Integrating Biological Monitoring Data from Diverse Sources:

Challenges in Database & Index Development for the Potomac Basinwide Assessments Project

Potomac River Basinwide Assessments

Enhance state water quality monitoring & assessment programs with consistent, watershed-wide assessments of stream health

"The ability to combine datasets is desirable to make judgements on the condition of the water resource." (Barbour et al. 1999)

"Combining information from separate monitoring surveys improves understanding of the biological integrity of riverine systems." (Handcock et al.)

The Data Synthesis Challenge:

Differing study designs

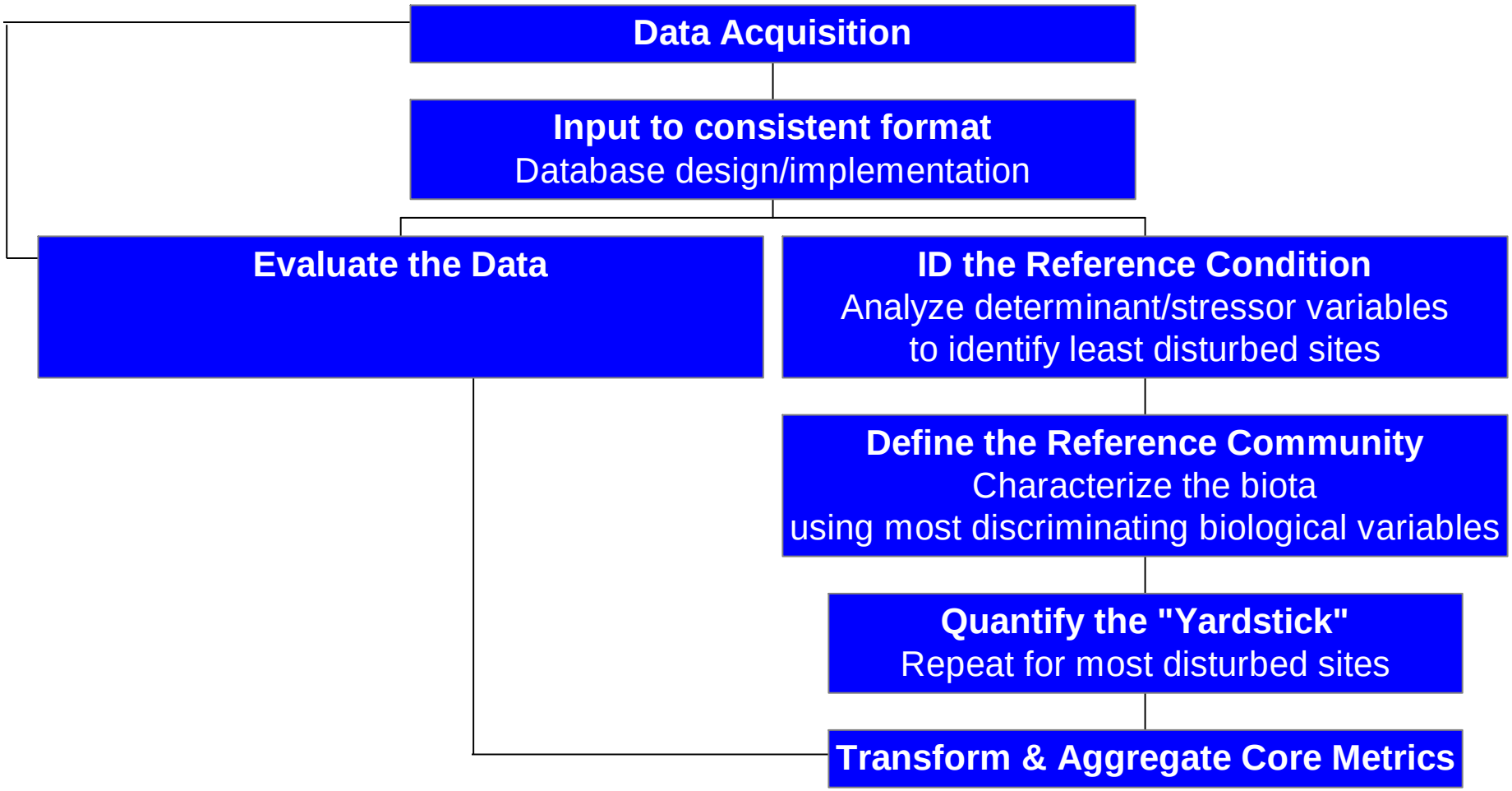
+ Differing methods

DIVERSE DATA!!

Solutions:

- **Unite datasets in a common form**
- **Create a common analysis framework**

Steps to Building a Framework



Assessment

Index Development

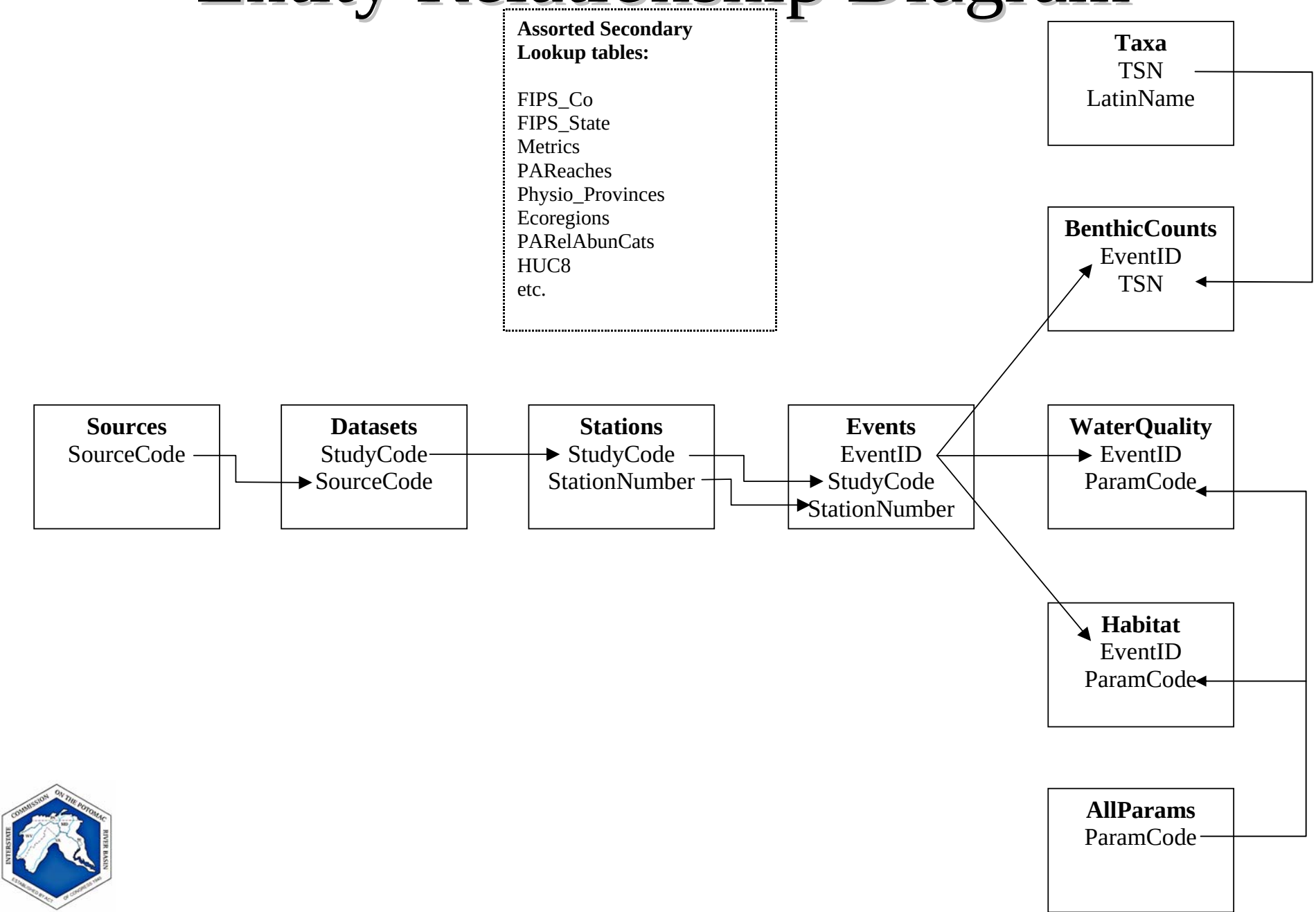
Data Acquisition

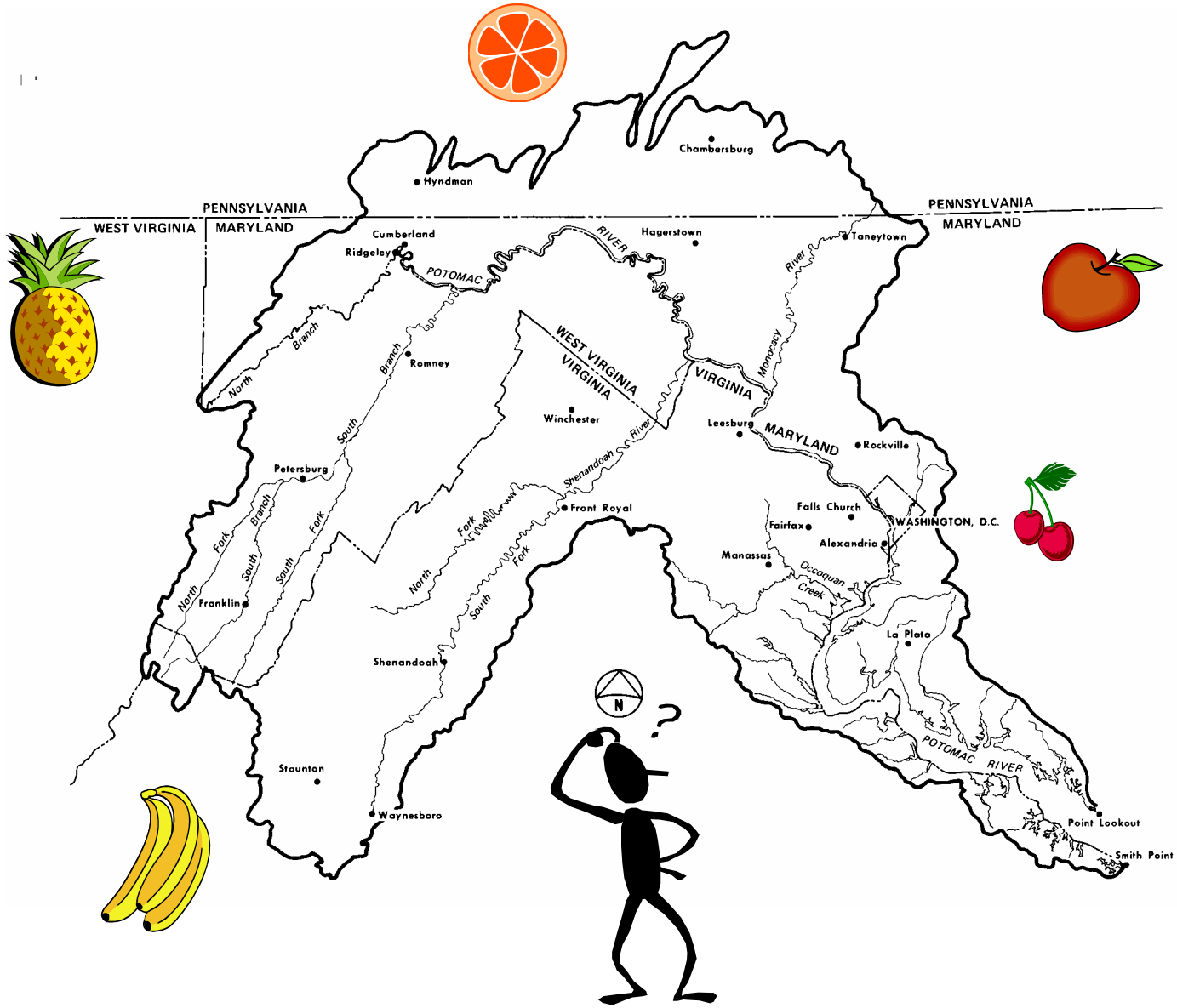
- Datasets (assessments + raw data) provided by member jurisdictions (305b/303d)
  - Maryland MBSS 1995-1997
  - Pennsylvania Unassessed Waters 1997-2001
  - Virginia WQ Assessment/Surface Water Monitoring 1994-2001
  - West Virginia WAP 1996- Spring 2001
- Assembled in a Microsoft Access database

Database Development Challenges

- Accommodating inherent differences among datasets
  - forms & formats
    - manual entry of hardcopy files
    - importing/adapting electronic files
  - accommodate ways datasets are customized (e.g. fieldnames, codes)
- Assuring data quality & database integrity
  - review sampling/processing/analysis/interpretation methods (lack of metadata!)
  - assume “primary quality” of contributed data
  - QA/QC during data entry (“secondary quality”)
  - improve geographical references (e.g. catchments, ecoregions, HUCs)

Entity Relationship Diagram





"Apples and oranges can be mixed if they are first converted to juice."
(Hale 2000)

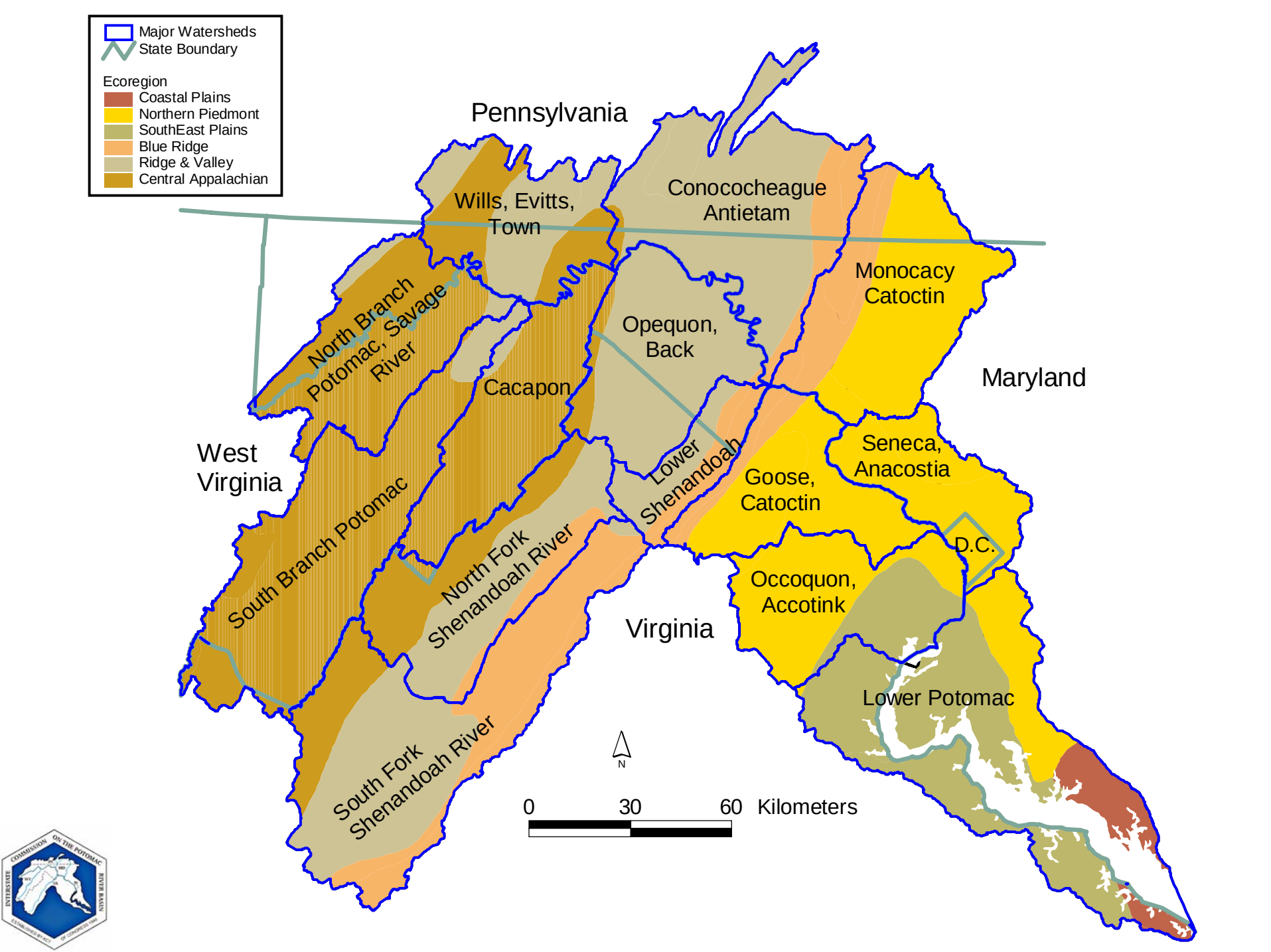
Real-World Example Across 3 Potomac Basin States

VA	PA	MD
•EPT	•EPT	•EPT
•Family	•Family	•Genus
•No formal training	•No formal training	•Training/certification required
•100-org subsample	•N/A; sort/ID in field and estimate RA's.	•120-org subsample
•Unknown (assume gridded pan)	•500 um kick net	•Tray w/100 5cmX5cm grids
•2 sq m area	•1 sq m area	•2 sq m area
•Multiple habitats sampled/composited	•Multiple replicates; not composited	•Multiple habitats sampled/composited
•BPJ	•Narrative only; attainment status determined in field	•Quantitative criteria
•Ecoregions?	•Subwatersheds	•Order, subwatersheds
•Targeted	•Targeted	•Stratified Random
•Judgement sampling	•Census sampling	•Probabilistic sampling

Data Synthesis Challenges

- **Study designs/goals**
  - **Solution: OK to combine for biological index development (e.g. MAIA)**
- **Index periods**
  - **Solution: seasonal differences negligible at Family-level ID**
- **Sampling/subsampling methods & gears**
  - **Solution: accept higher *p*-value**
- **Subsample sizes**
  - **Solution: differences in counts insignificant at Family ID**
- **Habitat assessment protocols & classification criteria**
  - **Solution: select common hab/WQ elements & equate to consistent scale**
- **Levels of taxonomic resolution**
  - **Solution: collapse IDs to Family where possible**
- **Analytical approaches (mix of qualitative & semi-quantitative data)**
  - **Solution: use minimum values associated with narrative categories as quantitative counts**

PA Relative Abundance Categories and Value Ranges				
Category	Range	LowestVal	AvgVal	HighestVal
Rare	<3	1	1.5	2
Present	3-9	3	6.5	9
Common	10-24	10	17	24
Abundant	25-100	25	62.5	100
Very Abundant	>100	101	101	sky's the limit


Major Watersheds
State Boundary
Ecoregion
Coastal Plains
Northern Piedmont
SouthEast Plains
Blue Ridge
Ridge & Valley
Central Appalachian
Pennsylvania
Wills, Evitts, Town
Conococheague Antietam
Monocacy Catoctin
North Branch Potomac, Savage River
Opequon, Back
Cacapon
Maryland
West Virginia
Lower Shenandoah
Seneca, Anacostia
Goose, Catoctin
D.C.
South Branch Potomac
North Fork Shenandoah River
Occoquon, Accotink
Virginia
Lower Potomac
South Fork Shenandoah River
N
0
30
60
Kilometers

Parameter	ParamCode	Which "rapid" habitat assessment parameters?
Instream Condition	INSTR_COND	Epifaunal Substrate+Cover/2 OR EpiSub&Cover Score
Habitat Heterogeneity	HAB_HETERO	Riffle Frequency OR Sinuosity OR Pool/Glide/Eddy Quality
Channel Alteration	**CHAN_ALT**	Channel Alteration
Bank Stability	BANK_STAB	Bank Stability
Substrate Quality	SUB_QUAL	Embeddedness OR Pool Substrate OR %Embeddedness scored to same scale
Riparian Zone	**RIP_ZONE**	Riparian Buffer score OR Riparian width (M) scored to same scale
Anthropogenic Alterations	**ANTHRO_ALT**	Grazing OR Aesthetic+Remoteness/2
Total Score	TOTSCORE	Sum of all parameter scores
pH	pH	
Conductivity	Cond	

Consistent Habitat/WQ Attributes

Reference Criteria (ALL of the following):				
Param	64	66	67	69
ANTHRO_ALT	≥70%	≥70%	≥70%	≥70%
BANK_STAB	≥70%	≥50%	≥70%	≥50%
CHAN_ALT	≥70%	≥50%	≥50%	≥50%
HAB_HETERO	>10%	>10%	>10%	>10%
INSTR_COND	>30%	>10%	>10%	>10%
SUB_QUAL	≥70%	≥70%	≥70%	≥70%
RIP_ZONE	≥50%	≥70%	≥70%	≥70%
	AND: (Both)			
pH	Between 6 and 9			
CON	<500			

Impairment Criteria (3 or more of the following):				
Param	64	66	67	69
ANTHRO_ALT	≤10%	<10%	<10%	<10%
BANK_STAB	≤10%	≤10%	≤10%	≤10%
CHAN_ALT	≤10%	≤10%	≤10%	≤10%
HAB_HETERO	<10%	<10%	<10%	<10%
INSTR_COND	<10%	<10%	<10%	<10%
SUB_QUAL	≤10%	≤10%	≤10%	≤10%
RIP_ZONE	≤10%	≤10%	≤10%	≤10%
	OR: (Either)			
pH	≤4.5			
CON	>1000			

ID Consistent Biological Indicators

- Select potential metrics from the literature (60)
- Equalize level of taxonomic resolution (Family)
- Screen out ref & stressed sites w/<u>both</u> TaxRich & TotAbun > or < 2 SD's from mean
- Range Test (can calculate for ≥90% of ref sites)
- Variability Test (C.V. ≤0.50 in ref sites)
- Discrimination Test - ID metrics that distinguish ref from stressed sites in each ecoregion
- Redundancy Test (Pearson Correlation coeff <0.75)

Metrics

Taxa Richness
EPT Taxa
Percent EPT
Index FBI
Percent Dom2 (except 69)
Percent Dom5 (69 only)
Percent Clingers
Percent Collectors (except 69)

Can Reference Data from Different Regions Be Combined?

- Increase the pool of available reference sites available to any 1 region
- Ensure that the best possible reference conditions are captured by the final index
- Test (t- and U-tests) to see if ecoregional reference communities are distinctly different when comparing core metric values
- In this case, the preferred answer is “NO”

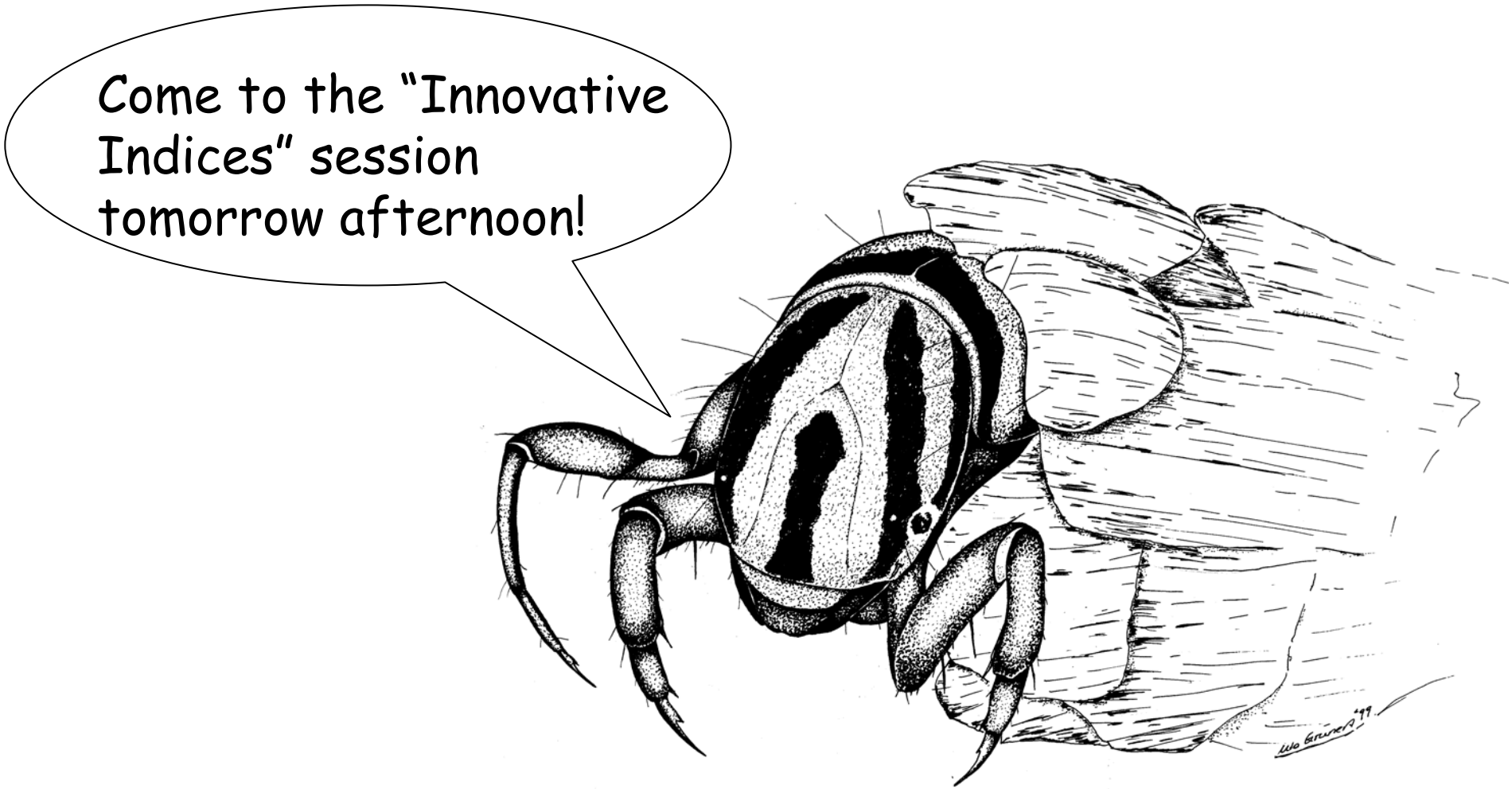
Ecoregion1	Ecoregion2	EPT	ENH	FBI	%CL	%CO	%D1	%D5	%EPT	TR
64	66	**	**	SS	SS	*	SS	SS	*	SS
64	67	**	**	SS	SS	**	SS	*	**	*
64	69	**	**	SS	SS	SS	SS	*	SS	*
66	67	SS	SS	*	SS	SS	SS	SS	SS	SS
66	69	SS	SS	SS	SS	SS	SS	SS	SS	SS
67	69	SS	SS	SS	SS	SS	SS	SS	SS	SS

- SS=Significantly similar (p>0.05)
- Reference communities in the Blue Ridge Mountain (66), Ridge & Valley (67), and Central Appalachian (69) ecoregions are almost indistinguishable
- Northern Piedmont (64) reference communities are quite dissimilar from those in the “mountain” ecoregions (66, 67, 69)

What We Know (Summary)

- We have a uniform framework for identifying zones of ecological distinctiveness & for defining biological potential of streams within ecoregions
- We have meaningful indicators for assessing community response to perturbation
- Reference data in certain ecoregions can be “pooled”
- If underlying methodologies are sufficiently similar, visual estimates of relative abundance are comparable to fixed-count subsampling
- Diverse data can be combined in a bioassessment framework *if the synthesis is done with care*

Want to Know More?



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