:52,659 --> 00:04:49,889
synthesis and particular with the stuff

128
00:04:54,439 --> 00:04:52,669
that I'm doing with the field work

129
00:04:55,670 --> 00:04:54,449
metabolic networks that microbial

130
00:04:58,850 --> 00:04:55,680
communities can be inferred from

131
00:05:00,800 --> 00:04:58,860
metagenomic data so if you sequence the

132
00:05:02,360 --> 00:05:00,810
genes then you can link those to a

133
00:05:04,580 --> 00:05:02,370
database and the database tells you what

134
00:05:05,930 --> 00:05:04,590
enzymes those genes code for and then

135
00:05:07,219 --> 00:05:05,940
there's another database that says what

136
00:05:09,320 --> 00:05:07,229
reactions are associated with those

137
00:05:12,740 --> 00:05:09,330
enzymes and so using all that data you

138
00:05:17,600 --> 00:05:12,750

can construct a big Network and infer

139
00:05:19,640 --> 00:05:17,610
the metabolism of a community ok so what

140
00:05:21,650 --> 00:05:19,650
our networks this is something that's

141
00:05:23,150 --> 00:05:21,660
probably need a lot of people so network

142
00:05:25,700 --> 00:05:23,160
when I say network I just mean nodes

143
00:05:27,200 --> 00:05:25,710
plus edges and to pot when I say to

144
00:05:28,610 --> 00:05:27,210
Paula gee I mean the physical properties

145
00:05:30,860 --> 00:05:28,620
of network so there are different things

146
00:05:32,510 --> 00:05:30,870
you can measure in a network such a

147
00:05:34,730 --> 00:05:32,520
shape connectivity or like degree

148
00:05:36,650 --> 00:05:34,740
distribution and that's example i'm

149
00:05:38,689 --> 00:05:36,660
giving you here so i'm left i have a

150
00:05:40,460 --> 00:05:38,699
random Network which is just the US

151
00:05:42,980 --> 00:05:40,470
highway map and on the right I have a

152
00:05:46,909 --> 00:05:42,990
scale-free Network which is the u.s.

153
00:05:49,700 --> 00:05:46,919
like airport system and the degree

154
00:05:51,529 --> 00:05:49,710
distribution of these nodes means how

155
00:05:55,610 --> 00:05:51,539
many nodes are connected how many other

156
00:05:58,939 --> 00:05:55,620
nodes so for example there's a small

157
00:06:01,339 --> 00:05:58,949
number of nodes that are that have a few

158
00:06:04,610 --> 00:06:01,349
links most nodes in this network have

159
00:06:07,520 --> 00:06:04,620
you know more than one but less than

160
00:06:10,010 --> 00:06:07,530
like 10 and then there's a few nodes

161
00:06:11,779 --> 00:06:10,020
which have way more than 10 so what you

162
00:06:14,029 --> 00:06:11,789
think about is like most cities are

163
00:06:15,649 --> 00:06:14,039

connected to only a few other cities and

164
00:06:17,600 --> 00:06:15,659
that's pretty consistent with the

165
00:06:19,100 --> 00:06:17,610
highway system in America which is

166
00:06:22,040 --> 00:06:19,110
unlike the airport system where you have

167
00:06:24,710 --> 00:06:22,050
big hubs where you have a few cities

168
00:06:29,300 --> 00:06:24,720
which are really highly connected so you

169
00:06:31,010 --> 00:06:29,310
have a lot of you have a lot of note or

170
00:06:32,600 --> 00:06:31,020
a lot of nodes with only a few links but

171
00:06:34,219 --> 00:06:32,610
you only have a few nodes with a lot of

172
00:06:35,540 --> 00:06:34,229
links and that's what this graph is

173
00:06:38,659 --> 00:06:35,550
showing so it follows a power law

174
00:06:40,999 --> 00:06:38,669
distribution and scale-free networks are

175
00:06:45,860 --> 00:06:41,009
really interesting because people use

176
00:06:46,820 --> 00:06:45,870
them to uncover scale-free networks are

177
00:06:49,840 --> 00:06:46,830
indicative of

178
00:06:52,160 --> 00:06:49,850
ecology and a lot of instances so that's

179
00:06:59,330 --> 00:06:52,170
something which we looked at in our

180
00:07:00,590 --> 00:06:59,340
research okay so Yellowstone we have

181
00:07:02,930 --> 00:07:00,600
some collaborators they got data from

182
00:07:05,390 --> 00:07:02,940
Yellowstone and there's these 26

183
00:07:07,580 --> 00:07:05,400
different sampled metagenomes that we

184
00:07:09,590 --> 00:07:07,590
have and like I saying earlier from the

185
00:07:11,420 --> 00:07:09,600
metagenomes we can infer the metabolic

186
00:07:13,670 --> 00:07:11,430
networks that are within these

187
00:07:15,380 --> 00:07:13,680
communities so you link them to the

188
00:07:17,030 --> 00:07:15,390

genes that you find in the metagenomes

189
00:07:19,520 --> 00:07:17,040
that you like the jeans the enzymes the

190
00:07:21,100 --> 00:07:19,530
enzymes the reactions and when I talk

191
00:07:24,320 --> 00:07:21,110
about metabolic network I'm just saying

192
00:07:25,700 --> 00:07:24,330
what is the metabolism facilitated by

193
00:07:27,320 --> 00:07:25,710
all the enzymes in this particular

194
00:07:30,950 --> 00:07:27,330
community so it's all the possible

195
00:07:32,660 --> 00:07:30,960
reactions as facilitated by enzymes okay

196
00:07:34,220 --> 00:07:32,670
so we can do this for phototrophic

197
00:07:36,140 --> 00:07:34,230
communities in kemah trophic communities

198
00:07:37,640 --> 00:07:36,150
and it ends up that you have different

199
00:07:39,410 --> 00:07:37,650
looking networks and these networks

200
00:07:40,850 --> 00:07:39,420
actually have different properties so

201
00:07:42,290 --> 00:07:40,860
just based on the properties in network

202
00:07:44,810 --> 00:07:42,300
you can figure out if the community is

203
00:07:46,310 --> 00:07:44,820
phototrophic or kim atrophic and just

204
00:07:48,170 --> 00:07:46,320
here's a visual example you wouldn't be

205
00:07:49,430 --> 00:07:48,180
will tell just from this image but you

206
00:07:51,380 --> 00:07:49,440
can look at different parameters of each

207
00:07:53,300 --> 00:07:51,390
of these networks and figure that out in

208
00:07:57,760 --> 00:07:53,310
the middle you have all communities put

209
00:07:59,960 --> 00:07:57,770
together plus all possible reactions

210
00:08:01,700 --> 00:07:59,970
okay so here's an example of two

211
00:08:03,920 --> 00:08:01,710
particular communities that of those 26

212
00:08:06,290 --> 00:08:03,930
that I was talking about and here's the

213
00:08:07,610 --> 00:08:06,300

degree distribution plots so these are

214
00:08:09,770 --> 00:08:07,620
the same plots that you saw under the

215
00:08:11,060 --> 00:08:09,780
random Network image and also under the

216
00:08:12,500 --> 00:08:11,070
scale-free Network image with the

217
00:08:15,110 --> 00:08:12,510
highway system and the airport system

218
00:08:16,910 --> 00:08:15,120
and if you notice these look a lot more

219
00:08:18,800 --> 00:08:16,920
like the airport systems these actually

220
00:08:20,720 --> 00:08:18,810
are scale-free networks so they follow

221
00:08:22,430 --> 00:08:20,730
up power law distribution and it's

222
00:08:23,570 --> 00:08:22,440
really interesting because like i was

223
00:08:24,980 --> 00:08:23,580
saying there's a lot of biological

224
00:08:27,500 --> 00:08:24,990
networks that follow the scale free

225
00:08:31,490 --> 00:08:27,510
distribution so maybe it's not too

226
00:08:33,260 --> 00:08:31,500
surprising that when you look at the

227
00:08:34,790 --> 00:08:33,270
metabolism of a whole community of

228
00:08:35,990 --> 00:08:34,800
organisms that it also follows a

229
00:08:37,100 --> 00:08:36,000
scale-free distribution but this

230
00:08:38,870 --> 00:08:37,110
actually isn't something that people

231
00:08:41,060 --> 00:08:38,880
have looked at before people looked at

232
00:08:43,370 --> 00:08:41,070
the distribution within particular

233
00:08:45,110 --> 00:08:43,380
organisms so within a single organism

234
00:08:47,090 --> 00:08:45,120
does F a scale-free distribution it

235
00:08:48,920 --> 00:08:47,100
turns out it does there's no reason that

236
00:08:50,150 --> 00:08:48,930
if you put a lot of them together that

237
00:08:51,470 --> 00:08:50,160
your distribution would still be

238
00:08:55,220 --> 00:08:51,480

scale-free so this is actually kind of

239
00:08:57,860 --> 00:08:55,230
an interesting result um another thing

240
00:08:59,590 --> 00:08:57,870
that we did is here's the 26 sampled

241
00:09:01,749 --> 00:08:59,600
metagenomes

242
00:09:03,759 --> 00:09:01,759
and we plotted a number of enzyme

243
00:09:05,710 --> 00:09:03,769
commission numbers which this is the

244
00:09:08,050 --> 00:09:05,720
number of basically unique enzymes or

245
00:09:10,240 --> 00:09:08,060
unique reactions coded by organisms in

246
00:09:12,100 --> 00:09:10,250
these communities on the y-axis and on I

247
00:09:13,870 --> 00:09:12,110
x-axis we did the number of taxonomic

248
00:09:18,340 --> 00:09:13,880
families so it's like number of species

249
00:09:22,780 --> 00:09:18,350
basically and the real metagenomes have

250
00:09:25,569 --> 00:09:22,790
a lot less number of enzymes for the

251
00:09:28,900 --> 00:09:25,579
number of families in a particular

252
00:09:31,689 --> 00:09:28,910
community and if we sample artificially

253
00:09:33,910 --> 00:09:31,699
which is the these blue dots random

254
00:09:35,920 --> 00:09:33,920
families and just put them together with

255
00:09:38,199 --> 00:09:35,930
this if you put the same number families

256
00:09:39,970 --> 00:09:38,209
together randomly assembled from these

257
00:09:42,519 --> 00:09:39,980
different communities then you end up

258
00:09:44,350 --> 00:09:42,529
with a lot more different enzymes that

259
00:09:47,259 --> 00:09:44,360
are being coded for which isn't that

260
00:09:48,370 --> 00:09:47,269
surprising basically this just means

261
00:09:50,559 --> 00:09:48,380
that reactions are shared across

262
00:09:52,840 --> 00:09:50,569
communities so these communities are

263
00:09:54,490 --> 00:09:52,850

more optimized for their environment and

264
00:09:55,990 --> 00:09:54,500
for the other organisms around them

265
00:09:58,509 --> 00:09:56,000
whereas these ones they use symbol

266
00:09:59,980 --> 00:09:58,519
artificially or not and that's pretty

267
00:10:01,840 --> 00:09:59,990
much what you'd expect because you

268
00:10:03,129 --> 00:10:01,850
wouldn't want to waste resources doing

269
00:10:07,720 --> 00:10:03,139
reactions that someone else in your

270
00:10:09,670 --> 00:10:07,730
communities already doing okay now I'm

271
00:10:11,079 --> 00:10:09,680
kind of going to jump into the other

272
00:10:12,910 --> 00:10:11,089
aspect of what i was talking about which

273
00:10:15,749 --> 00:10:12,920
is that I do this computational modeling

274
00:10:19,629 --> 00:10:15,759
stuff and so in these models that I make

275
00:10:21,429 --> 00:10:19,639
I simulate the evolution of organisms

276
00:10:23,590 --> 00:10:21,439
and the organisms are defined by the

277
00:10:25,509 --> 00:10:23,600
enzymes that they contain so on this

278
00:10:26,679 --> 00:10:25,519
picture on the right here I just show

279
00:10:29,319 --> 00:10:26,689
you each of these little circles

280
00:10:30,400 --> 00:10:29,329
represents an organism and then they're

281
00:10:33,610 --> 00:10:30,410
divided into different little

282
00:10:37,210 --> 00:10:33,620
communities and they catalyze reactions

283
00:10:39,370 --> 00:10:37,220
based on their propensity and propensity

284
00:10:40,569 --> 00:10:39,380
is just a fancy way of saying well if

285
00:10:42,220 --> 00:10:40,579
you have a higher concentration of

286
00:10:43,540 --> 00:10:42,230
different substrates that's more likely

287
00:10:44,920 --> 00:10:43,550
directions going to be catalyzed

288
00:10:50,290 --> 00:10:44,930

especially if the reaction rate

289
00:10:51,670 --> 00:10:50,300
constants higher okay so this is some

290
00:10:52,929 --> 00:10:51,680
preliminary results for my model which

291
00:10:55,689 --> 00:10:52,939
basically just shows that it's behaving

292
00:10:57,309 --> 00:10:55,699
as it should be so look at this bottom

293
00:10:59,050 --> 00:10:57,319
plot first and this is just showing you

294
00:11:00,519 --> 00:10:59,060
species count over time so each of these

295
00:11:03,420 --> 00:11:00,529
different lines is a different species

296
00:11:05,889 --> 00:11:03,430
as defined by the enzymes it contains

297
00:11:08,639 --> 00:11:05,899
and you kind of see here that after some

298
00:11:10,489 --> 00:11:08,649
system time that a few species become

299
00:11:12,769 --> 00:11:10,499
more fit than

300
00:11:13,939 --> 00:11:12,779
rest of the things in the system but

301
00:11:15,619 --> 00:11:13,949
then they'd eventually die out just

302
00:11:17,809 --> 00:11:15,629
because the system is closed and there's

303
00:11:19,699 --> 00:11:17,819
no energy input to you burning all your

304
00:11:21,229 --> 00:11:19,709
energy that you have and then this top

305
00:11:23,479 --> 00:11:21,239
plot is just showing you the fraction

306
00:11:25,849 --> 00:11:23,489
the total organismal energy contained

307
00:11:28,699 --> 00:11:25,859
within a particular species so the total

308
00:11:31,519 --> 00:11:28,709
organismal energy combined all hundred

309
00:11:32,749 --> 00:11:31,529
species at the beginning is going to be

310
00:11:35,479 --> 00:11:32,759
one it's going to be one at the end

311
00:11:37,519 --> 00:11:35,489
because that doesn't change but you can

312
00:11:39,499 --> 00:11:37,529
just see the fraction of energy in these

313
00:11:42,709 --> 00:11:39,509

two species that dominate ends up

314
00:11:44,029 --> 00:11:42,719
increasing as you'd expect so this isn't

315
00:11:46,069 --> 00:11:44,039
supposed to be anything mind-blowing but

316
00:11:48,589 --> 00:11:46,079
I'm just showing you that I'm starting

317
00:11:52,129 --> 00:11:48,599
to replicate how microbial systems can

318
00:11:53,809 --> 00:11:52,139
evolve on my computer and that we can

319
00:11:55,039 --> 00:11:53,819
use this eventually to make networks to

320
00:11:58,249 --> 00:11:55,049
compare to those same networks I was

321
00:11:59,839 --> 00:11:58,259
showing you earlier okay so just going

322
00:12:01,329 --> 00:11:59,849
through few working conclusions these

323
00:12:03,949 --> 00:12:01,339
are bullet points I showed you earlier

324
00:12:05,629 --> 00:12:03,959
but Camino metabolic networks inferred

325
00:12:07,429 --> 00:12:05,639
from metagenomic data is indicated that

326
00:12:08,839 --> 00:12:07,439
they have a scale-free degree

327
00:12:12,229 --> 00:12:08,849
distribution just like organismal

328
00:12:13,639 --> 00:12:12,239
metabolic networks Rio metagenomes have

329
00:12:15,499 --> 00:12:13,649
much less Cadillac diversity than

330
00:12:16,639 --> 00:12:15,509
artificial metagenomes suggesting the

331
00:12:18,889 --> 00:12:16,649
reactions are shared across communities

332
00:12:20,029 --> 00:12:18,899
and that I've constructed this model and

333
00:12:22,279 --> 00:12:20,039
then it were working on it so that we

334
00:12:38,299 --> 00:12:22,289
can compare it to the empirical data

335
00:12:39,439 --> 00:12:38,309
that we have so thank you questions so I

336
00:12:41,529 --> 00:12:39,449
thought that plot that you have is

337
00:12:44,019 --> 00:12:41,539
really interesting that showing that

338
00:12:47,269 --> 00:12:44,029

these reactions are shared across

339
00:12:48,739 --> 00:12:47,279
communities because I think lots of

340
00:12:50,479 --> 00:12:48,749
times when you think about the origin of

341
00:12:52,189 --> 00:12:50,489
life we talk about RNA worlds or

342
00:12:54,379 --> 00:12:52,199
whatever and we sort of assumed that

343
00:12:55,939 --> 00:12:54,389
some geochemistry would be providing

344
00:12:58,069 --> 00:12:55,949
some functionality for primitive life

345
00:12:59,960 --> 00:12:58,079
but I think it's really cool to see that

346
00:13:01,249 --> 00:12:59,970
you know you don't even need to assume

347
00:13:03,109 --> 00:13:01,259
that primitive life was doing that

348
00:13:06,469 --> 00:13:03,119
modern life is very clearly doing that

349
00:13:08,539 --> 00:13:06,479
and it's really observable so do you

350
00:13:10,639 --> 00:13:08,549
have any insight about what kinds of

351
00:13:12,249 --> 00:13:10,649
functions might be more easily shared or

352
00:13:14,689 --> 00:13:12,259
do you have any way to get at that data

353
00:13:16,129 --> 00:13:14,699
we do have ways to get that data and we

354
00:13:17,899 --> 00:13:16,139
do have that data we just haven't

355
00:13:19,819 --> 00:13:17,909
investigated it this is kind of like the

356
00:13:21,409 --> 00:13:19,829
first level thing that we've done so

357
00:13:22,230 --> 00:13:21,419
that's probably the next goal is we want

358
00:13:23,940 --> 00:13:22,240
to investigate

359
00:13:32,449 --> 00:13:23,950
exactly what reactions tend to be shared

360
00:13:39,000 --> 00:13:36,510
have my own mic so if you don't have a

361
00:13:42,860 --> 00:13:39,010
closed system how do you how would you

362
00:13:48,800 --> 00:13:45,449
that's a good question and it's really

363
00:13:51,180 --> 00:13:48,810

hard to predict just gonna top my head

364
00:13:52,829 --> 00:13:51,190
but it'd be interesting because you

365
00:13:55,710 --> 00:13:52,839
wouldn't I mean like you'd be able to

366
00:13:57,840 --> 00:13:55,720
see things evolve more so in this system

367
00:14:00,690 --> 00:13:57,850
obviously whatever we put in the initial

368
00:14:02,040 --> 00:14:00,700
conditions if it's close it's going to

369
00:14:03,570 --> 00:14:02,050
live for a while and it's going to die

370
00:14:05,220 --> 00:14:03,580
but it's not really going to change and

371
00:14:07,050 --> 00:14:05,230
so if you had some open conditions r you

372
00:14:09,060 --> 00:14:07,060
I had energy flowing or you had a flow

373
00:14:10,530 --> 00:14:09,070
of metabolites in then you can probably

374
00:14:13,050 --> 00:14:10,540
see somewhere interesting dynamics

375
00:14:19,320 --> 00:14:13,060
that's a very vague answer but that's