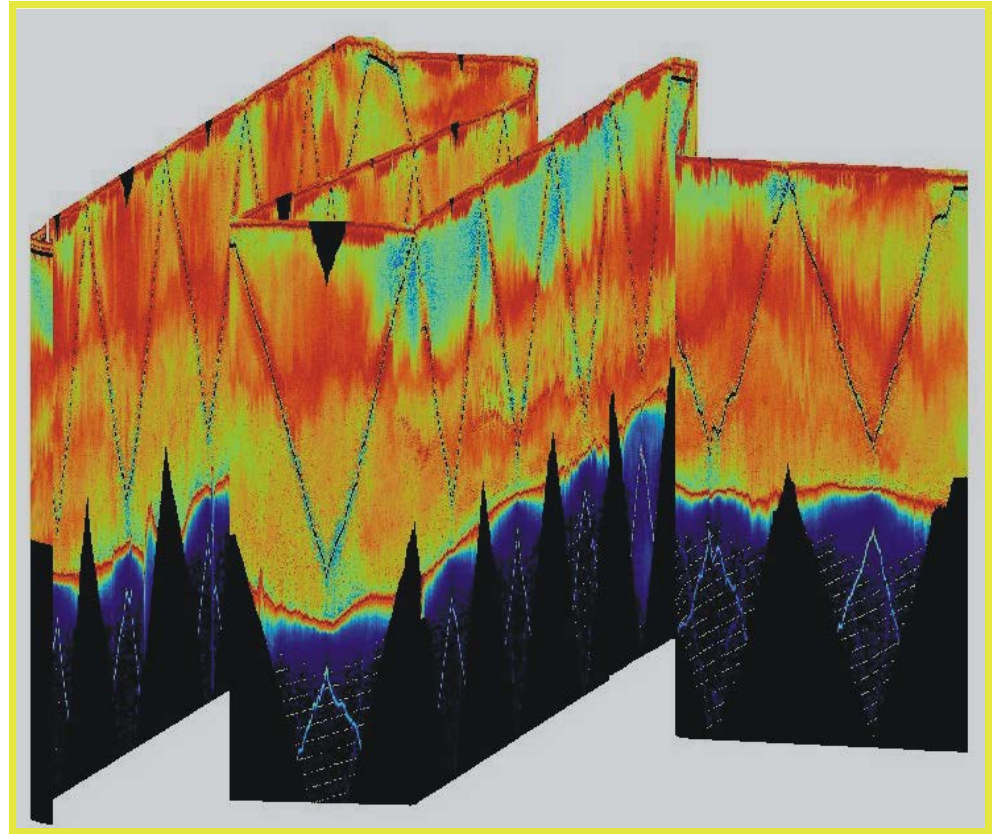
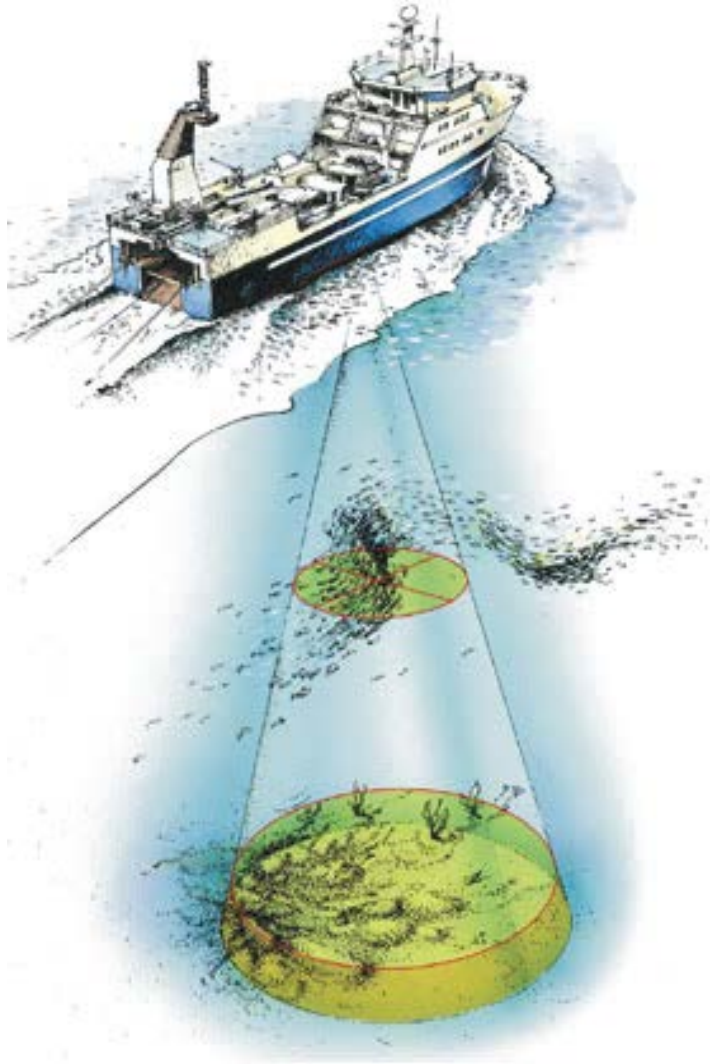
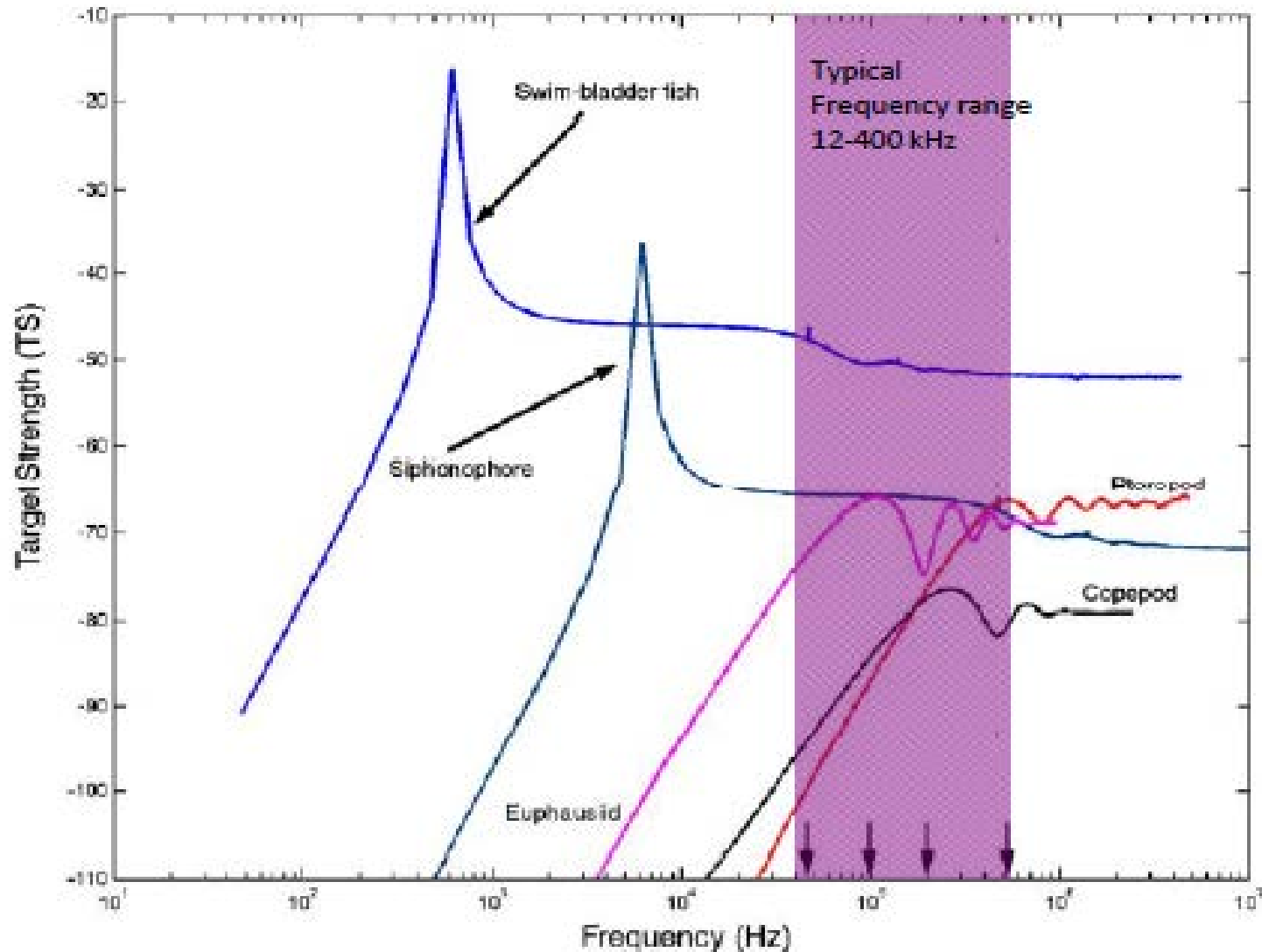


Data Processing & Analysis I



Acoustic Scattering Regions



Factors Influencing Acoustic Data Quality

1. Sensor: echosounder, transducer
2. Sampling platform: vessel, transducer mounting, electrical supply, grounding
3. Environment: water structure, surface conditions
4. Targets: behavior, material properties, orientation
5. Operator: parameter settings, biological sampling, recording
6. Analyst: size and density translations, abundance or biomass estimates

Echosounder Outputs: Sample Data

'Raw' Data

- sample power (units watts)
- sample angle (units degrees) along: fore, aft; athwart: port, starboard

Processed Data

- area backscatter strength: S_a
- (Mean) volume backscatter strength: S_v
- Nautical Area Backscattering Strength: S_A , NASC
- target strength: TS

Processing Steps

1. Pre-Processing: passive noise calculation, calibration tuning, data editing (bottom, noise, empty pings)
2. Processing: gridding, classification,
3. Exports: densities, distributions for maps, demographics (e.g. length frequencies), behaviors (e.g. target tracks)

Partitioning Backscattered Energy aka Scrutinizing

- the division of recorded backscatter into categories
- 3 components: quality control, dividing echo integrals, associating integrals with user-defined categories
- can be subjective (e.g. single frequency) or objective (e.g. multifrequency)
- each transect partitioned by operator or objective rules
- species mixtures complicates the task

Backscatter Categories

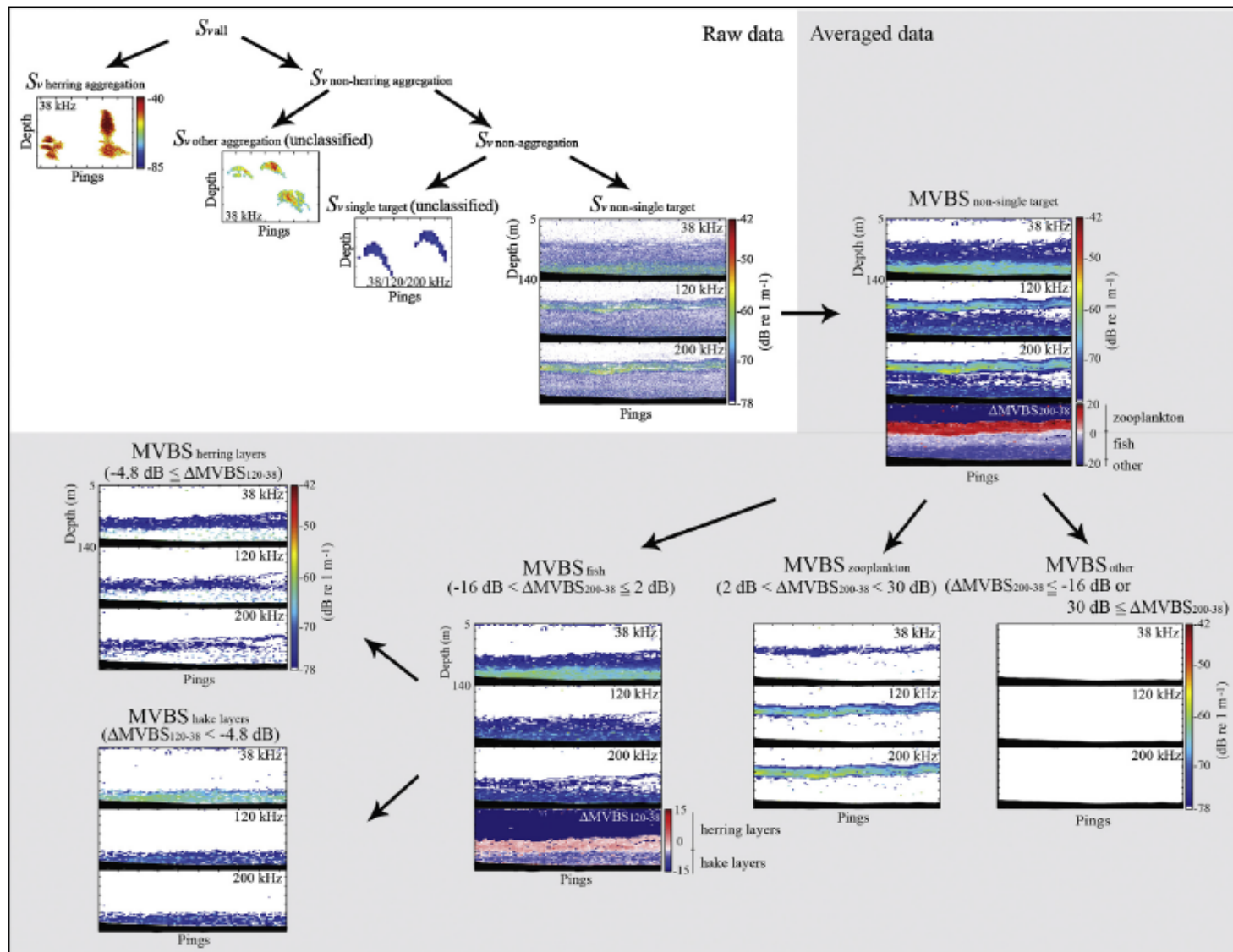
Subjective:

- analyst determined
- species and/or size/length classes
- based on prior knowledge, echogram, direct samples

Objective

- rule determined (*rules set by analyst*)
- frequency- and/or amplitude-dependent backscatter
- trawl catches for species compositions and length frequencies and when constituents unknown
- proportion energy by % species composition or weight

Mean Volume Backscatter Differencing



Relative Frequency Response

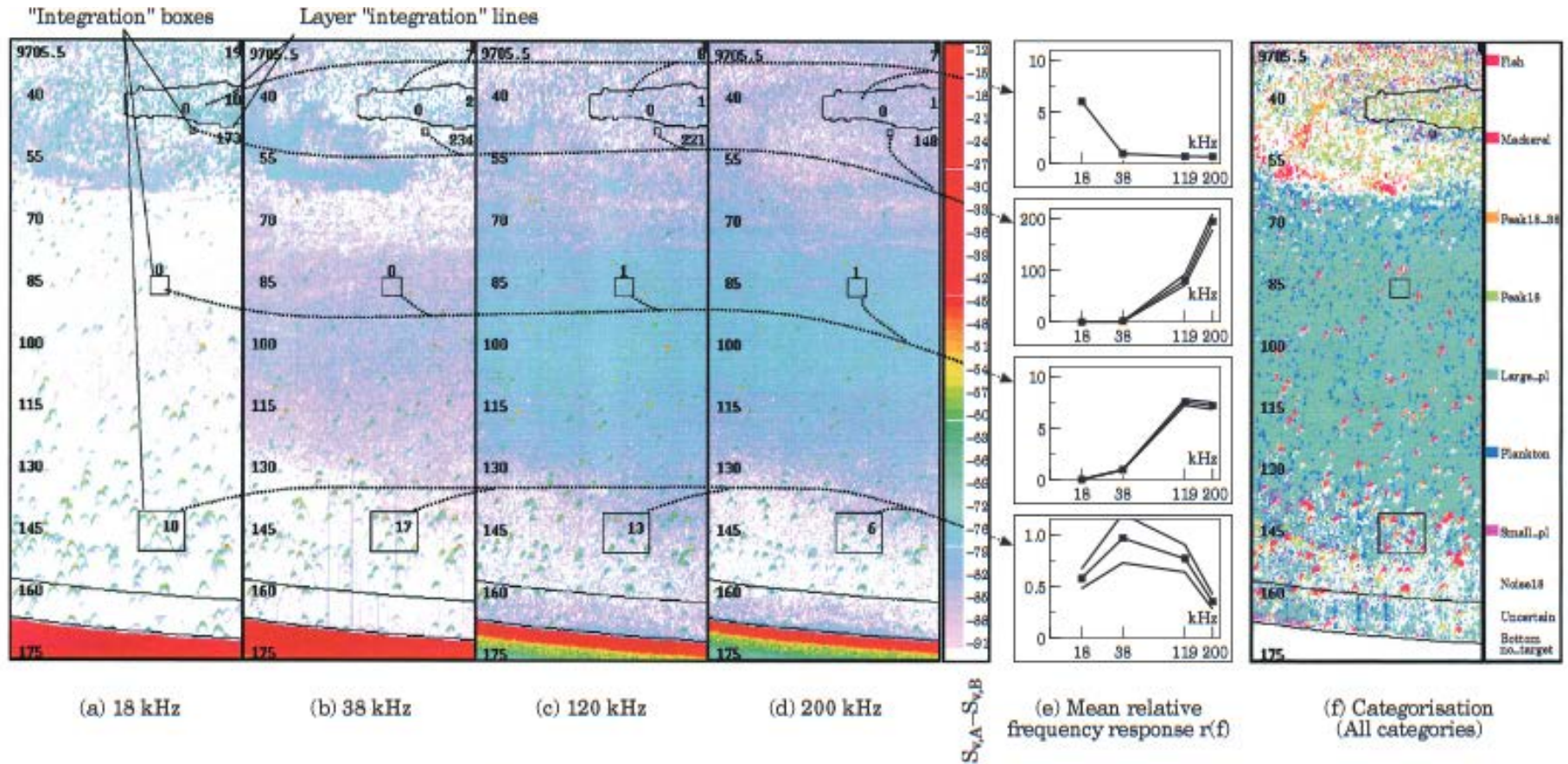
- Choose a baseline frequency ($f = 38$ kHz typical) and compare backscatter integral amplitudes to that frequency

$$r(f) = \frac{S_v(f)}{S_v(f_{ref})} = \frac{S_A(f)}{S_A(f_{ref})} \quad (\text{Korneliussen and Ona 2002})$$

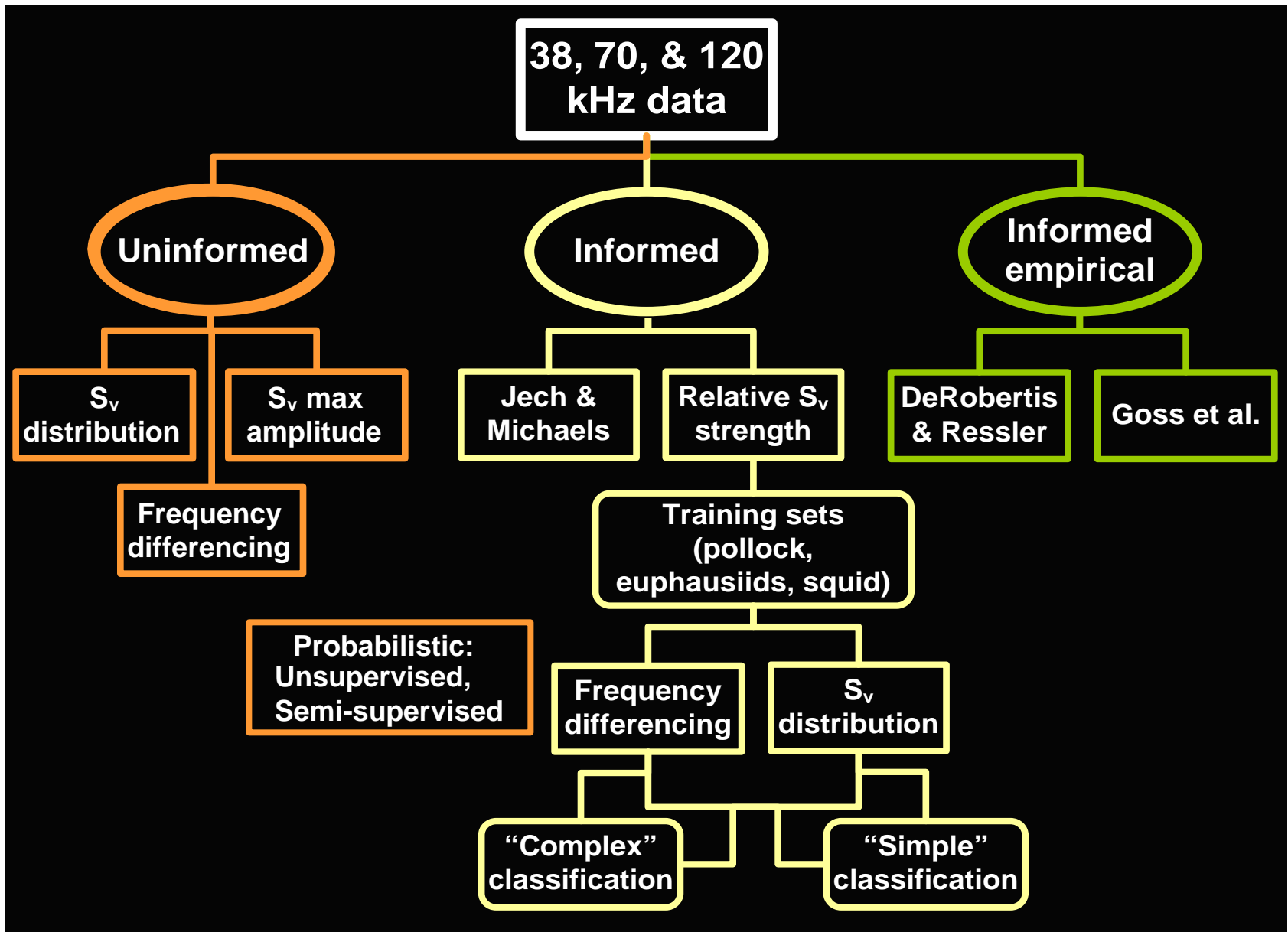
For Single
Targets

$$r_T(f) = \frac{\sigma_{bs,T,i}(f)}{\sigma_{bs,T,i}(f_{ref})} \quad (\text{Pedersen and Korneliussen 2009})$$

Frequency Response Example



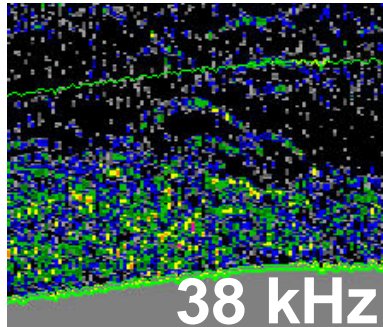
Multifrequency Classification Approaches



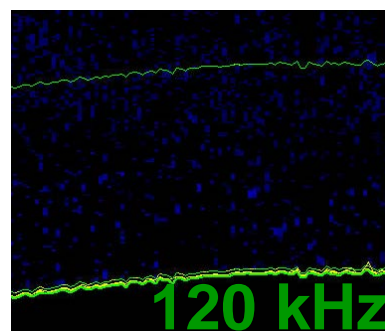
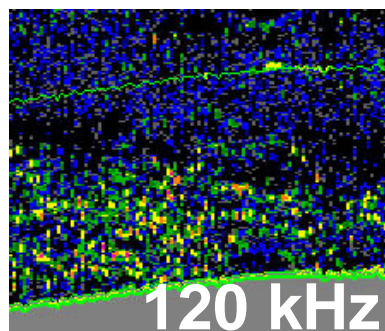
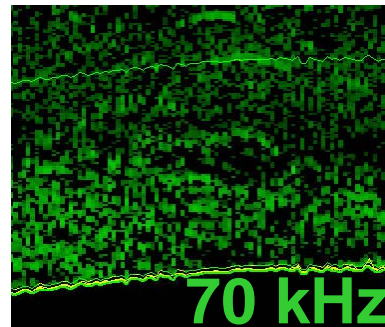
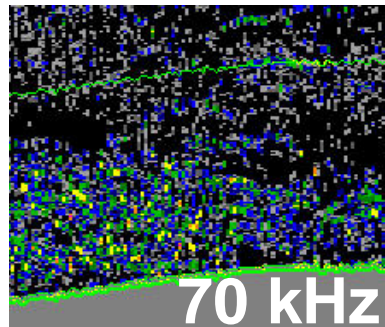
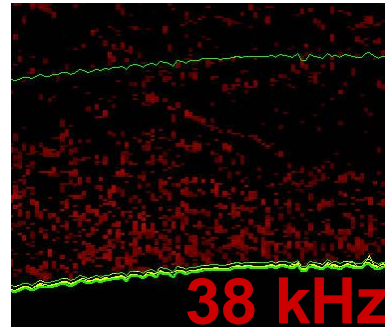
Unsupervised Classification

S_v maximum amplitude

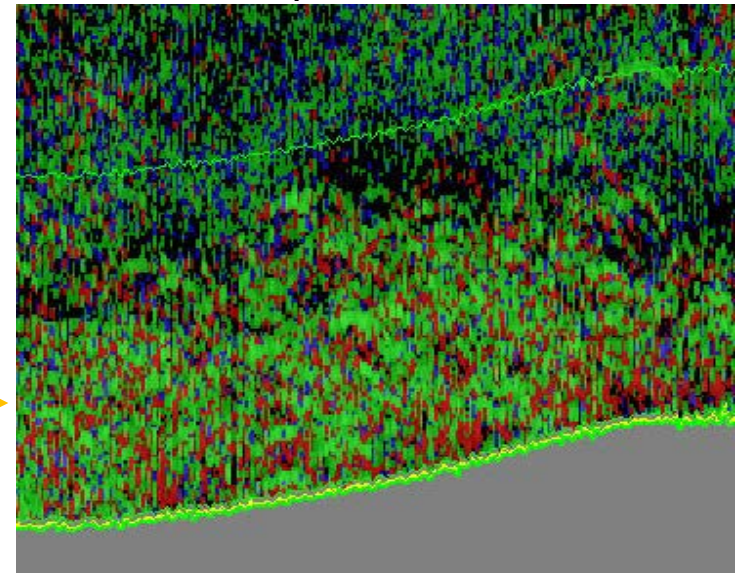
Original



Maximum



S_v confetti

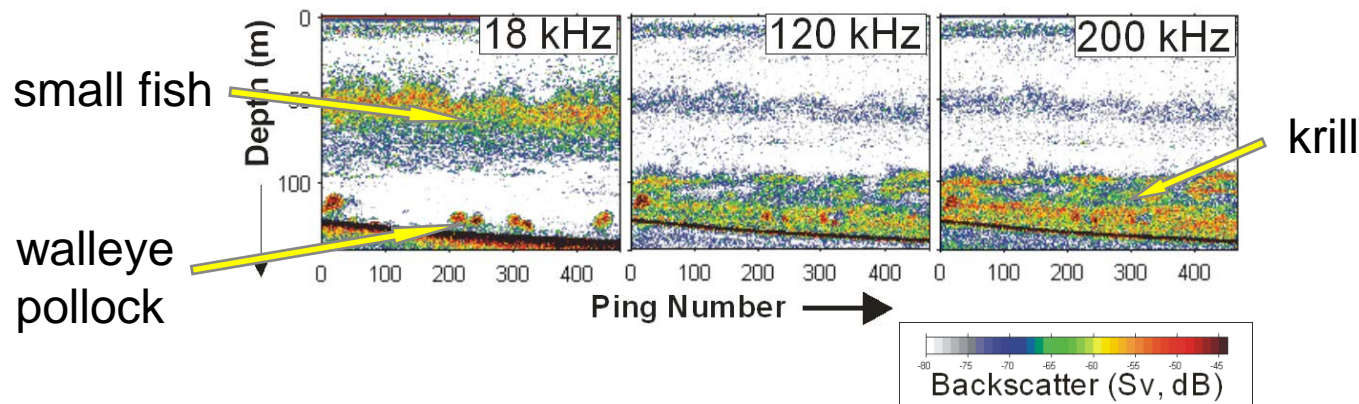


Masked onto 38, 70, 120

Kloser et al. 2002

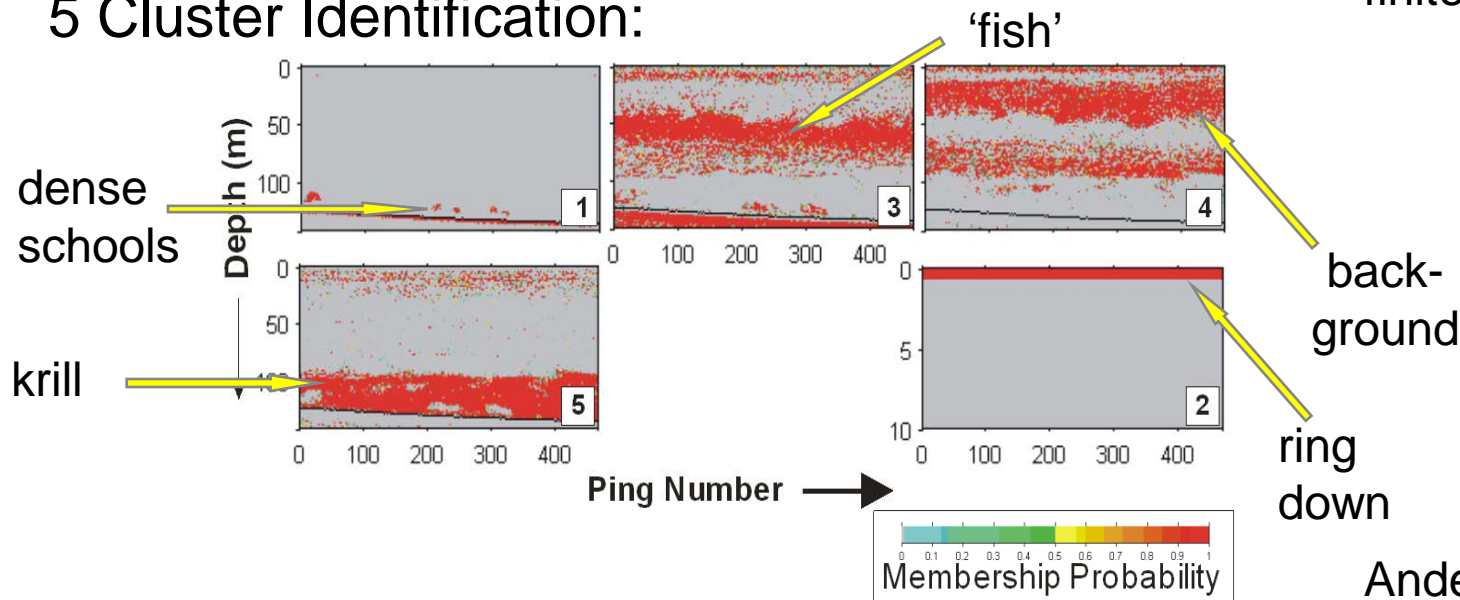
Unsupervised Probabilistic Classification

3 Frequency Backscatter:



Expectation
maximization of
finite mixture models

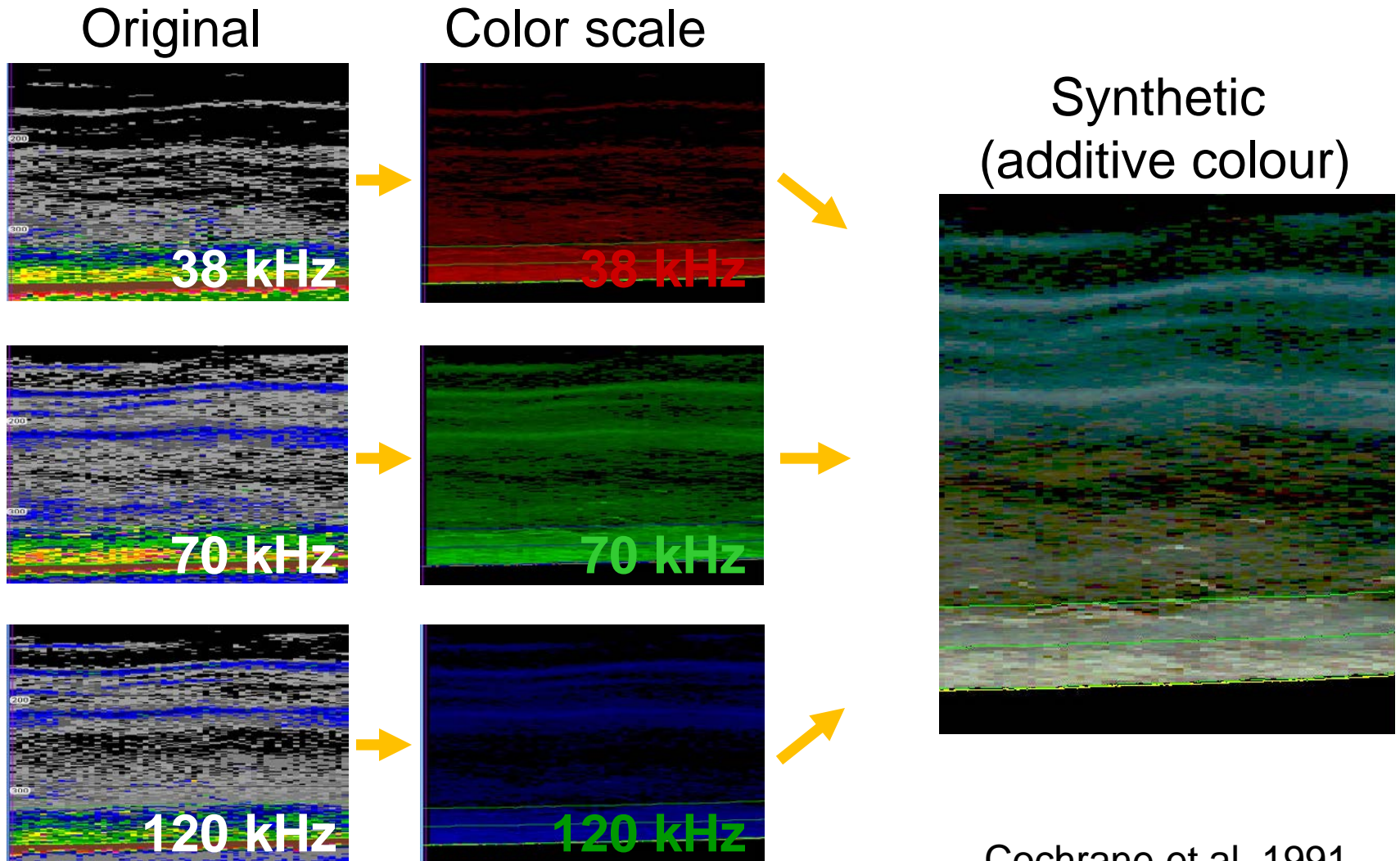
5 Cluster Identification:



Anderson et al. 2007

Supervised Classification: Integral Amplitude

S_v relative strength, verified samples

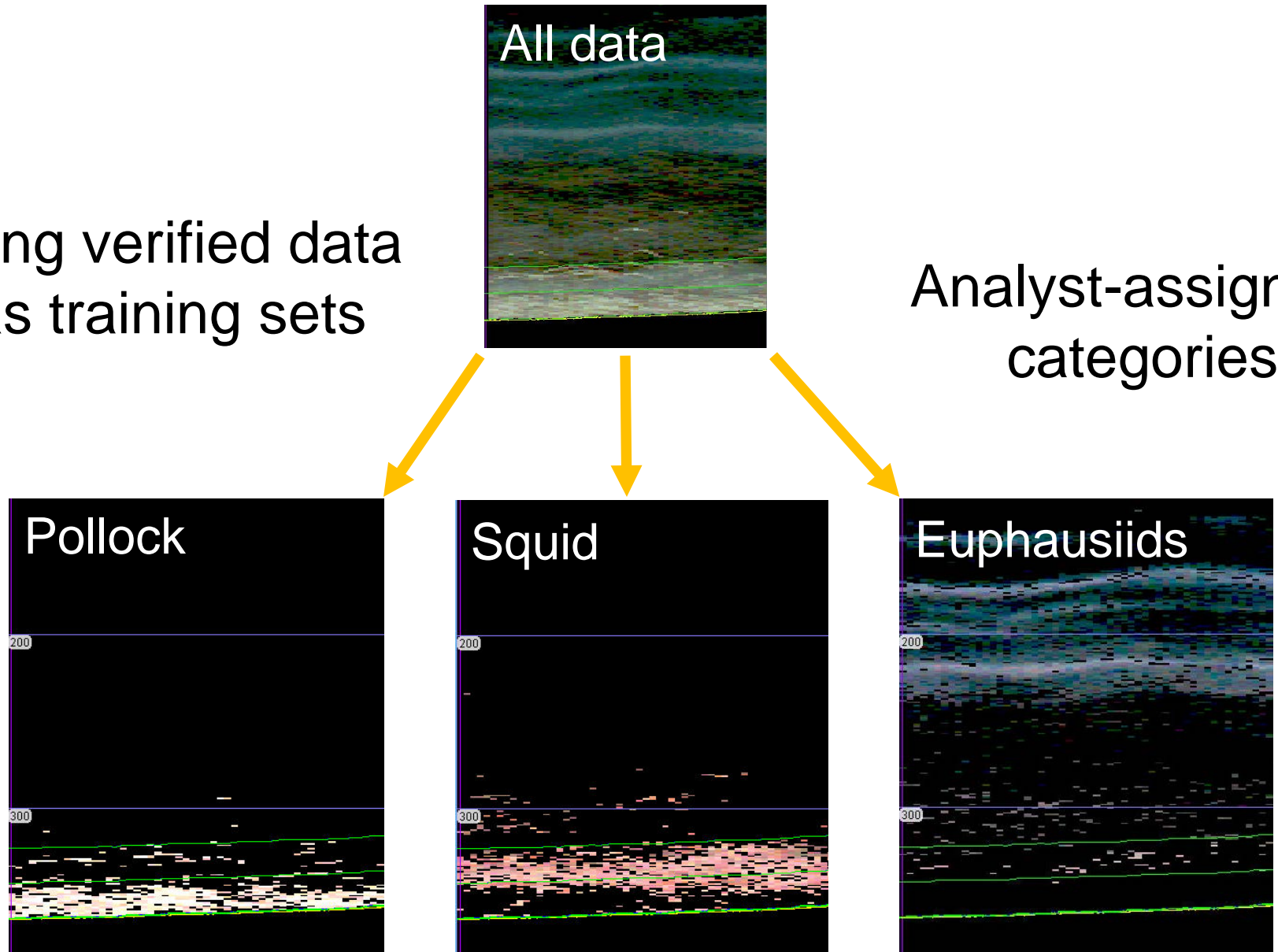


Cochrane et al. 1991

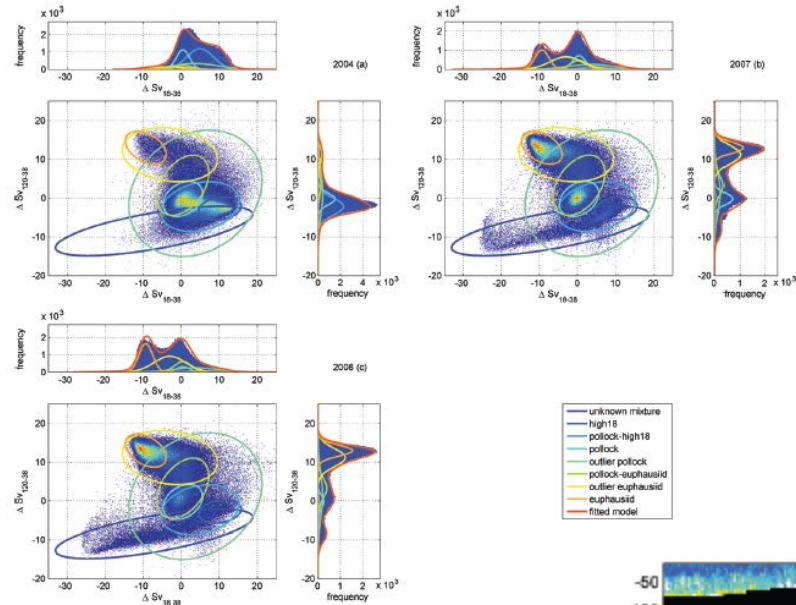
Supervised Classification: Ref Library

Using verified data
as training sets

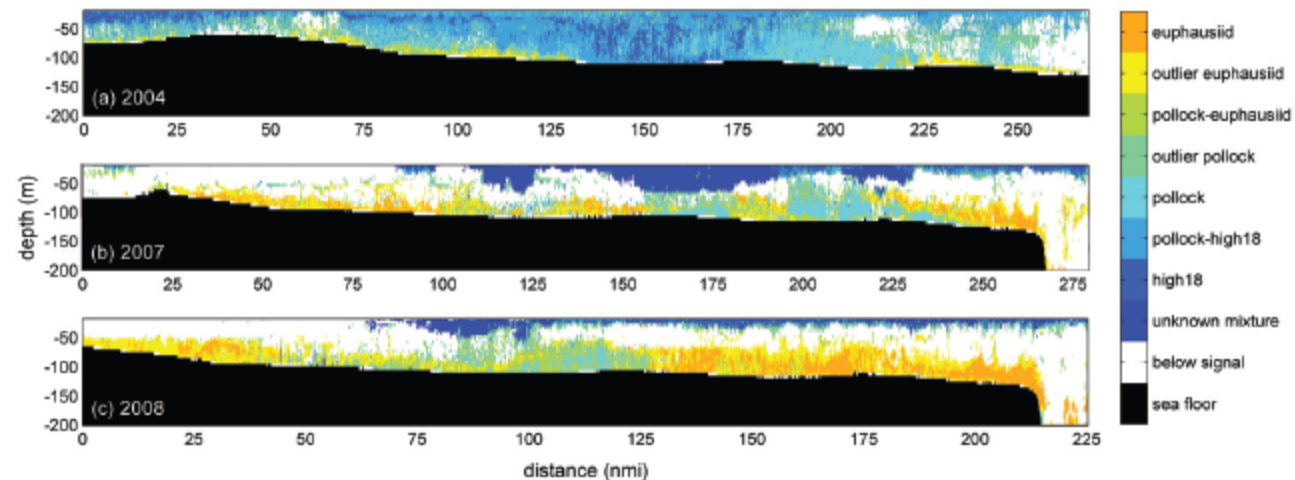
Analyst-assigned
categories



Seimi-supervised Probabilistic Classification



Generalized Gaussian mixture model with class discovery



Trawl Classification

Trawl Catches, length-based single or multiple species:

- numbers and weight by species
- lengths by species
- lengths by sex

Proportion (P) of catch by species i in length class j :

$$P_{ij} = \sum_{k=1}^{M_i} (n_{ijk} / N_{ik}) / M_i$$

where

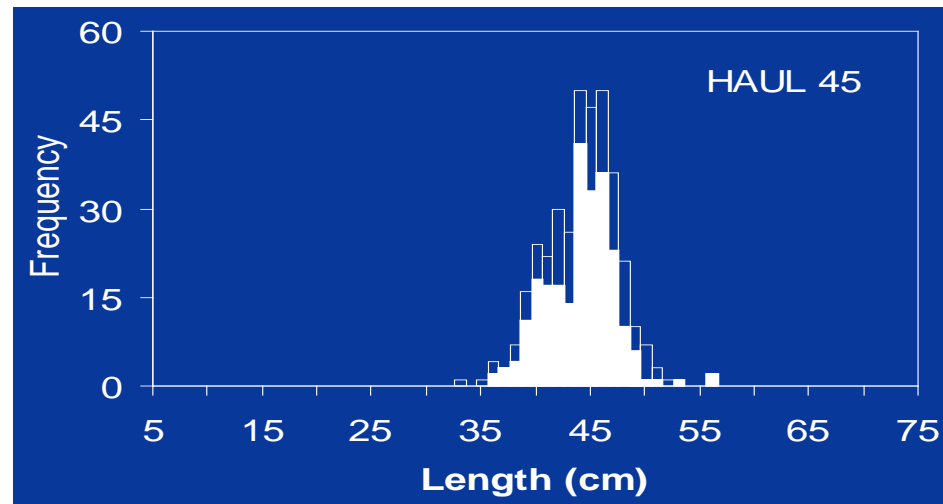
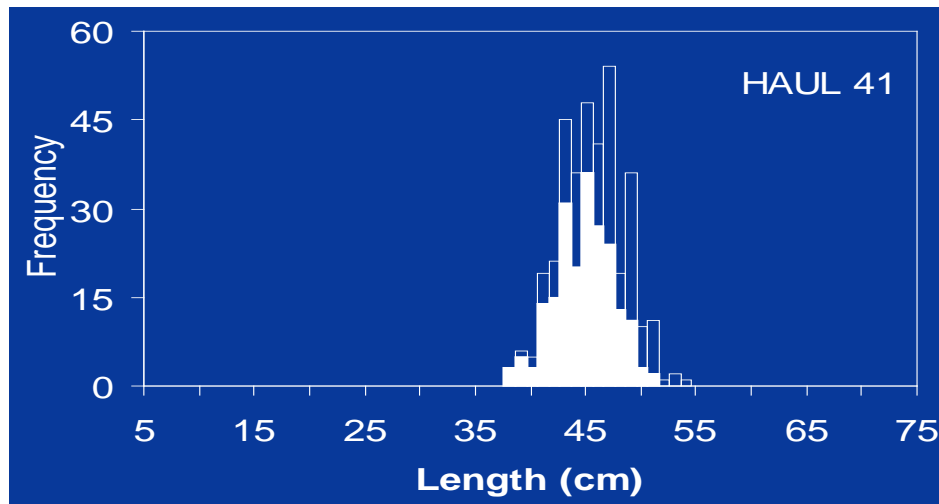
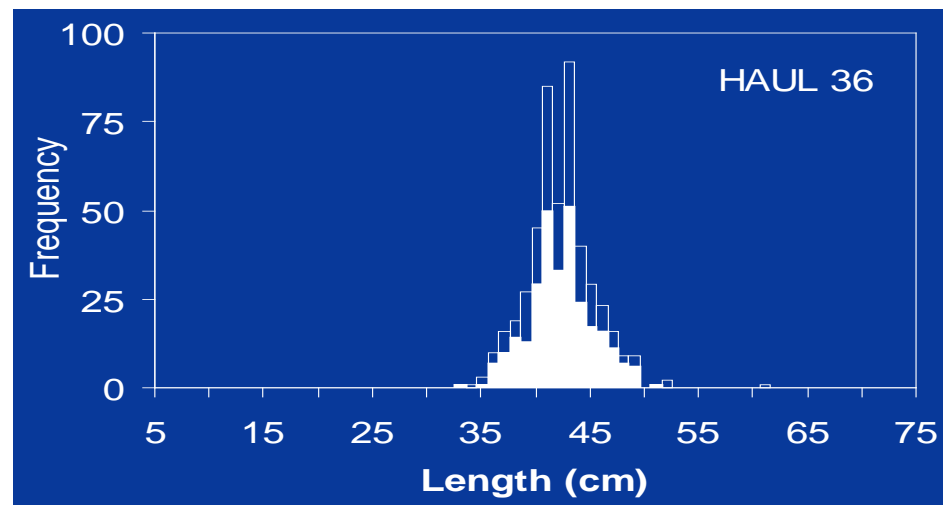
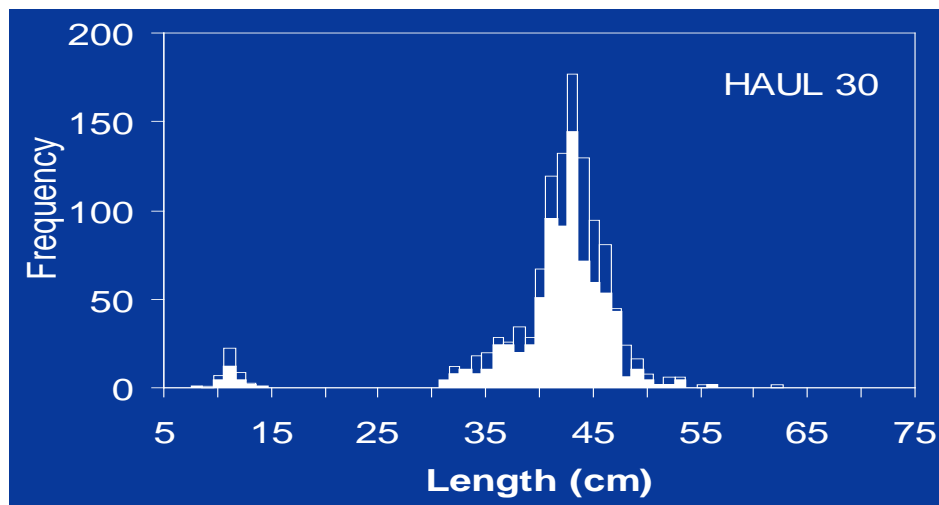
M_i is # hauls, n_{ijk} is number in length class j , and N_{ik} is total # species

- equal weight by catch rate of each species
- weight by echo integrals in area

Length Frequency Data

best case scenario

Walleye Pollock, Bering Sea, 2000



Proportions By Species

Trawl Catches, Mixed Species:

Equal weight (w) to each species i at station k :

$$w_i = \sum_{k=1}^{M_i} (q_{ik} / q_k) / M$$

where

M_i is # hauls, q_{ik} is quantity of i th species at station k , and q_k is total catch

- weight by catch rate
- weight by echo integrals in area

Grouping Homogeneous Regions

- once all transect segments are categorized, homogeneous regions are grouped (typically species and/or length structured)
- can use Kolmogorov-Smirnov test to examine differences in distribution of two trawl catches (Campbell 1974):

D statistic: range 0 (identical) to 1 (no similarity)

if $0.1 < p < 0.3$ then samples same

0.1 threshold to incorporate sampling error

Converting Echo Integrals

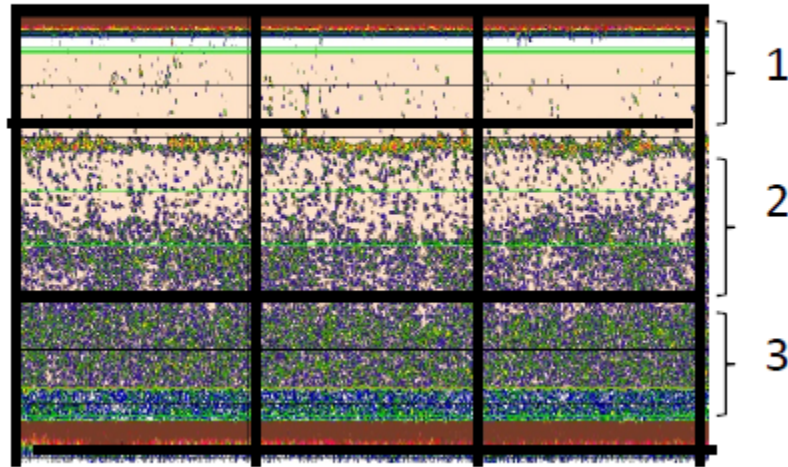
- estimate density of targets ρ_i from the observed echo integrals E_i

$$\rho_i = C_E \frac{E_i}{\langle \sigma_{bsi} \rangle}$$

where C_E is a equipment calibration factor, $\langle \sigma_{bsi} \rangle$ is the mean backscattering cross section of class or species i

Aggregating Backscatter: SVAH

Along-track intervals →



Sum Vertically

Depth layer	Along-track interval S_a [$m^2 m^{-2}$]		
	$1 \cdot 10^{-6}$	$2 \cdot 10^{-6}$	$1 \cdot 10^{-6}$
	$10 \cdot 10^{-6}$	$8 \cdot 10^{-6}$	$8 \cdot 10^{-6}$
	$5 \cdot 10^{-6}$	$5 \cdot 10^{-6}$	$5 \cdot 10^{-6}$

Along-track interval S_a [$m^2 m^{-2}$]			
$16 \cdot 10^{-6}$	$15 \cdot 10^{-6}$	$14 \cdot 10^{-6}$	

Average Horizontally

Average S_a [$m^2 m^{-2}$] in area	
$15 \cdot 10^{-6} m^2 m^{-2}$	

Determining $\langle \sigma_{bsi} \rangle$

In situ measurements (may or may not be direct samples)

- dual or split beam transducer required
- more common in fresh water surveys than in marine

Acoustic size - target size relationship

$$\langle \sigma_{bsi} \rangle = \frac{1}{n} \sum_i f_{ij} 10^{[(a_i + b_i \log L)/10]}$$

$$\langle \sigma_{bsi} \rangle = \frac{1}{n} \sum \left[r^2 I_{bs}(r) 10^{\alpha r/10} \right] / I_o$$

Determining $\langle \sigma_{bs}^i \rangle$

Model estimates (requires acoustic size-animal size (length) relationship):

- numerous models available, most combine anatomical representation with material properties to estimate backscatter

$$\langle \sigma_{bsi} \rangle = \frac{1}{n} \sum RSL * L = \frac{1}{n} \sum \frac{l_{bs}}{L} * L$$

RSL is a non dimensional, linear measure

$$TS = 20\log(RSL) + 20\log(L)$$

* log of the means \neq mean of the logs*

Determining $\langle \sigma_{bs} i \rangle$

Challenge of Multiple species (need direct sample data):

weight by backscatter proportions using catch, catch-rate of each species, or echo integrals in vicinity of catches

Direct biomass estimate:

derive TS -Weight relationship and adjust parameters accordingly (by size class as L-W curves are non-linear)

Example: Pacific Hake (*Merluccius productus*)

-36 dB kg⁻¹ for 50 to 55 cm fish

(Williamson and Traynor 1984)

Abundance Estimates

- calculate densities independently for each EDSU, species or category of target, and depth interval (resolution depends on distributions of animals)
- if randomly distributed then mean density x area of interest
- if contagious then calculate abundance in each region and sum
- partition abundances by length classes
- interpolation among transects: area includes up to $\frac{1}{2}$ the distance between two transects, assume observed density throughout area, sum areal or volumetric estimates
- other methods: contour maps, geostatistical (e.g. kriging)
- extrapolation outside of transects: don't do it! adjust your survey design and transect layout

Abundance/Biomass Estimates by Length

Assume you have:

σ_{bs} for each length class i

frequency f of each length class i

known distance between transects

defined homogeneous regions j

length-weight relationship (a & b constants) for each length class

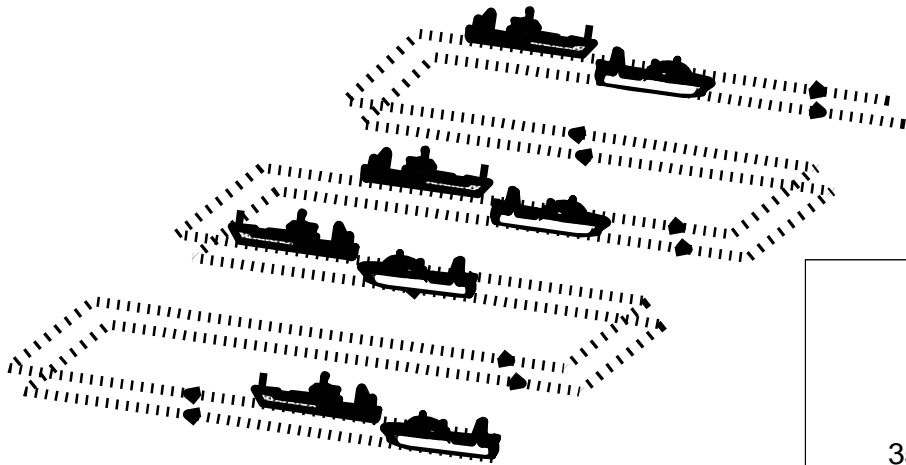
$$\text{Abundance} \quad N_{i,j} = S_{a,j} \times area_j \times \frac{1}{\sigma_{bsi}} \times f_{i,j}$$

$$\text{Biomass} \quad B_{i,j} = N_{i,j} \times a \times (L_{i,j})^b$$

$$Total = \sum_i^n \sum_j^m N_{i,j} \text{ or } B_{i,j}$$

Intercalibration

- use of multiple vessels to obtain a single estimate
- new vessel replacing an older vessel



- quiet vs non-quiet vessel
- ideally amounts will match

See also: De Robertis et al.
2008, 2010a,b,

