Microbial Enhanced Coalbed Systems (MECS)

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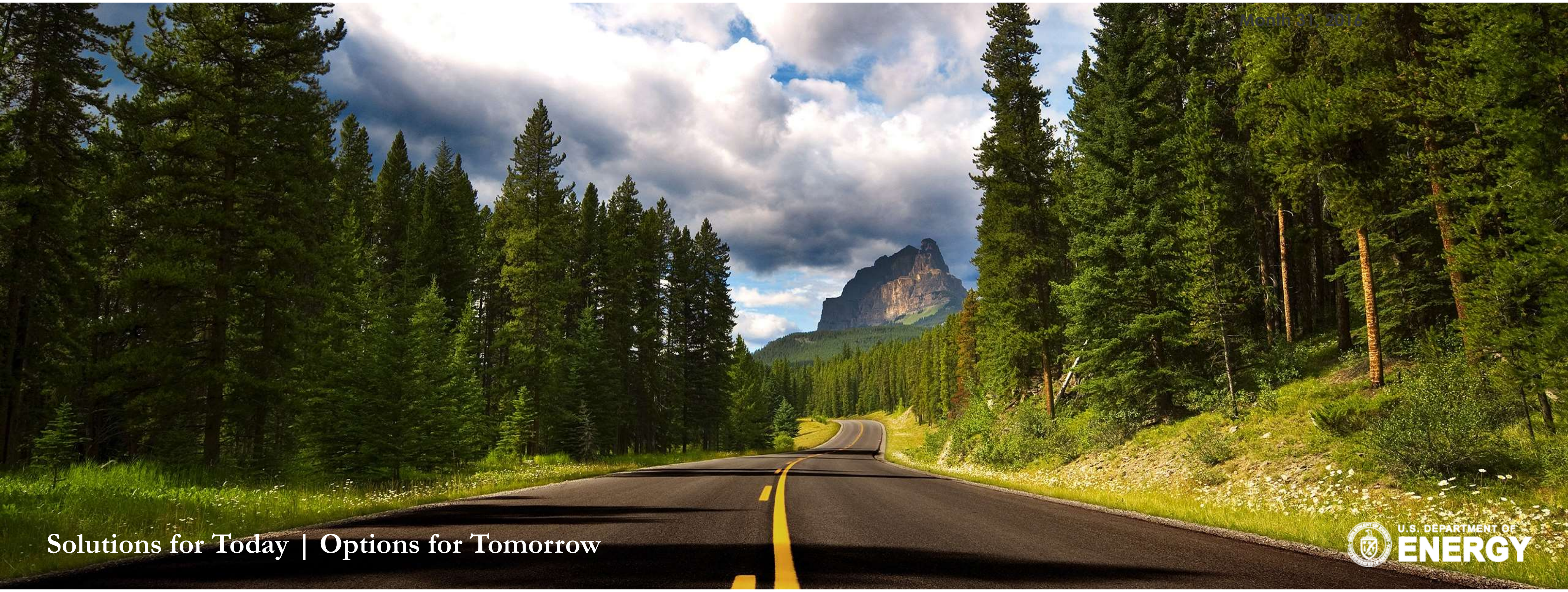
03/20/2017



Month 31, 2016

Solutions for Today | Options for Tomorrow

MECS Team

NATIONAL ENERGY TECHNOLOGY LABORATORY

AECOM

OAK RIDGE INSTITUTE FOR SCIENCE AND EDUCATION
Managed by ORAU for DOE

MECS and ARS

Objective: Move away from “bigger is better” to a decentralized locality based processes that utilizes local feed stocks to create needed products in the most economic method

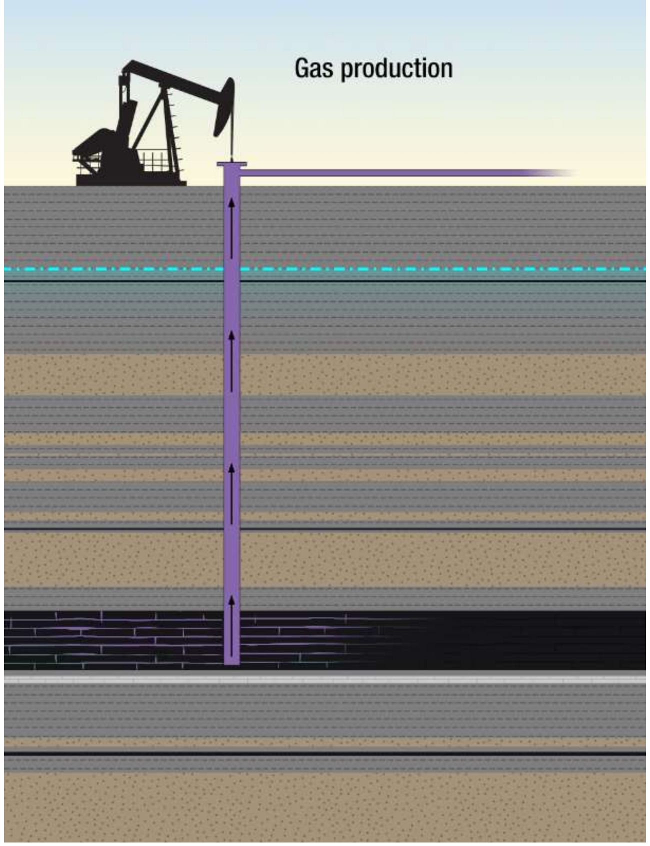
Local feedstock

Coal

Reaction Systems

Needed product

CH_4



Goal: Increase coal-to-methane production utilizing the native microbial consortia

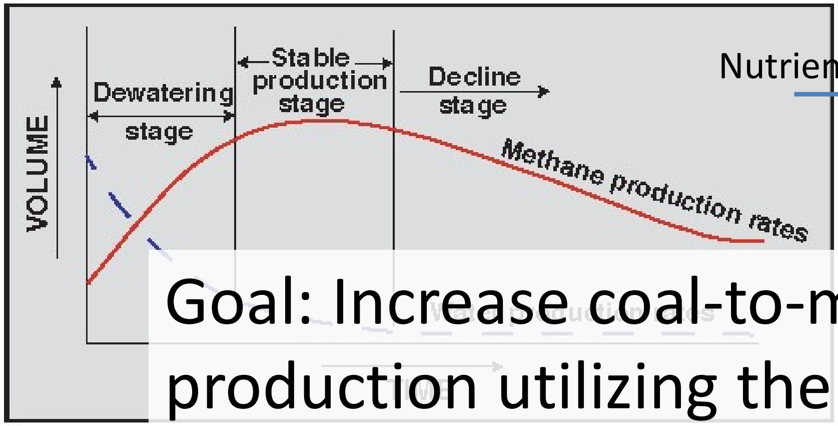
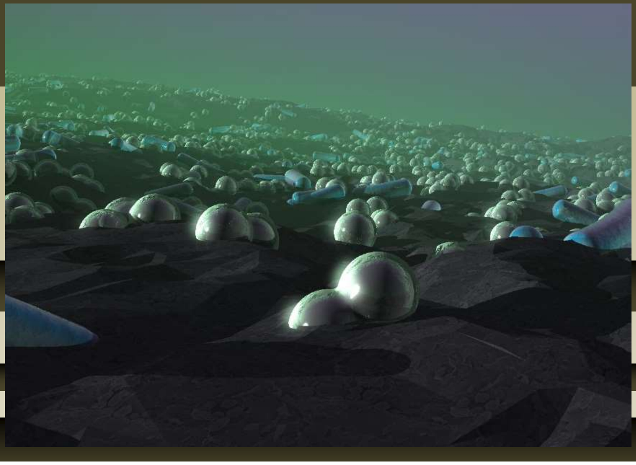


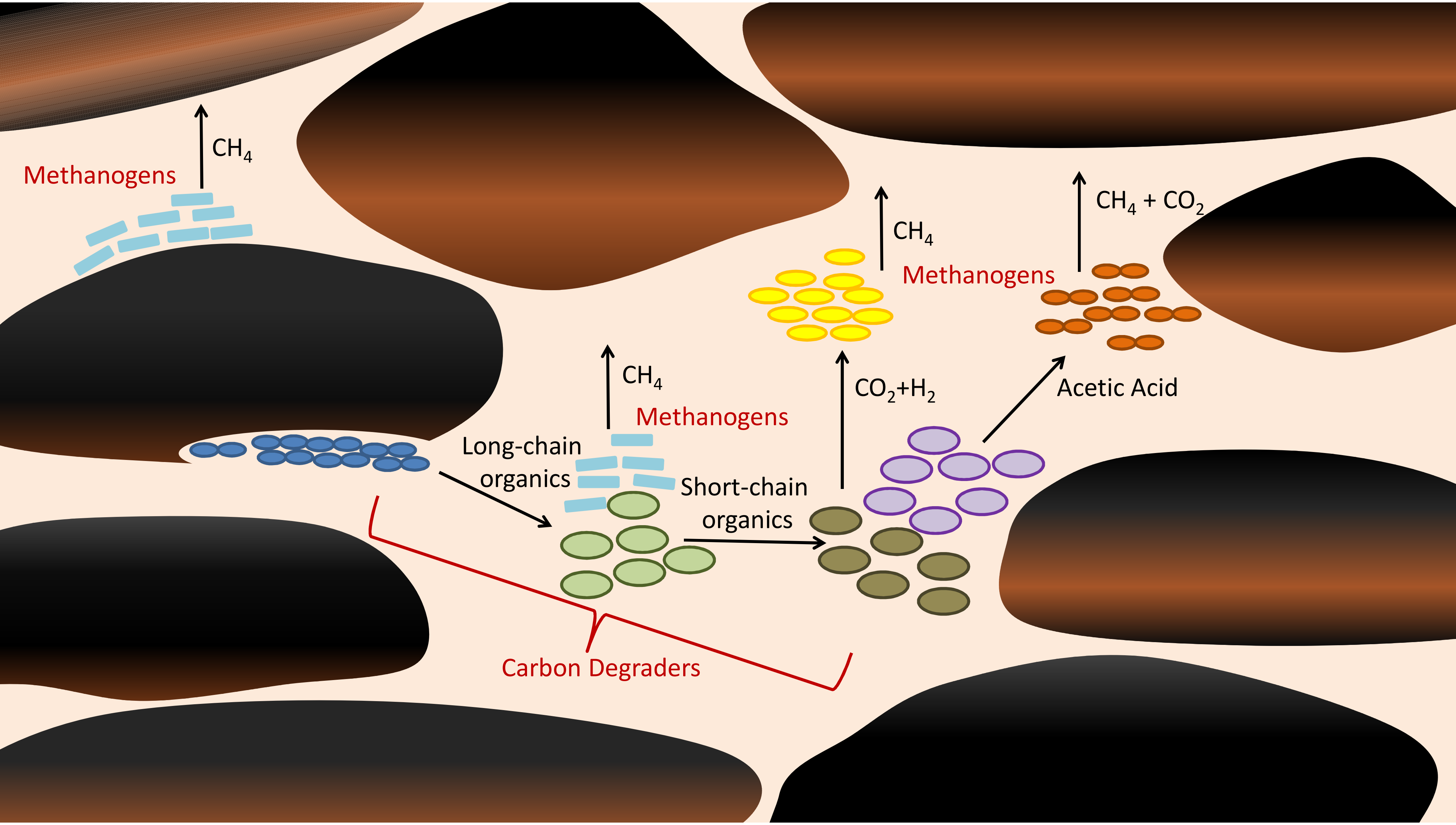
Figure 2. Typical production curves for a coal-bed methane well showing relative volumes of methane and water through time. Modified from Kuuskraa and Brandenberg (1989).

Nutrient Solution

CH_4
Produced Fluids

Coalbed




CH$_4$
Methanogens
CH$_4$
Methanogens
CH$_4$
Methanogens
CH$_4$ + CO$_2$
CO$_2$+H$_2$
Acetic Acid
Long-chain organics
Short-chain organics
Carbon Degraders

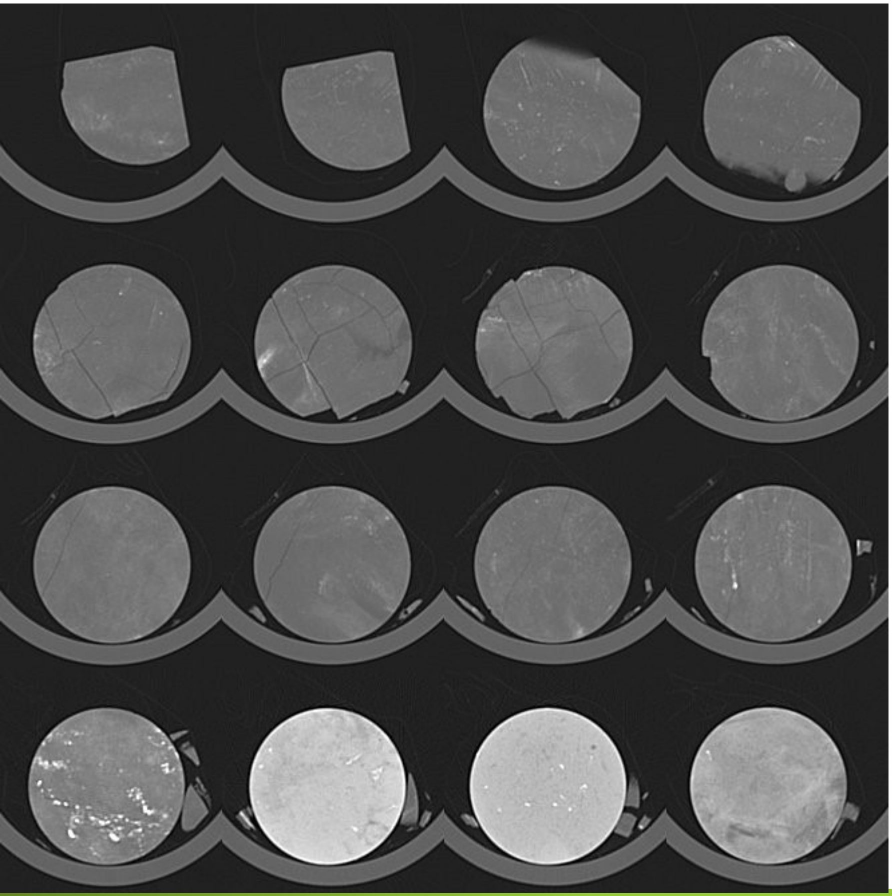
Outline – Preliminary Characterization

- Coal/Coalbed Characteristics – Ongoing, flow pathways
- Microbial Analysis
  - 16S rRNA Gene Sequencing of 5 coal basins – What microorganisms are present
  - Metagenomic Analysis of Appalachian basin – What microorganisms are present

    – What is the functional potential

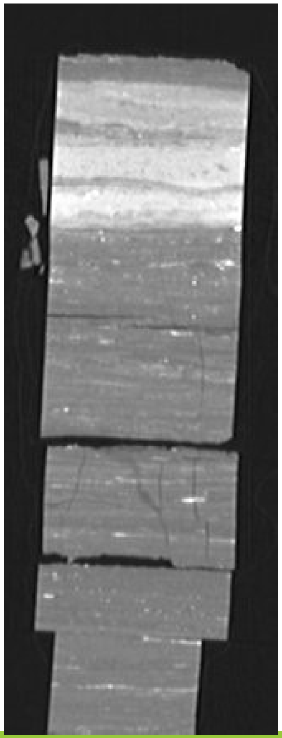
Coal Characterization

Coal CT scans – slices through 2 inch diameter cores

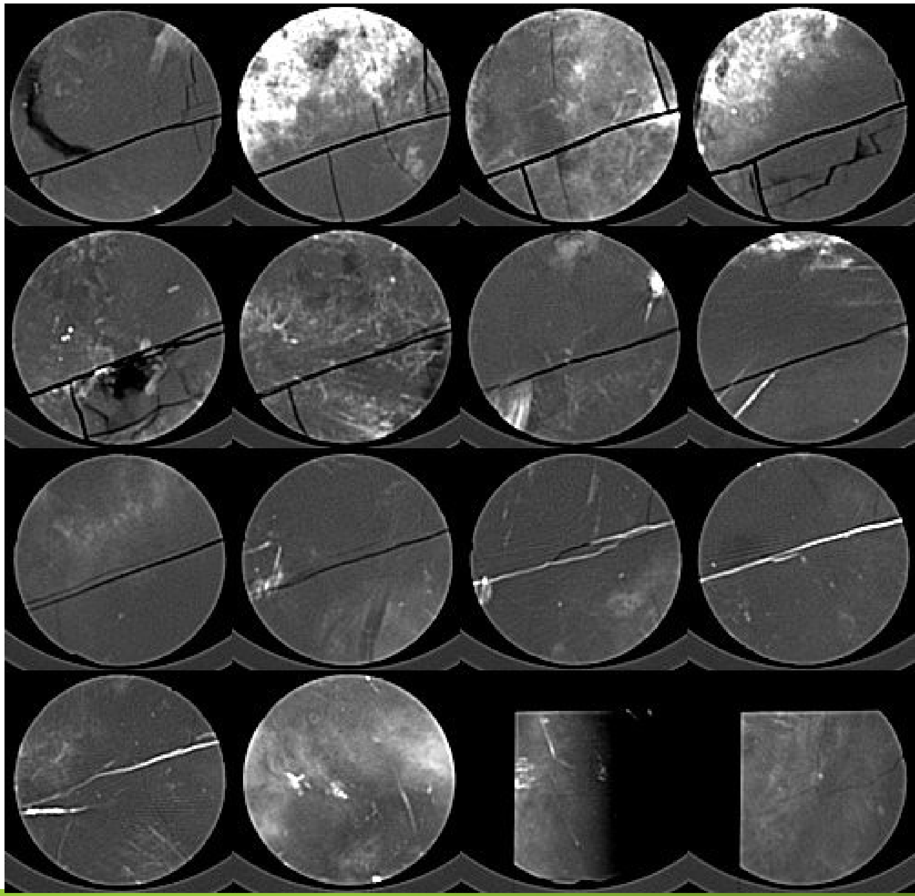


Waynsesburg montage

Dark transmits X-rays/bright blocks X-rays



Waynesburg XZ

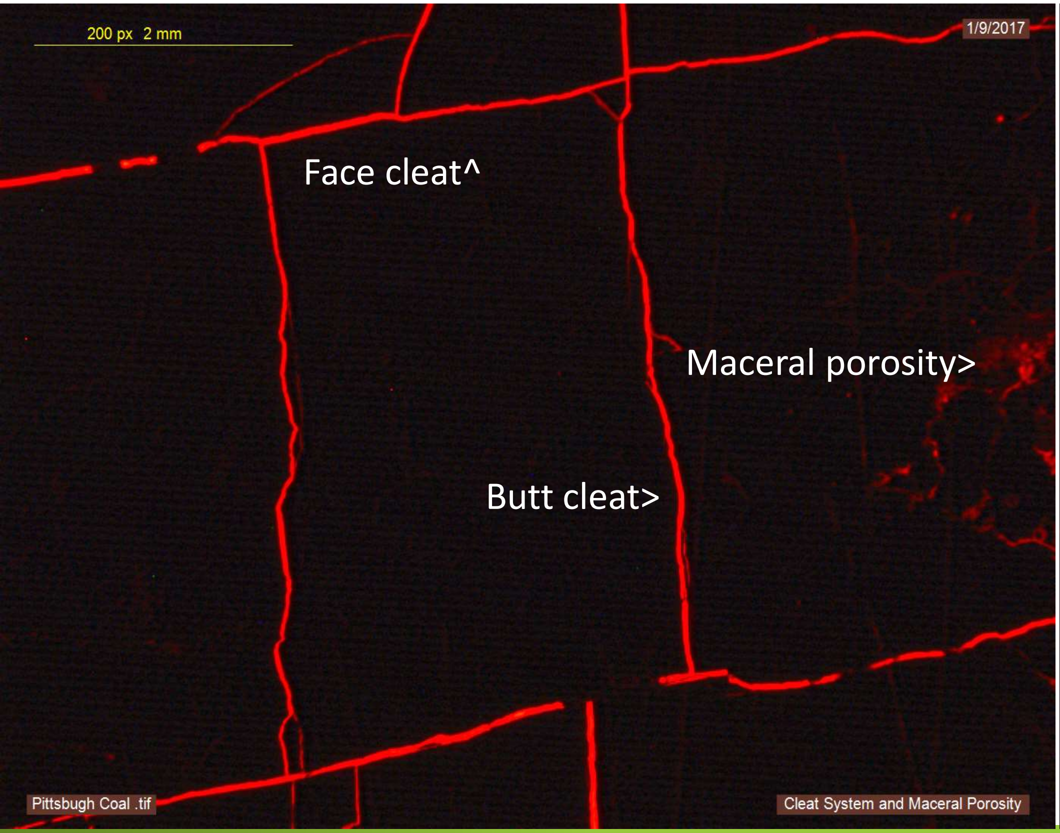


Sewickley montage

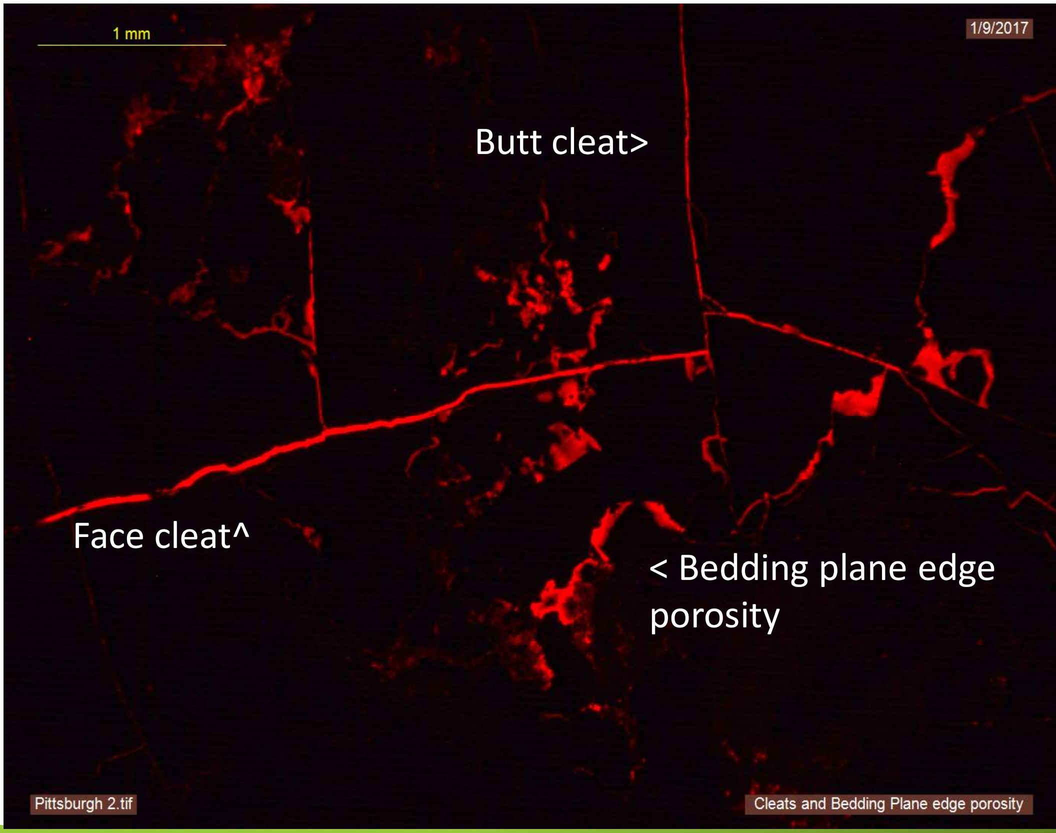
Coal Characterization

Pittsburgh Coal polished sections – impregnated with rhodamine-b dyed epoxy

Vertical slice



Horizontal slice



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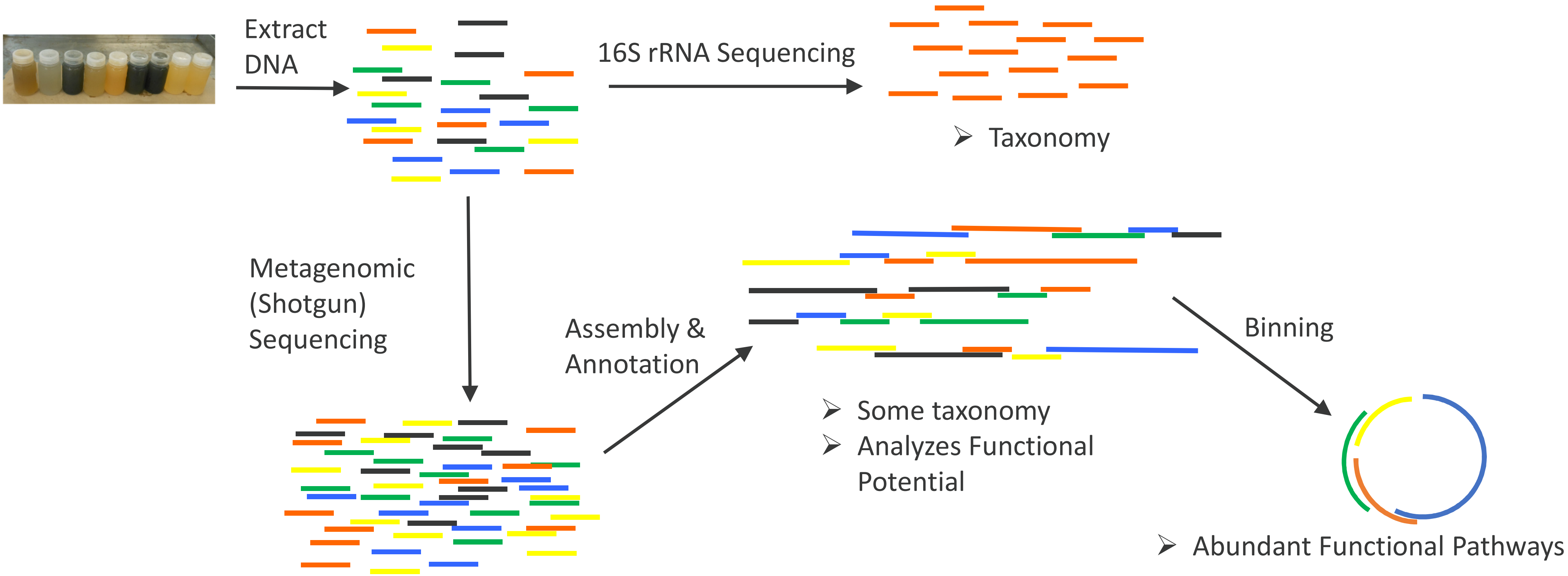
Microbiology Methods



Extract DNA

16S rRNA Sequencing

- Taxonomy

Metagenomic (Shotgun) Sequencing

Assembly & Annotation

- Some taxonomy
- Analyzes Functional Potential

Binning

- Abundant Functional Pathways

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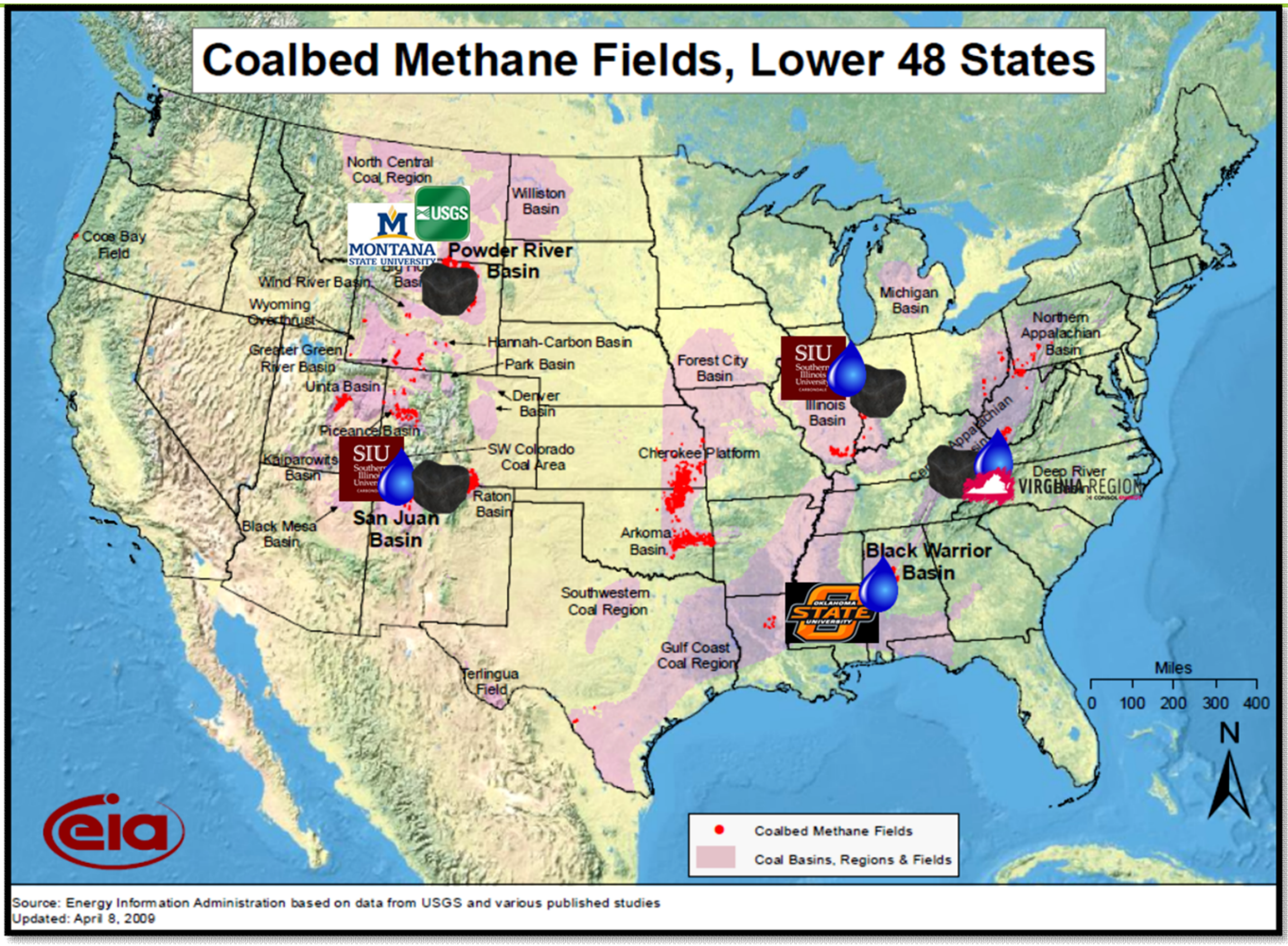
16S rRNA Gene Sequencing



Coalbed Methane Fields, Lower 48 States

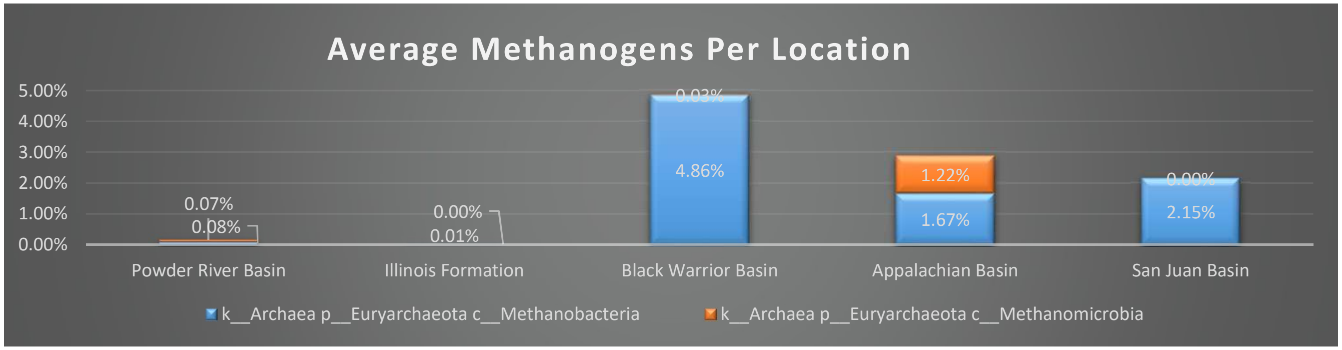
Source: Energy Information Administration based on data from USGS and various published studies
Updated: April 8, 2009

20 samples analyzed by 16S sequencing with Earth Microbiome Project (EMP)

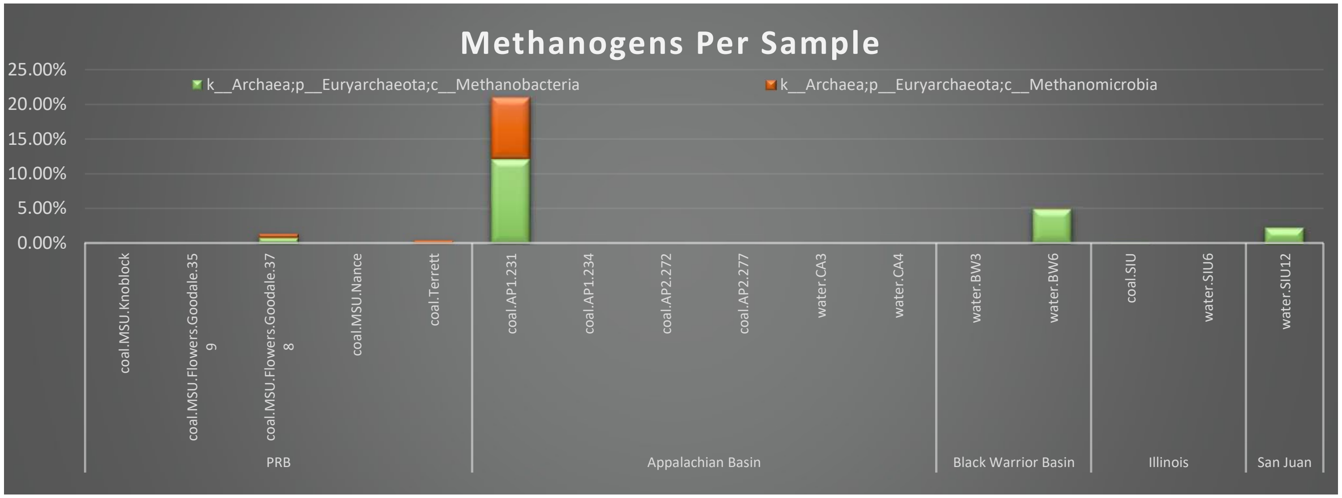
48 samples analyzed by 16S sequencing in house

16S rRNA Gene Sequencing

EMP

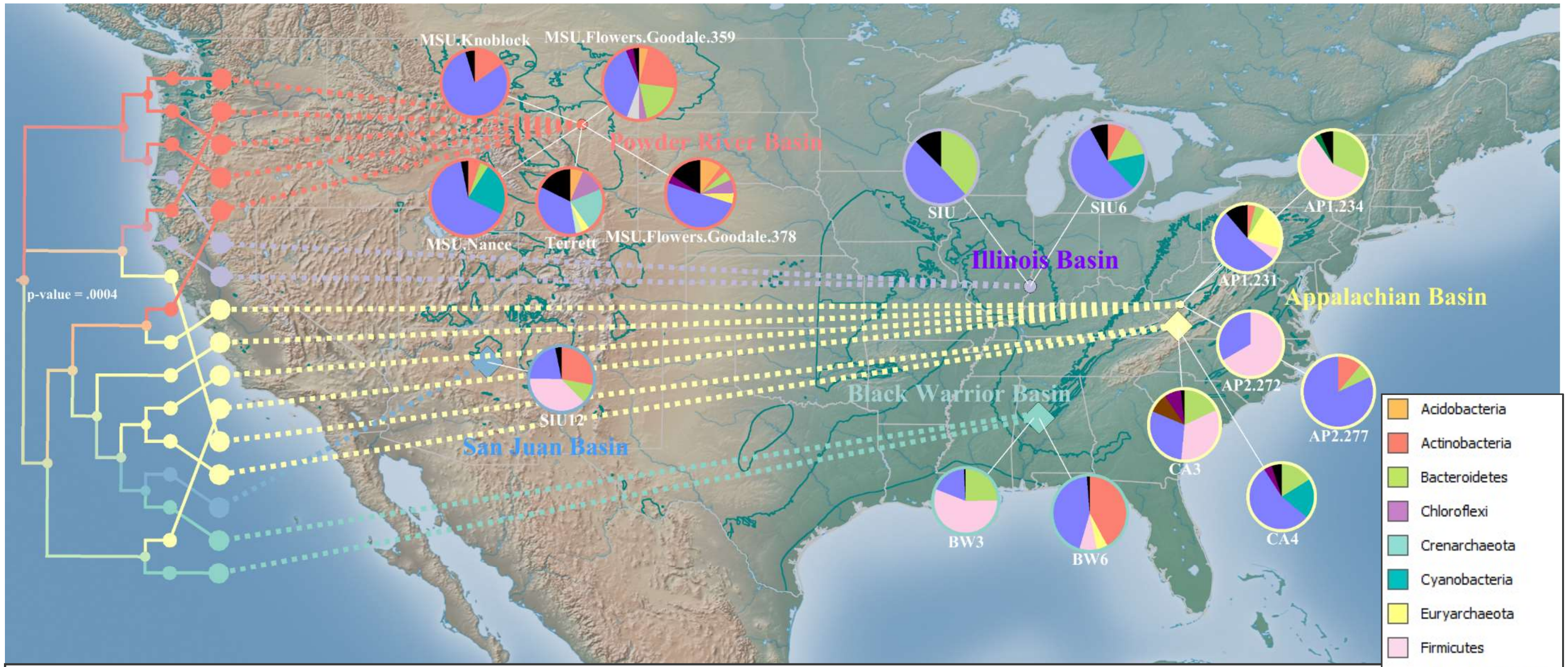


Although methanogens were found in each region, variations of population were great.
The highest percentage was seen in the Appalachian coal sample at 20% but the average was closer to 3-5%



16S rRNA Gene Sequencing

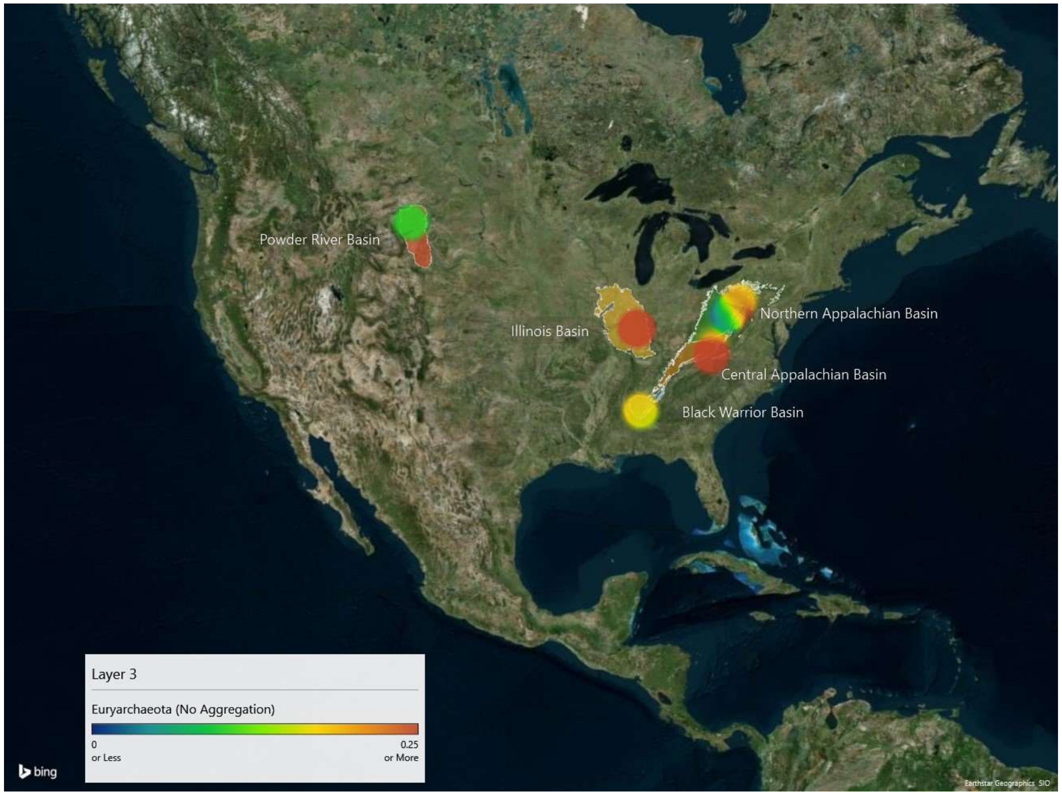
EMP



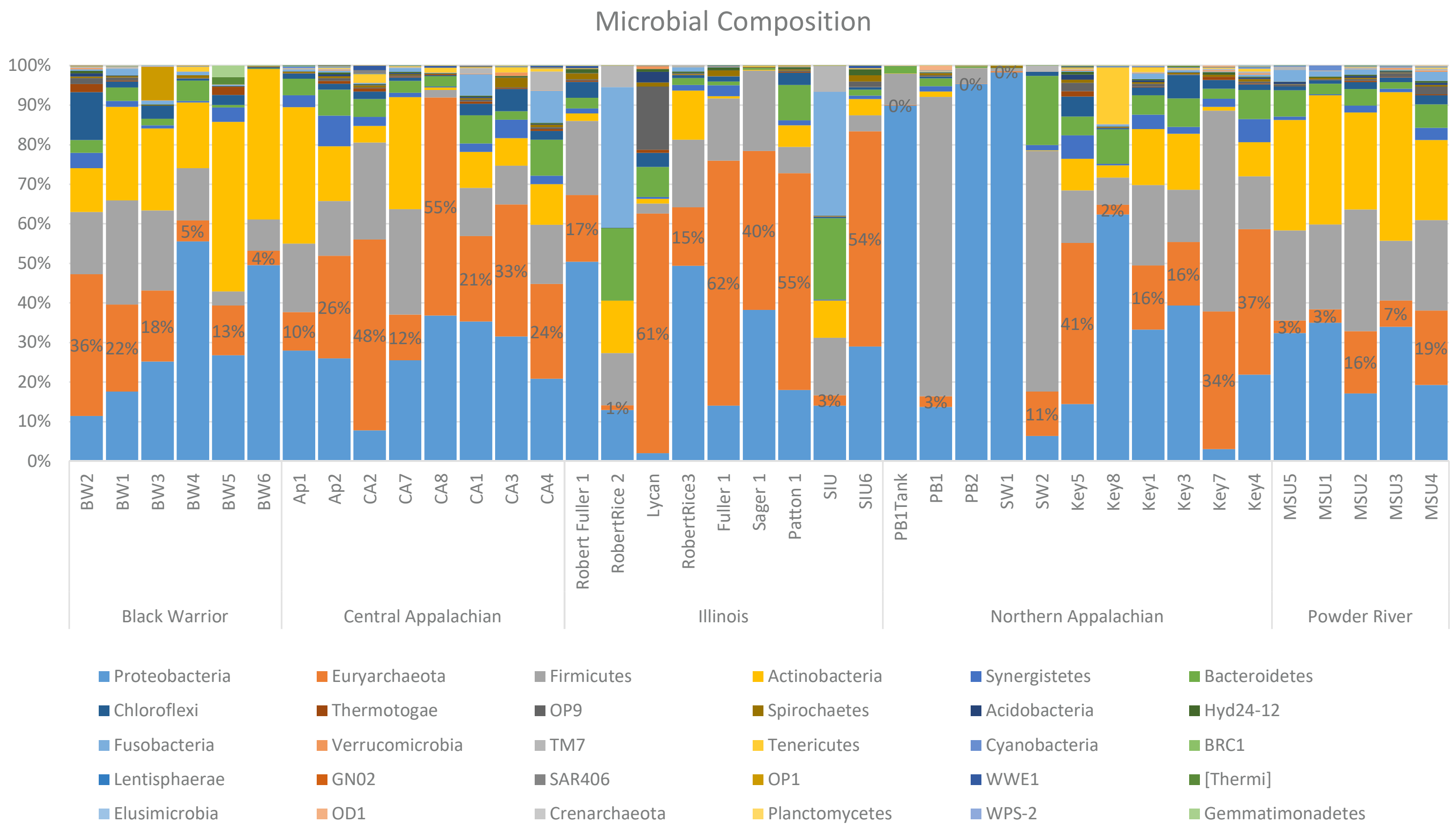
<u>Sequencing Data from the Earth Microbiome Project Collaboration:</u>
Samples denoted SIU and MSU come from respective collaborators. Euryarchaeota indicates methanogen group (yellow). P-value (0.0004) of unweighted Unifrac tree suggests that changes in microbial communities can be attributed to geographic relationships. However, differences exist between samples from the same seam, even in core samples a few feet apart. Coal core samples are noted by circles and diamonds indicate water samples. Size of circle or diamond indicates depth (deeper samples are larger).

16S rRNA Gene Sequencing

In-House



16S rRNA Gene Sequencing



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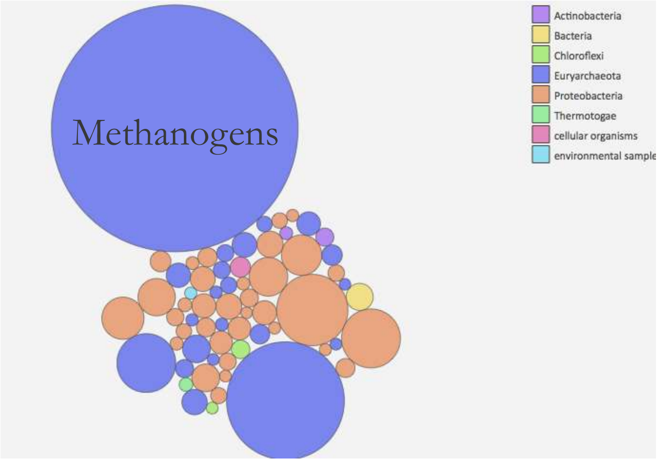
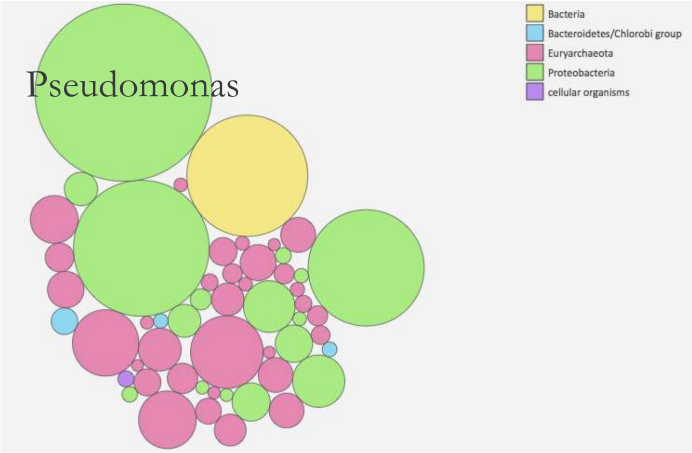
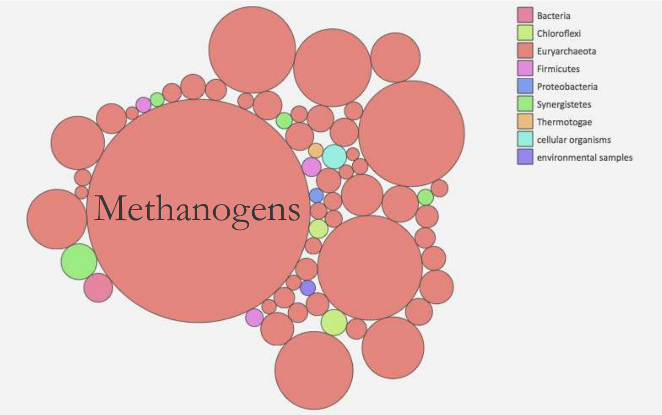
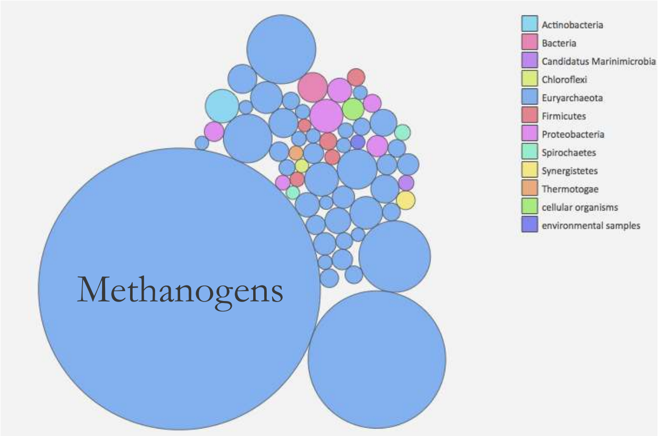
Inferred taxonomy of metagenome

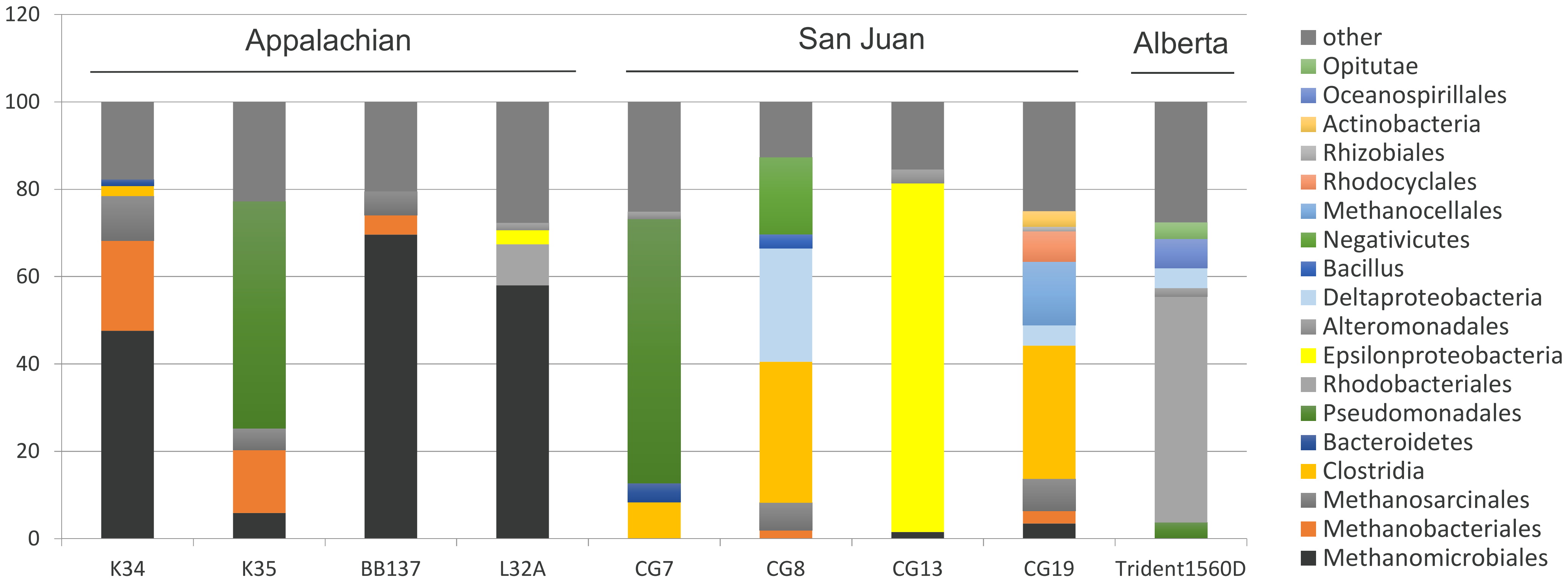








Inferred taxonomy of coalbed metagenomes

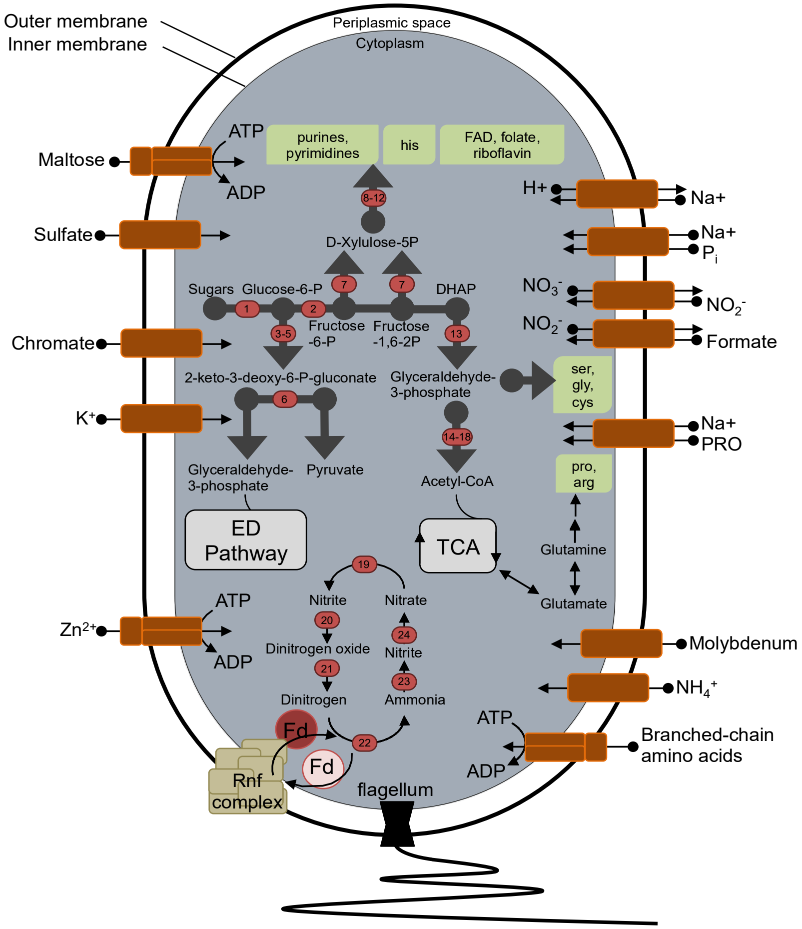


Pangenome of coalbed metagenomes

Pseudomonas Stutzeri draft genome

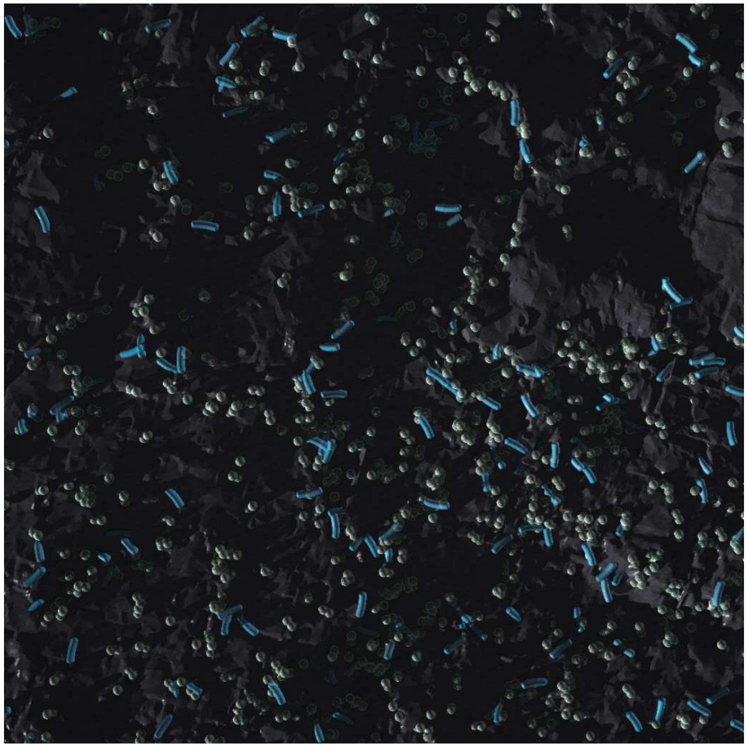
Psuedomonas stutzeri strain	Size (Mb)	GC%	Scaffolds	Completeness	Contamination
K35	**4.79969**	**62.9**	**194**	**99.2**	**0.72**
SDM-LAC	4.23321	60.6	199	99.04	0.82
TS44	4.27882	64.4	78	99.04	1.35
KOS6	4.94721	62.7	5	99	0.64
273	5.03094	60.3	1	98.96	0.95
DSM 10701	4.17412	63.2	1	98.85	0.29
P. xanthomarina S11	5.05197	62.3	73	99.31	0.4
P. chloritidismutans AW-1	5.06	62.5	77	95.03	5.42

P. Stutzeri Pathways



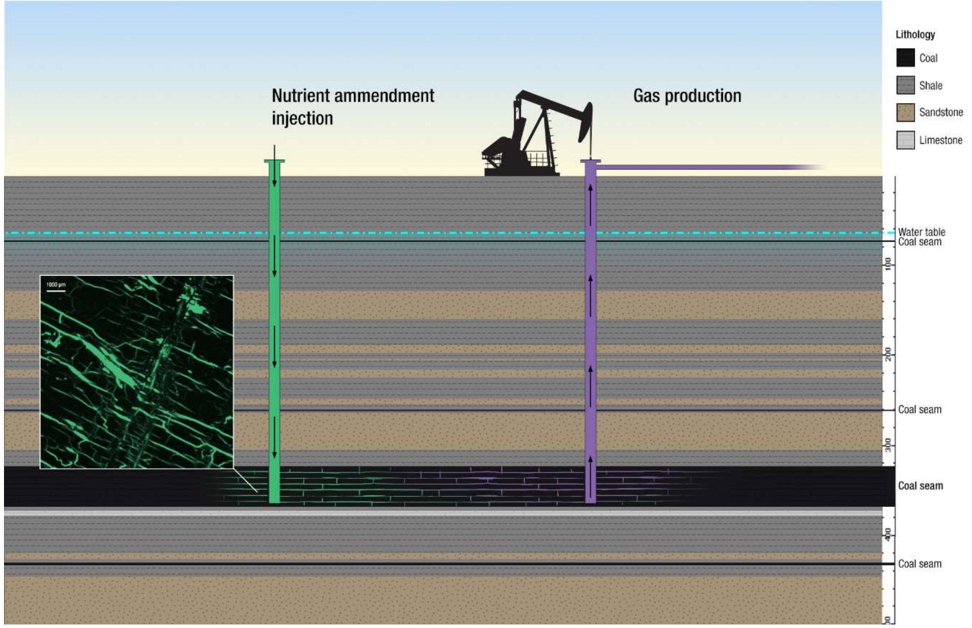
Future Work

- **Production and geochemistry correlations with 16S rRNA gene sequencing**
- **Metagenome analysis of Appalachian Basin**
- **Methanogen draft genome**
- **Coal characterization**
- **Nutrient amendment tests**
    - Carbon degraders
    - Methanogens



For More Information

MEC Systems



Website:

https://edx.netl.doe.gov/mecsystems/

Questions

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