
AB
GRAD
CON23

1
00:00:13,310 --> 00:00:10,870
[Music]

2
00:00:16,070 --> 00:00:13,320
so thank you

3
00:00:18,109 --> 00:00:16,080
um yeah I'm here to talk about a

4
00:00:20,029 --> 00:00:18,119
different kind of biosignature um to

5
00:00:21,349 --> 00:00:20,039
introduce assembly Theory

6
00:00:23,390 --> 00:00:21,359
I don't know if this is the right group

7
00:00:25,670 --> 00:00:23,400
to be very controversial about it with

8
00:00:27,769 --> 00:00:25,680
or if you guys all accept it so we're

9
00:00:30,769 --> 00:00:27,779
gonna we're gonna see what happens

10
00:00:31,970 --> 00:00:30,779
um but mostly the main reason I'm a fan

11
00:00:33,950 --> 00:00:31,980
of this Theory the reason really talked

12
00:00:37,130 --> 00:00:33,960
about it is that there's two major

13
00:00:39,590 --> 00:00:37,140

problems that is currently in the field

14
00:00:40,850 --> 00:00:39,600
of astrobiology at least from my opinion

15
00:00:43,130 --> 00:00:40,860
um the first one is that we don't have a

16
00:00:44,630 --> 00:00:43,140
universal definition of life

17
00:00:45,830 --> 00:00:44,640
um again not sure if you guys agree with

18
00:00:47,330 --> 00:00:45,840
this or if that's really controversial

19
00:00:49,310 --> 00:00:47,340
no idea

20
00:00:53,209 --> 00:00:49,320
um but honestly we don't know what we're

21
00:00:55,369 --> 00:00:53,219
looking for out elsewhere and

22
00:00:57,650 --> 00:00:55,379
because of that kind of the biochemistry

23
00:00:59,630 --> 00:00:57,660
that we see or could potentially see we

24
00:01:02,750 --> 00:00:59,640
have no idea what that could look like

25
00:01:06,710 --> 00:01:02,760
comparison on Earth so kind of what we

26
00:01:07,789 --> 00:01:06,720
need to do is find a universal pattern

27
00:01:09,710 --> 00:01:07,799
of life

28
00:01:11,929 --> 00:01:09,720
first and then build our detection

29
00:01:13,370 --> 00:01:11,939
methods based on that

30
00:01:14,929 --> 00:01:13,380
um I think going out there seeing what

31
00:01:16,910 --> 00:01:14,939
we see is incredibly useful incredibly

32
00:01:18,710 --> 00:01:16,920
interesting but then you end up with

33
00:01:20,450 --> 00:01:18,720
like a phosphine problem of how do we

34
00:01:21,830 --> 00:01:20,460
explain what we see

35
00:01:23,870 --> 00:01:21,840
um if we determine what we're looking

36
00:01:26,149 --> 00:01:23,880
for first and then build a method based

37
00:01:28,730 --> 00:01:26,159
on that Universal Property we're able to

38
00:01:29,810 --> 00:01:28,740

be a little more stringent a little more

39
00:01:31,490 --> 00:01:29,820
um

40
00:01:32,749 --> 00:01:31,500
a little more robust about what we're

41
00:01:35,510 --> 00:01:32,759
actually finding

42
00:01:36,830 --> 00:01:35,520
so given that given that kind of

43
00:01:39,230 --> 00:01:36,840
solution

44
00:01:42,289 --> 00:01:39,240
um the basic idea of assembly theory is

45
00:01:43,850 --> 00:01:42,299
that life produces complex things

46
00:01:46,010 --> 00:01:43,860
um for example if we were to go to

47
00:01:47,630 --> 00:01:46,020
Enceladus and find an iPhone sitting on

48
00:01:48,289 --> 00:01:47,640
the bottom of the ocean

49
00:01:50,810 --> 00:01:48,299
um

50
00:01:52,490 --> 00:01:50,820
somehow unless Steve Jobs flew on a

51
00:01:54,889 --> 00:01:52,500
plane and put it there

52
00:01:57,950 --> 00:01:54,899
um we would say something Enceladus made

53
00:01:59,870 --> 00:01:57,960
a complex thing made it made an iPhone

54
00:02:01,069 --> 00:01:59,880
um that's weird that's interesting that

55
00:02:02,389 --> 00:02:01,079
would certainly be a really interesting

56
00:02:03,050 --> 00:02:02,399
battle signature

57
00:02:05,090 --> 00:02:03,060
um

58
00:02:07,609 --> 00:02:05,100
especially if we saw thousands of them

59
00:02:09,710 --> 00:02:07,619
if it was littered in iPhones there'd be

60
00:02:13,369 --> 00:02:09,720
some kind of process on Enceladus that

61
00:02:14,630 --> 00:02:13,379
would create and select for a complex

62
00:02:17,270 --> 00:02:14,640
object

63
00:02:19,369 --> 00:02:17,280

so this kind of idea is that life makes

64
00:02:21,949 --> 00:02:19,379
complex things it makes a lot of them

65
00:02:24,229 --> 00:02:21,959
and what assembly Theory does is

66
00:02:25,910 --> 00:02:24,239
specifically measure that give a measure

67
00:02:26,809 --> 00:02:25,920
of the complexity good measure of how

68
00:02:30,710 --> 00:02:26,819
much

69
00:02:35,150 --> 00:02:30,720
memory is part of the system that makes

70
00:02:37,190 --> 00:02:35,160
something really complex in a lot of it

71
00:02:39,589 --> 00:02:37,200
so kind of what this is what we're

72
00:02:41,809 --> 00:02:39,599
talking about is specifically it's a

73
00:02:43,729 --> 00:02:41,819
number of joining steps required to

74
00:02:45,710 --> 00:02:43,739
build an object from a base set of

75
00:02:47,270 --> 00:02:45,720
fragments that's a lot of words that's

76
00:02:49,610 --> 00:02:47,280
really confusing

77
00:02:50,809 --> 00:02:49,620
um so start with Legos and we'll go up

78
00:02:53,449 --> 00:02:50,819
from there

79
00:02:56,270 --> 00:02:53,459
um if you were to make this thing like

80
00:02:58,130 --> 00:02:56,280
this big Square rectangle whatever thing

81
00:03:00,530 --> 00:02:58,140
you would start with this green and

82
00:03:02,089 --> 00:03:00,540
green and red block and you would start

83
00:03:03,949 --> 00:03:02,099
joining them together in the most

84
00:03:05,990 --> 00:03:03,959
optimal way possible essentially the way

85
00:03:07,790 --> 00:03:06,000
that minimizes the joining steps to make

86
00:03:09,470 --> 00:03:07,800
that thing at the end

87
00:03:12,470 --> 00:03:09,480
um specifically there's five of them

88
00:03:15,890 --> 00:03:12,480

here you notice that you reuse this

89
00:03:18,290 --> 00:03:15,900
double a couple times and you reuse the

90
00:03:20,089 --> 00:03:18,300
square once as well so you're able to

91
00:03:22,130 --> 00:03:20,099
reuse the thing you already make there's

92
00:03:24,649 --> 00:03:22,140
five joining steps the ma of this

93
00:03:26,149 --> 00:03:24,659
particular Lego block will be five

94
00:03:27,589 --> 00:03:26,159
um and you can do this for lots of

95
00:03:29,869 --> 00:03:27,599
different things you can do this for

96
00:03:31,430 --> 00:03:29,879
Strings like Gage was talking about

97
00:03:34,070 --> 00:03:31,440
um yesterday where if you want to make

98
00:03:35,330 --> 00:03:34,080
Abracadabra you're going to have a

99
00:03:38,990 --> 00:03:35,340
number of steps particularly seven

100
00:03:41,149 --> 00:03:39,000
you're going to reuse Abra along the way

101
00:03:44,750 --> 00:03:41,159
and you can do this for chemicals which

102
00:03:46,130 --> 00:03:44,760
is kind of more astrological relevance

103
00:03:49,369 --> 00:03:46,140
um you're able to start with your base

104
00:03:50,809 --> 00:03:49,379
fragments in this case it's a element a

105
00:03:52,570 --> 00:03:50,819
bond and a different elements which is

106
00:03:55,070 --> 00:03:52,580
defined by the thing you're looking for

107
00:03:56,030 --> 00:03:55,080
and you're able to build up the steps

108
00:03:57,710 --> 00:03:56,040
along the way

109
00:03:59,330 --> 00:03:57,720
I think one thing I want to emphasize is

110
00:04:01,490 --> 00:03:59,340
that these steps don't necessarily have

111
00:04:04,550 --> 00:04:01,500
any physical meaning like this windmill

112
00:04:06,589 --> 00:04:04,560
guy isn't maybe maybe you can't make

113
00:04:08,630 --> 00:04:06,599

this in a lab who knows

114
00:04:10,970 --> 00:04:08,640
um and it doesn't particularly matter

115
00:04:12,770 --> 00:04:10,980
for this metric um this is not what I'm

116
00:04:16,250 --> 00:04:12,780
saying this is a physical property it's

117
00:04:18,770 --> 00:04:16,260
a theoretical way of reusing the

118
00:04:21,170 --> 00:04:18,780
symmetry of the object that you're

119
00:04:23,030 --> 00:04:21,180
ending up with so

120
00:04:23,629 --> 00:04:23,040
kind of keep that in mind

121
00:04:25,490 --> 00:04:23,639
um

122
00:04:28,310 --> 00:04:25,500
when you're doing this this is all from

123
00:04:30,469 --> 00:04:28,320
paper in 2021 from Stuart Marshall and

124
00:04:33,890 --> 00:04:30,479
Cole Mathis both at the University of

125
00:04:35,150 --> 00:04:33,900
Glasgow and we're able to do ma over a

126
00:04:37,249 --> 00:04:35,160
ton of things

127
00:04:39,350 --> 00:04:37,259
um and unsurprisingly correlates with

128
00:04:41,450 --> 00:04:39,360
molecular weights because as things get

129
00:04:43,909 --> 00:04:41,460
bigger you get more steps to make them

130
00:04:45,890 --> 00:04:43,919
but it's not a one-to-one ratio there's

131
00:04:47,150 --> 00:04:45,900
a lot of things kind of here that are

132
00:04:49,310 --> 00:04:47,160
high molecular weight below assembly

133
00:04:51,950 --> 00:04:49,320
Theory because they have high symmetry

134
00:04:54,530 --> 00:04:51,960
um so they're not necessarily as complex

135
00:04:57,409 --> 00:04:54,540
they require less steps to make

136
00:04:59,629 --> 00:04:57,419
um just again keep that in mind

137
00:05:00,950 --> 00:04:59,639
and the reason why we're so excited

138
00:05:03,650 --> 00:05:00,960

about this the reason why we want to use

139
00:05:06,770 --> 00:05:03,660
this for an astrobiological signature is

140
00:05:08,510 --> 00:05:06,780
that when you look at these compounds in

141
00:05:10,610 --> 00:05:08,520
a mass spec

142
00:05:13,850 --> 00:05:10,620
um you're able to see a lot of these

143
00:05:16,189 --> 00:05:13,860
different Peaks a mass spec takes a

144
00:05:17,450 --> 00:05:16,199
compound fragments it based on

145
00:05:19,249 --> 00:05:17,460
ionization a lot of different things

146
00:05:21,530 --> 00:05:19,259
there's lots of ways to do it this one

147
00:05:23,870 --> 00:05:21,540
particularly was an orbitrap so if

148
00:05:26,450 --> 00:05:23,880
fragments things twice and you end up

149
00:05:28,249 --> 00:05:26,460
with a number of different Peaks now

150
00:05:30,170 --> 00:05:28,259
kind of notice there's a correlation the

151
00:05:31,850 --> 00:05:30,180
lower things the lower ma things the

152
00:05:34,909 --> 00:05:31,860
less complex things don't have as many

153
00:05:36,290 --> 00:05:34,919
Peaks as the higher complex things

154
00:05:37,930 --> 00:05:36,300
um again kind of make sense bigger

155
00:05:39,830 --> 00:05:37,940
things are more complex

156
00:05:41,090 --> 00:05:39,840
there's a really strong correlation

157
00:05:43,430 --> 00:05:41,100
between the two

158
00:05:46,249 --> 00:05:43,440
which is really really exciting again

159
00:05:47,629 --> 00:05:46,259
it's not intuitively obvious that you

160
00:05:49,610 --> 00:05:47,639
have a theoretical measure that has no

161
00:05:52,670 --> 00:05:49,620
correlation physical reality actually

162
00:05:56,150 --> 00:05:52,680
corresponds to a mass spec signature

163
00:05:57,469 --> 00:05:56,160

um so when we saw this we kind of ran

164
00:05:59,029 --> 00:05:57,479
with this and we're saying hey we can

165
00:06:01,490 --> 00:05:59,039
put a mask back in space we've done it

166
00:06:03,950 --> 00:06:01,500
before we've done it since the 1970s so

167
00:06:05,270 --> 00:06:03,960
why don't we look at what kind of mass

168
00:06:07,370 --> 00:06:05,280
specs are needed

169
00:06:09,650 --> 00:06:07,380
think about ma as a specific bio

170
00:06:12,170 --> 00:06:09,660
signature and then

171
00:06:13,670 --> 00:06:12,180
um use Mass Spec to go out and find it

172
00:06:15,770 --> 00:06:13,680
and

173
00:06:18,469 --> 00:06:15,780
the thing we're looking for specifically

174
00:06:21,050 --> 00:06:18,479
again from this 2021 paper is that all

175
00:06:22,550 --> 00:06:21,060
of biochemistry has an MA greater than

176
00:06:24,770 --> 00:06:22,560
15.

177
00:06:25,490 --> 00:06:24,780
um anything below 15 at least we see on

178
00:06:27,770 --> 00:06:25,500
Earth

179
00:06:30,050 --> 00:06:27,780
is a mixture of biotic abiotic things

180
00:06:31,189 --> 00:06:30,060
they're found throughout the geosphere

181
00:06:33,409 --> 00:06:31,199
and everything

182
00:06:35,450 --> 00:06:33,419
but above 15 is only things made by

183
00:06:38,029 --> 00:06:35,460
things that we know are alive

184
00:06:39,230 --> 00:06:38,039
um like whiskey a few other things they

185
00:06:41,270 --> 00:06:39,240
kind of had some fun at Glasgow

186
00:06:44,390 --> 00:06:41,280
measuring a bunch of stuff but

187
00:06:46,189 --> 00:06:44,400
essentially anything above 15 what we

188
00:06:48,230 --> 00:06:46,199

say is hey this

189
00:06:49,909 --> 00:06:48,240
from what we know about life on Earth

190
00:06:53,510 --> 00:06:49,919
let's extrapolate it to be a universal

191
00:06:55,490 --> 00:06:53,520
property that's something that's complex

192
00:06:58,249 --> 00:06:55,500
um for the rest of the talk I think just

193
00:06:59,930 --> 00:06:58,259
15 it might be a little fuzzy I also

194
00:07:02,330 --> 00:06:59,940
measured 20.

195
00:07:04,010 --> 00:07:02,340
um I consider 20 as about as a specific

196
00:07:06,110 --> 00:07:04,020
bio signature so you'll see two numbers

197
00:07:07,249 --> 00:07:06,120
later on um that's where the 20 comes

198
00:07:08,450 --> 00:07:07,259
from is just give it a little wiggle

199
00:07:10,490 --> 00:07:08,460
room

200
00:07:11,870 --> 00:07:10,500
so now the issue with that if we're

201
00:07:13,550 --> 00:07:11,880
going to send a mass back into space it

202
00:07:14,930 --> 00:07:13,560
needs to be high resolution

203
00:07:16,909 --> 00:07:14,940
um you can't have something like this or

204
00:07:19,010 --> 00:07:16,919
you only have a couple Peaks

205
00:07:20,089 --> 00:07:19,020
you need something that has the right

206
00:07:22,370 --> 00:07:20,099
number of peaks in order to find

207
00:07:23,689 --> 00:07:22,380
something that's high and complex

208
00:07:25,129 --> 00:07:23,699
um if you find something send something

209
00:07:26,570 --> 00:07:25,139
that's low resolution it's not going to

210
00:07:28,249 --> 00:07:26,580
be good enough

211
00:07:31,430 --> 00:07:28,259
um so

212
00:07:33,050 --> 00:07:31,440
and when we look at stuff today you'll

213
00:07:34,790 --> 00:07:33,060

see this chart a couple times so we want

214
00:07:35,870 --> 00:07:34,800
to explain it real fast this is

215
00:07:41,450 --> 00:07:35,880
essentially

216
00:07:43,430 --> 00:07:41,460
of how big the molecule is and this is

217
00:07:47,029 --> 00:07:43,440
the mass resolution of the particular

218
00:07:49,550 --> 00:07:47,039
object times 10 000.

219
00:07:51,350 --> 00:07:49,560
um all of these ones off here are off

220
00:07:53,689 --> 00:07:51,360
the chart like they just have really

221
00:07:55,790 --> 00:07:53,699
have Big M over Z ratios and these two

222
00:07:57,469 --> 00:07:55,800
would have a really high resolution

223
00:08:00,469 --> 00:07:57,479
um so this is good

224
00:08:02,089 --> 00:08:00,479
now these things take up rooms

225
00:08:04,070 --> 00:08:02,099
um like an orbit traps not that big but

226
00:08:06,170 --> 00:08:04,080
you need a bunch of vacuum stuff like

227
00:08:07,909 --> 00:08:06,180
it's about as big as this Podium roughly

228
00:08:09,230 --> 00:08:07,919
if you want a really good one

229
00:08:10,730 --> 00:08:09,240
um you can't just launch that on a

230
00:08:13,730 --> 00:08:10,740
spaceship NASA gets really mad when you

231
00:08:16,249 --> 00:08:13,740
launch something that big so how do we

232
00:08:18,290 --> 00:08:16,259
like the stuff we do today it's roughly

233
00:08:20,330 --> 00:08:18,300
down here um Ricky ravalo's group in

234
00:08:24,050 --> 00:08:20,340
University Maryland College Park

235
00:08:27,409 --> 00:08:24,060
um has this mini orbitrap that's decent

236
00:08:29,390 --> 00:08:27,419
but still like not still on that scale

237
00:08:31,490 --> 00:08:29,400
um so how could how good can we get how

238
00:08:34,969 --> 00:08:31,500

is that good enough how much do we need

239
00:08:36,110 --> 00:08:34,979
in order to determine definitively that

240
00:08:38,570 --> 00:08:36,120
you have a mass spec signal stick

241
00:08:40,430 --> 00:08:38,580
signature

242
00:08:43,130 --> 00:08:40,440
um so what we did we did some chemical

243
00:08:45,050 --> 00:08:43,140
enumeration we built some graphs

244
00:08:47,150 --> 00:08:45,060
um specifically built some formulas and

245
00:08:49,490 --> 00:08:47,160
said hey given a specific number of

246
00:08:51,710 --> 00:08:49,500
chemicals this case Zero to six carbons

247
00:08:53,750 --> 00:08:51,720
any number of hydrogens the nitrogen

248
00:08:55,370 --> 00:08:53,760
Oxford phosphorus sulfur how many

249
00:08:56,329 --> 00:08:55,380
different formulas do we get how big is

250
00:08:58,790 --> 00:08:56,339
the chemical space that could

251
00:09:00,470 --> 00:08:58,800
potentially be out there answer is

252
00:09:02,509 --> 00:09:00,480
pretty big you've got lots of different

253
00:09:05,090 --> 00:09:02,519
formulas unsurprising

254
00:09:07,670 --> 00:09:05,100
um they can be modeled with a normal

255
00:09:10,070 --> 00:09:07,680
normal curve so I can do this for any

256
00:09:13,070 --> 00:09:10,080
number of upper limit and any number

257
00:09:14,750 --> 00:09:13,080
like up to 10 atoms up to five atoms if

258
00:09:16,610 --> 00:09:14,760
I want to measure more I can do a

259
00:09:17,570 --> 00:09:16,620
different normal curve

260
00:09:19,430 --> 00:09:17,580
um

261
00:09:23,090 --> 00:09:19,440
at this next slide might trigger people

262
00:09:25,190 --> 00:09:23,100
I apologize I did random chemistry based

263
00:09:28,130 --> 00:09:25,200

on that because again we don't know what

264
00:09:29,870 --> 00:09:28,140
that is going to look like so I built

265
00:09:31,370 --> 00:09:29,880
random I built random structures from

266
00:09:33,610 --> 00:09:31,380
random formulas essentially building

267
00:09:35,870 --> 00:09:33,620
putting random bonds together

268
00:09:38,870 --> 00:09:35,880
this might not exist this probably

269
00:09:39,889 --> 00:09:38,880
doesn't exist anywhere but um I kind of

270
00:09:41,090 --> 00:09:39,899
hope it doesn't because that would be

271
00:09:44,570 --> 00:09:41,100
weird

272
00:09:46,550 --> 00:09:44,580
um but what we what we did is we built

273
00:09:48,230 --> 00:09:46,560
it we put it through Rd kits 3D and

274
00:09:49,370 --> 00:09:48,240
better software so we know this is at

275
00:09:50,810 --> 00:09:49,380
least physically possible it doesn't

276
00:09:52,190 --> 00:09:50,820
break the rules of physics the

277
00:09:55,009 --> 00:09:52,200
thermodynamics are really weird who

278
00:09:56,150 --> 00:09:55,019
knows how long this lasts but again our

279
00:09:57,110 --> 00:09:56,160
assumptions we don't know what this

280
00:09:58,190 --> 00:09:57,120
looks like

281
00:09:59,690 --> 00:09:58,200
um and this actually is a good

282
00:10:00,889 --> 00:09:59,700
assumption you'll see a few graphs later

283
00:10:02,690 --> 00:10:00,899
that we're not actually that far off

284
00:10:05,210 --> 00:10:02,700
from reality but

285
00:10:07,970 --> 00:10:05,220
um just bear with me for now so I did

286
00:10:09,350 --> 00:10:07,980
this for 10 000 different structures

287
00:10:12,050 --> 00:10:09,360
um made a bunch of made a bunch of

288
00:10:14,329 --> 00:10:12,060

random chemicals and found the m a of

289
00:10:15,650 --> 00:10:14,339
them so if molecular weights we have

290
00:10:17,269 --> 00:10:15,660
assembly index

291
00:10:18,650 --> 00:10:17,279
and you see that most of them started to

292
00:10:21,350 --> 00:10:18,660
get high Ma

293
00:10:24,230 --> 00:10:21,360
and you get a likelihood very quickly of

294
00:10:26,870 --> 00:10:24,240
well what is the likelihood of finding a

295
00:10:28,250 --> 00:10:26,880
high ma object at a particular molecular

296
00:10:29,509 --> 00:10:28,260
weight

297
00:10:31,310 --> 00:10:29,519
so

298
00:10:33,350 --> 00:10:31,320
we have number we have the size of

299
00:10:34,670 --> 00:10:33,360
chemical space we have molecular weights

300
00:10:37,490 --> 00:10:34,680
and we know how often those things are

301
00:10:39,829 --> 00:10:37,500
high m a we're essentially able to then

302
00:10:41,750 --> 00:10:39,839
put that on a Precision curve and say

303
00:10:43,670 --> 00:10:41,760
what's the Precision which can be

304
00:10:44,650 --> 00:10:43,680
translated into resolution of the

305
00:10:46,790 --> 00:10:44,660
particular

306
00:10:48,889 --> 00:10:46,800
number of

307
00:10:50,870 --> 00:10:48,899
chemical species that have a high ma in

308
00:10:54,230 --> 00:10:50,880
that case or that particular M over Z

309
00:10:55,850 --> 00:10:54,240
ratio we take the integral of that

310
00:10:59,329 --> 00:10:55,860
particular line our goal is to find 10

311
00:11:00,410 --> 00:10:59,339
or fewer just to put a number on it and

312
00:11:01,850 --> 00:11:00,420
then we end up with something looks like

313
00:11:05,090 --> 00:11:01,860

this

314
00:11:08,590 --> 00:11:05,100
um so our in an ideal case

315
00:11:11,750 --> 00:11:08,600
what we have is something about 552 000

316
00:11:13,009 --> 00:11:11,760
M over Delta M Mass resolution Which is

317
00:11:14,930 --> 00:11:13,019
far fewer than what we have in

318
00:11:17,509 --> 00:11:14,940
commercial orbitraps those are on the

319
00:11:19,130 --> 00:11:17,519
orders like Millions 10 Millions

320
00:11:21,050 --> 00:11:19,140
um but it's not what we've sent to space

321
00:11:22,910 --> 00:11:21,060
it's about four times better than what

322
00:11:23,569 --> 00:11:22,920
we've sent the space so far

323
00:11:25,550 --> 00:11:23,579
um

324
00:11:27,230 --> 00:11:25,560
those ones we send so those ones set

325
00:11:29,449 --> 00:11:27,240
into space are decent like in this

326
00:11:31,850 --> 00:11:29,459
little curve here they're good they're

327
00:11:34,190 --> 00:11:31,860
able to determine highma molecules but

328
00:11:35,810 --> 00:11:34,200
we still want to get as high up on this

329
00:11:36,889 --> 00:11:35,820
graph as possible

330
00:11:38,750 --> 00:11:36,899
um so it's more of an engineering

331
00:11:40,250 --> 00:11:38,760
challenge this is more saying hey

332
00:11:42,230 --> 00:11:40,260
Engineers if you can go out and build

333
00:11:43,610 --> 00:11:42,240
something like this give an unknown

334
00:11:45,230 --> 00:11:43,620
chemical space we're confident that

335
00:11:47,389 --> 00:11:45,240
you'll be able to detect a high ma

336
00:11:50,630 --> 00:11:47,399
molecule if it's out there

337
00:11:52,970 --> 00:11:50,640
um and quickly just to finish up

338
00:11:56,030 --> 00:11:52,980

um I know the chemicals were really bad

339
00:11:58,790 --> 00:11:56,040
and really not Earth-like

340
00:12:01,250 --> 00:11:58,800
um so we determined our spacecraft our

341
00:12:04,310 --> 00:12:01,260
sermon our resolution based on existing

342
00:12:06,290 --> 00:12:04,320
chemistry we used keg keto Encyclopedia

343
00:12:08,930 --> 00:12:06,300
of genes of genomes I'm mostly saying

344
00:12:10,449 --> 00:12:08,940
how good is our prediction based on

345
00:12:13,370 --> 00:12:10,459
those random chemicals

346
00:12:15,530 --> 00:12:13,380
this is MOMA this is the one that's

347
00:12:17,449 --> 00:12:15,540
launching soon to Mars

348
00:12:18,650 --> 00:12:17,459
um it's not that great at distinguishing

349
00:12:21,230 --> 00:12:18,660
formulas

350
00:12:22,730 --> 00:12:21,240
um there's a lot of overlaps but if you

351
00:12:24,949 --> 00:12:22,740
look at something like corals or our

352
00:12:26,269 --> 00:12:24,959
recommended one you're not you're really

353
00:12:28,850 --> 00:12:26,279
not that bad you're getting maximum of

354
00:12:29,630 --> 00:12:28,860
five so it's pretty good

355
00:12:34,370 --> 00:12:29,640
um

356
00:12:35,930 --> 00:12:34,380
and even better when we start saying hey

357
00:12:37,370 --> 00:12:35,940
does random chemistry correspond with

358
00:12:39,590 --> 00:12:37,380
reality

359
00:12:41,630 --> 00:12:39,600
um it does thankfully

360
00:12:44,629 --> 00:12:41,640
um kind of as a test we took 200

361
00:12:46,069 --> 00:12:44,639
formulas from that formal enumeration

362
00:12:47,449 --> 00:12:46,079
um got a hundred different isomers of

363
00:12:49,670 --> 00:12:47,459

those formulas but from pubchem so

364
00:12:51,170 --> 00:12:49,680
existing chemistry GDB which from John

365
00:12:53,150 --> 00:12:51,180
Louise Raymond's group and burn which is

366
00:12:55,009 --> 00:12:53,160
a generated database of potential

367
00:12:58,069 --> 00:12:55,019
chemistry here on Earth and then random

368
00:12:59,690 --> 00:12:58,079
structure generation like we did and if

369
00:13:02,329 --> 00:12:59,700
they were separate we'd say we have a

370
00:13:03,590 --> 00:13:02,339
problem but all of these kind of the m a

371
00:13:07,190 --> 00:13:03,600
space of all those chemicals is about

372
00:13:09,410 --> 00:13:07,200
the same so we actually end up roughly a

373
00:13:11,269 --> 00:13:09,420
recommendation on random chemistry seems

374
00:13:12,590 --> 00:13:11,279
to be sufficient based on life we see

375
00:13:13,310 --> 00:13:12,600
today

376
00:13:16,009 --> 00:13:13,320
um

377
00:13:17,690 --> 00:13:16,019
so kind of a recommendation if we take

378
00:13:18,949 --> 00:13:17,700
this metal micro assembly Theory as a

379
00:13:21,530 --> 00:13:18,959
biosignature

380
00:13:24,350 --> 00:13:21,540
we have a mass range of mass specs to

381
00:13:26,389 --> 00:13:24,360
shoot for we have a resolution and it's

382
00:13:28,430 --> 00:13:26,399
a worst case scenario and what we're

383
00:13:31,430 --> 00:13:28,440
showing is that this roughly represents

384
00:13:33,530 --> 00:13:31,440
m a of chemical space

385
00:13:35,389 --> 00:13:33,540
um there's lots of people to thank

386
00:13:37,069 --> 00:13:35,399
um mostly the ASU group that is mostly

387
00:13:45,110 --> 00:13:37,079
sitting at the front table so thank you

388
00:13:45,120 --> 00:13:49,730

thank you John any questions

389
00:13:49,740 --> 00:13:54,710
felt all freaked out by the chemistry

390
00:14:01,910 --> 00:13:58,129
hi great talk

391
00:14:05,750 --> 00:14:01,920
um I'm wondering why is the random set

392
00:14:07,069 --> 00:14:05,760
smaller on the area that it takes than a

393
00:14:08,269 --> 00:14:07,079
pumpkin

394
00:14:10,970 --> 00:14:08,279
yeah

395
00:14:14,090 --> 00:14:10,980
um that is a that's a great question

396
00:14:17,389 --> 00:14:14,100
um I think my answer is that it's

397
00:14:20,569 --> 00:14:17,399
possibly a sampling issue of random

398
00:14:22,850 --> 00:14:20,579
space is probably bigger but the density

399
00:14:24,949 --> 00:14:22,860
of different compounds that it could

400
00:14:27,230 --> 00:14:24,959
sample in random chemistry is just so

401
00:14:29,329 --> 00:14:27,240
high on that little part right there

402
00:14:31,129 --> 00:14:29,339
like I'm just not sampling enough to get

403
00:14:34,009 --> 00:14:31,139
a distribution

404
00:14:36,290 --> 00:14:34,019
um or or or I am and I'm not

405
00:14:37,610 --> 00:14:36,300
um getting the edges as much

406
00:14:39,230 --> 00:14:37,620
um I think it's interesting question of

407
00:14:40,910 --> 00:14:39,240
how life can be a little more spread out

408
00:14:44,150 --> 00:14:40,920
I think there's an interesting function

409
00:14:46,490 --> 00:14:44,160
a functionality argument going on um I

410
00:14:49,129 --> 00:14:46,500
think yeah random chemistry I think it's

411
00:14:50,389 --> 00:14:49,139
so dense in the middle that I'm just not

412
00:14:51,110 --> 00:14:50,399
exploring the edges as well as I could

413
00:14:55,670 --> 00:14:51,120

be

414
00:15:02,210 --> 00:14:59,389
hi uh this is very very interesting so

415
00:15:04,129 --> 00:15:02,220
um I guess would you mind uh maybe going

416
00:15:05,150 --> 00:15:04,139
over the

417
00:15:08,090 --> 00:15:05,160
um

418
00:15:10,250 --> 00:15:08,100
uh basically what led you to your

419
00:15:14,269 --> 00:15:10,260
resolution and

420
00:15:16,310 --> 00:15:14,279
um and uh Max M over Z calculations a

421
00:15:20,509 --> 00:15:16,320
little bit uh

422
00:15:22,009 --> 00:15:20,519
I guess more in detail uh about how that

423
00:15:25,970 --> 00:15:22,019
connects to

424
00:15:30,230 --> 00:15:25,980
um msms uh measurements is is this

425
00:15:31,790 --> 00:15:30,240
um just with M over Z or okay yeah so um

426
00:15:34,550 --> 00:15:31,800
yeah it's a great question so I'm not

427
00:15:36,050 --> 00:15:34,560
assuming any fragmentation here

428
00:15:37,310 --> 00:15:36,060
um mostly because we don't know exactly

429
00:15:40,009 --> 00:15:37,320
what we're going to send or if it's an

430
00:15:41,769 --> 00:15:40,019
ms1 or MS2 machine

431
00:15:44,930 --> 00:15:41,779
um so I'm just assuming that there's a

432
00:15:48,110 --> 00:15:44,940
there's a particular structure it's

433
00:15:50,269 --> 00:15:48,120
ionized so I knock off a hydrogen and

434
00:15:52,430 --> 00:15:50,279
then that's a single Peak that you get

435
00:15:55,250 --> 00:15:52,440
what's the resolution to distinguish

436
00:15:57,710 --> 00:15:55,260
those Peaks um which one thing is worst

437
00:15:59,990 --> 00:15:57,720
case add fragmentation and add like a

438
00:16:02,269 --> 00:16:00,000

really add a decent orbitrap and this

439
00:16:03,350 --> 00:16:02,279
probably becomes a lot better but it's

440
00:16:04,730 --> 00:16:03,360
hard to predict exactly what that

441
00:16:06,470 --> 00:16:04,740
fragmentation is

442
00:16:07,970 --> 00:16:06,480
um there's a team in Glasgow

443
00:16:09,470 --> 00:16:07,980
um led by Emma kyrick that's like trying

444
00:16:10,069 --> 00:16:09,480
to figure that out right now

445
00:16:11,990 --> 00:16:10,079
um

446
00:16:13,310 --> 00:16:12,000
as you can imagine it's a difficult like

447
00:16:14,509 --> 00:16:13,320
Mass specs are weird

448
00:16:15,650 --> 00:16:14,519
um it's a difficult problem to predict

449
00:16:19,069 --> 00:16:15,660
and extrapolate

450
00:16:20,509 --> 00:16:19,079
yeah because I guess I'm wondering you

451
00:16:22,490 --> 00:16:20,519
know obviously

452
00:16:24,590 --> 00:16:22,500
um ion neutral Mass spectrometer and

453
00:16:28,550 --> 00:16:24,600
Cassini did not have nearly this

454
00:16:30,410 --> 00:16:28,560
resolution uh but if the fragmentation

455
00:16:32,810 --> 00:16:30,420
that you can assume happened when those

456
00:16:34,670 --> 00:16:32,820
ice grains collided with it

457
00:16:38,269 --> 00:16:34,680
um could be assumed to be an MS2 like

458
00:16:40,129 --> 00:16:38,279
event then and if that you know if MS2

459
00:16:42,050 --> 00:16:40,139
makes it that much better then maybe you

460
00:16:45,230 --> 00:16:42,060
could look at it from this perspective

461
00:16:47,210 --> 00:16:45,240
yeah no I didn't I think if he hadn't I

462
00:16:49,129 --> 00:16:47,220
think I would love to see a number of

463
00:16:49,790 --> 00:16:49,139

how much that correlates

464
00:16:51,769 --> 00:16:49,800
um

465
00:16:53,990 --> 00:16:51,779
yeah I think that's the I think that's

466
00:16:55,430 --> 00:16:54,000
probably the next step on where to go

467
00:16:58,430 --> 00:16:55,440
with this yeah

468
00:17:02,990 --> 00:17:01,069
okay uh we could probably take one more

469
00:17:04,970 --> 00:17:03,000
question and you're the lucky man right

470
00:17:07,010 --> 00:17:04,980
next to me

471
00:17:09,289 --> 00:17:07,020
it's a very interesting talk uh you

472
00:17:11,750 --> 00:17:09,299
talked about the lower limit on Ma is

473
00:17:14,030 --> 00:17:11,760
there any upper limit on Ma

474
00:17:16,309 --> 00:17:14,040
so like under up a little bit of how far

475
00:17:17,750 --> 00:17:16,319
biochemistry can go yeah

476
00:17:19,870 --> 00:17:17,760
um it's a great question

477
00:17:25,549 --> 00:17:19,880
so

478
00:17:27,590 --> 00:17:25,559
small small molecules we're not using

479
00:17:29,690 --> 00:17:27,600
this in peptides or anything mostly

480
00:17:31,549 --> 00:17:29,700
because the base fragments that we're

481
00:17:33,350 --> 00:17:31,559
talking about in this case are elements

482
00:17:36,169 --> 00:17:33,360
to bonds and we talked like something

483
00:17:38,810 --> 00:17:36,179
like DNA molecule then Things become so

484
00:17:41,210 --> 00:17:38,820
massive so massive that since it's an NP

485
00:17:43,010 --> 00:17:41,220
complex NP complete problem it that'll

486
00:17:46,070 --> 00:17:43,020
take forever to compute

487
00:17:47,990 --> 00:17:46,080
um so I think like it quickly depends on

488
00:17:49,430 --> 00:17:48,000

your definition of a base fragment and

489
00:17:51,289 --> 00:17:49,440
what you want your what you want those

490
00:17:53,750 --> 00:17:51,299
joining steps to be

491
00:17:57,110 --> 00:17:53,760
um it's essentially DNA I imagine would

492
00:18:00,110 --> 00:17:57,120
be in tens of millions if not higher if

493
00:18:02,029 --> 00:18:00,120
we're using this particular definition

494
00:18:03,950 --> 00:18:02,039
um freezing amino acids or base pairs

495
00:18:05,810 --> 00:18:03,960
Things become a little different

496
00:18:07,070 --> 00:18:05,820
um I have some interesting results in

497
00:18:09,049 --> 00:18:07,080
like patent chemistry that I'm happy to

498
00:18:10,250 --> 00:18:09,059
share afterwards to show like we have a

499
00:18:12,169 --> 00:18:10,260
little bit of upper limit of like what

500
00:18:14,330 --> 00:18:12,179
chemistry can look like but um

501
00:18:15,710 --> 00:18:14,340
I mean that's more of a computational

502
00:18:17,680 --> 00:18:15,720
limit than anything