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SST variability could be used to build a seasonal outlook for U.S. regional tornado outbreaks
Environmental Research Letters (4.090)

Comment on 'Slow adaptation in the face of rapid warming leads to the collapse of Atlantic cod in the Gulf of Maine'
Science (33.611)

Bycatch avoidance in the west coast ocean salmon fishery: making progress on a complex problem by way of a transdisciplinary approach
ICES Journal of Marine Science (2.377)

A Surface Plasmon Resonance system for the underwater detection of domoic acid
Limnology and Oceanography Methods (2.25)

Long distance dispersal and vertical gene flow in the Caribbean brooding coral *Porites astreoides*
Nature Scientific Reports (5.578)

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Validation of back-calculated body lengths and timing of growth mark deposition in Hawaiian green sea turtles.
Ecology and Evolution (1.658)

Habitat suitability of the Atlantic bluefin tuna by size class: an ecological niche approach
Progress in Oceanography (3.986)

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Identifying copy number variation of the dominant virulence factor msa within genomes of the fish pathogen *Renibacterium salmoninarum*
Microbial Genomics

Life history diversity of steelhead (*Oncorhynchus mykiss*) in two coastal Washington watersheds
Transactions of the American Fisheries Society (1.314)

Pretty good multispecies yield
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A trans-Atlantic examination of haddock (*Melanogrammus aeglefinus*) food habits
Journal of Fish Biology (1.658)

Monitoring Oregon coastal harmful algae: observations and implications of a harmful algal bloom-monitoring project
Harmful Algae (3.874)

Techniques for improving estimates of maturity ogives in groundfish using double-reads and measurement error models
Fisheries Research (1.903)

Assessment of sodium channel mutations in Makah Tribal members of the U.S. Pacific Northwest as a potential mechanism of resistance to paralytic shellfish poisoning
Harmful Algae (3.34)

Residency and movement of juvenile Chinook salmon at multiple spatial scales in a tidal marsh of the Columbia River estuary
Transactions of the American Fisheries Society (1.468)

What influences the worldwide genetic structure of sperm whales (*Physeter macrocephalus*)?
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Life history traits and effective population size in species with overlapping generations revisited: the importance of adult mortality
Heredity (3.805)

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Using Citizen Science Reports to Evaluate Estimates of Surface Precipitation Type
Bulletin of the American Meteorological Society (11.57)

Multifunction phased array radar for aircraft and weather surveillance
Proceedings of the IEEE (6.810)

Project Sagebrush: revisiting the value of the horizontal plume spread parameter σy
Journal of Applied Meteorology and Climatology (2.099)

Is the melting Arctic changing midlatitude weather?
Physics Today (5.648)

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Analysis of Ice-to-Liquid Ratios during Freezing Rain and the Development of an Ice Accumulation Model
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OTHER REPORTS, BOOK CHAPTERS, AND INTERNAL PUBLICATIONS

NOS

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OSTP Report

HIGHLIGHTED ARTICLES

SST variability could be used to build a seasonal outlook for U.S. regional tornado outbreaks
Environmental Research Letters (4.090)
S. K. Lee (OAR/AOML/CIMAS), **A. Wittenberg (OAR/AOML)**, **D. Enfield (OAR/AOML/CIMAS)**, S. Weaver, **C. Wang and R. Atlas (OAR/AOML)**

- This is the first study to show that the most frequently occurring spring sea surface temperature (SST) patterns in the tropical Pacific and North Atlantic are linked to distinctive spatial patterns of the probability of U.S. regional tornado outbreaks. An important implication is that these leading patterns of Pacific and Atlantic SST variability could be used to build a seasonal outlook for U.S. regional tornado outbreaks.
- At present, our capacity to predict U.S. tornado and other severe weather risk does not extend beyond seven days. A seasonal outlook could potentially better help prepare communities and position resources for recovery.

Seasonal predictability of U.S. regional tornado outbreaks may be possible by measuring springtime ENSO phases and the North Atlantic SST tripole variability. At present, our capacity to predict U.S. tornado and other severe weather risk does not extend beyond seven days. A seasonal outlook could potentially better help prepare communities and position resources for recovery.
Expected publication date: Late March or early April 2016

NOAA SCIENTIFIC PUBLICATIONS REPORT
APRIL 11, 2016

Comment on 'Slow adaptation in the face of rapid warming leads to the collapse of Atlantic cod in the Gulf of Maine'
Science (33.611)
M. C. Palmer, J. J. Deroba, C. M. Legault, E. N. Brooks (NMFS/NEFSC)

- The Pershing et al. Science publication concluded that failure to account for temperature induced mortality in the assessment and management of Gulf of Maine Atlantic cod caused overfishing.
- Palmer et al. provide technical comments on the conclusions of the Pershing et al. paper stating that they are based on inappropriate calculations and misinterpretation of the data and that the Pershing et al. paper provides no evidence that a failure to account for temperature led to the persistent overfishing of the Gulf of Maine stock.

Pershing et al. (Reports, 13 November, p.809) concluded that failure to account for temperature in the assessment and management of Gulf of Maine Atlantic cod caused overfishing. We argue the "extra mortality" calculation driving this conclusion is an artifact. Environmental factors affect all stocks but attribution of additional mortality to temperature alone by Pershing et al. is unsupported by the data.
Acceptance date: 25 March 2016

Bycatch avoidance in the west coast ocean salmon fishery: making progress on a complex problem by way of a transdisciplinary approach
ICES Journal of Marine Science (2.377)
S. Otto, S. Simons, J. Stoll, **P. W. Lawson (NMFS/NWFSC)**

- Explores potential of broad new approaches to fisheries management including use of high-resolution data and incorporation of environmental and economic analysis.
- This document is a product of the Transdisciplinary Academy in marine resource sustainability, organized by Lorenzo Ciannelli and Kathryn Sobocinski, and held in Newport for two weeks in August, 2014. It is to be published, along with several other papers from the same Academy, in a special edition of ICES Journal of Marine Science.

The spatio-temporal overlap of morphologically undistinguishable weak and healthy fish stocks is a major concern for the Pacific Northwest troll Chinook salmon fishery. Regular fishery closures have led to major financial losses and socioeconomic hardship in past years calling more and more for alternative

regulatory measures. One promising approach for such complex and pressing socio-ecological challenges is the transition towards transdisciplinary research that spans disciplinary boundaries. This study applies this approach and combines natural and human sciences with stakeholder participation. Based on a unique genetic dataset collected by fishermen, fine-scale patterns of fishing effort, stock distributions and spatial stock overlaps were assessed. Two hot spots of weak Klamath Chinook in the Northern and Central Oregon coast regions were identified and related partly to the topography. This new knowledge was then used to develop a simple bioeconomic model to evaluate costs and benefits of re-allocating effort to avoid bycatch of the weak stock. The developed model is a dynamic, spatially-explicit feedback model, composed of several sub-modules, that runs on a monthly basis. A status quo and an alternative scenario of a 50% cut of Klamath catch were tested with the model. The scenarios show that effort re-allocation can lead to reduction in Klamath catch as well as to increases in net profit but outcomes depend on the distance from the fleet's home port to the new fishing area. The output of the model at its current stage should be regarded strategically, providing a qualitative understanding of the types of best fleet strategies. Despite some challenges in transdisciplinarity discussed in this study and the present limitations to incorporate fine-scale changes of Chinook salmon stock distributions in management regulations, this is the direction that fishery management needs eventually to be headed.
Acceptance date: 16 March 2016

A Surface Plasmon Resonance system for the underwater detection of domoic acid
Limnology and Oceanography Methods (2.25)
F. Colas, M. P. Crassous, S. Laurent, **R.W. Litaker (NOS/NCCOS/CCFHR)**, E. Rinnert, E. Le Gall, M. Lunven, L. Delauney and C. Compère

- A surface plasmon resonance (SPR) transducer for submarine experiments was presented and characterized. Its sensitivity enabled accurate measurement of the refractive index from a boat or at different ocean depths.
- An inhibition assay for detecting a biotoxin in a seawater matrix was then developed and assessed during shipboard experiments.
- The newly developed SPR method has the potential to significantly improve the ability to measure domoic acid (DA) contamination in the environment using gliders, moored arrays, and ships. DA in shellfish is of concern because it causes amnesic shellfish poisoning.

Over the past decade Surface Plasmon Resonance (SPR) techniques have been applied to the measurement of numerous analytes. In this paper, an SPR biosensor system deployed from an oceanographic vessel was used to measure dissolved domoic acid (DA), a common and harmful phycotoxin produced by certain microalgae species belonging to the genus Pseudo-nitzschia. During the biosensor deployment, concentrations of Pseudo-nitzschia cells were very low over the study area and measured domoic acid concentrations were below detection. However, the in situ operational detection limit of the system was established using calibrated seawater solutions spiked with DA. The system could detect the toxin at concentration as low as to 0.1 ng.mL-1 and presented a linear dynamic range from 0.1 – 2.0 ng.mL-1. This sensor showed promise for in situ detection of DA.
Published: 31 March 2016
Available online: http://onlinelibrary.wiley.com/wol1/doi/10.1002/lom3.10104/full

Long distance dispersal and vertical gene flow in the Caribbean brooding coral Porites astreoides
Nature Scientific Reports (5.578)
X. M. Serrano (OAR/AOML), I. Baums, T. B. Smith, R. J. Jones, T. L. Shearer, and A. C. Baker

- Shallow-reef corals in Florida are more closely related to their shallow-water counterparts over a thousand miles away than they are to deep-water corals on the same reef
- Shallow-water corals that die due to bleaching or other damage will not locally recruit coral larvae from deeper waters of the same reef, which could slow recovery

To date, most assessments of coral connectivity have emphasized long-distance horizontal dispersal of propagules from one shallow reef to another. The extent of vertical connectivity, however, remains largely understudied. Here, we used newly-developed and existing DNA microsatellite loci for the brooding coral *Porites astreoides* to assess patterns of horizontal and vertical connectivity in 590 colonies collected from three depth zones (≤10 m, 15–20 m and ≥25 m) at sites in Florida, Bermuda and the U.S. Virgin Islands (USVI). We also tested whether maternal transmission of algal symbionts (*Symbiodinium* spp.) might limit effective vertical connectivity. Overall, shallow *P. astreoides* exhibited high gene flow between Florida and USVI, but limited gene flow between these locations and Bermuda. In contrast, there was significant genetic differentiation by depth in

Florida (Upper Keys, Lower Keys and Dry Tortugas), but not in Bermuda or USVI, despite strong patterns of depth zonation in algal symbionts at two of these locations. Together, these findings suggest that *P. astreoides* is effective at dispersing both horizontally and vertically despite its brooding reproductive mode and maternal transmission of algal symbionts. In addition, these findings might help explain the ecological success reported for *P. astreoides* in the Caribbean in recent decades.
Published: 22 February 2016
Available online: http://www.nature.com/articles/srep21619

ADDITIONAL ARTICLES

NMFS Publications

Validation of back-calculated body lengths and timing of growth mark deposition in Hawaiian green sea turtles
Ecology and Evolution (1.658)
L. Goshe, M. Snover, **A. Hohn (SEFSC-Beaufort)**, G. Balazs

- Use of tetracycline marked bones allowed calibration of use of growth-layer thickness as a proxy for carapace length in green sea turtles.
- Use of growth-layers as an indicator of size-at-size allows for back-calculation of growth and correlation of growth variability to other factors, such as environmental conditions or animal health.
- Results strengthen support for use of growth-layers in bones for sea turtles for age estimation and growth.

1. Somatic growth rate data for wild sea turtles can provide insight into life-stage durations, time maturation, and total lifespan. When appropriately validated, the technique of skeletochronology allows prior growth rates of sea turtles to be calculated with considerably less time and labor than required by mark-recapture studies.
2. We applied skeletochronology to 10 dead, stranded green turtles *Chelonia mydas* that had previously been measured, tagged, and injected with oxytetracycline (OTC) during mark-recapture studies in Hawaii for the purpose of validating skeletochronological analysis. We the validity of back-calculating carapace lengths (CLs) from diameters of lines of arrested growth (LAGs), which mark the outer boundaries of individual skeletal growth increments. This validation was achieved by comparing CLs estimated from measurements

of the LAG proposed to have been deposited closest to the time of tagging to actual CLs measured at the time of tagging. Measureable OTC-mark diameters in five turtles also allowed us to investigate the time of year when LAGs are deposited.

3. We found no significant difference between CLs measured at tagging and those estimated through skeletochronology, which supports calculation of somatic growth rates by taking the difference between CLs estimated from successive LAG diameters in humerus bones for this species. Back-calculated CLs associated with the OTC mark and growth mark deposited closest to tagging indicated that annual LAGs are deposited in the spring.
4. The results of this validation study increase confidence in utilization of skeletochronology to rapidly obtain accurate age and growth data for green turtles.

Acceptance date: 13 March 2016

Habitat suitability of the Atlantic bluefin tuna by size class: an ecological niche approach

Progress in Oceanography (3.986)

J. Druon, PhD, J. Fromentin, A. Hanke, H. Arrizabalaga, D. Damalas, V. Tičina, G. Quílez-Badia, K. Ramirez, I. Arregui, G. Tserpes, P. Reglero, M. Deflorio, I. Oray, S. F. Karakulak, P. Megalofonou, T. Ceyhan, L. Grubišić, B. R. MacKenzie, **J. Lamkin (SEFSC Miami)**, P. Afonso, P. Addis

- This model predicts a wider temperature tolerance for larger fish allowing them to feed in the northern – high chlorophyll levels – latitudes up to the Norwegian Sea in the eastern Atlantic and to the Gulf of Saint Lawrence in the western basin.
- Other secondary potential spawning grounds not supported by observations were predicted in the Azores area and off Morocco to Senegal during July and August when extrapolating the model settings from the Gulf of Mexico into the North Atlantic.

An ecological niche modelling (ENM) approach was used to predict the potential feeding and spawning habitats of small (5-25kg, only feeding) and large (> 25kg) Atlantic bluefin tuna (ABFT), *Thunnus thynnus*, in the Mediterranean Sea, the

North Atlantic and the Gulf of Mexico. The ENM was built bridging knowledge on ecological traits of ABFT (e.g. temperature tolerance, mobility, feeding and spawning strategy) with patterns of selected environmental variables (chlorophyll-a fronts and concentration, sea surface current and temperature, sea surface height anomaly) that were identified using an extensive set of precisely geo-located presence data. The results highlight a wider temperature tolerance for larger fish allowing them to feed in the northern – high chlorophyll levels - latitudes up to the Norwegian Sea in the eastern Atlantic and to the Gulf of Saint Lawrence in the western basin. Permanent suitable feeding habitat for small ABFT was predicted to be mostly located in temperate latitudes in the North Atlantic and in the Mediterranean Sea, as well as in subtropical waters off northwest Africa, while summer potential habitat in the Gulf of Mexico was found to be unsuitable for both small and large ABFTs. Potential spawning grounds were found to occur in the Gulf of Mexico from March-April in the southeast to April-May in the north, while favorable conditions evolve in the Mediterranean Sea from mid-May in the eastern to mid-July in the western basin. Other secondary potential spawning grounds not supported by observations were predicted in the Azores area and off Morocco to Senegal during July and August when extrapolating the model settings from the Gulf of Mexico into the North Atlantic. The presence of large ABFT off Florida and the Bahamas in spring was not explained by the model as is; however, the environmental variables other than the sea surface height anomaly appeared to be favorable for spawning in part of this area. Defining key spatial and temporal habitats should further help in building spatially-explicit stock assessment models, thus improving the spatial management of bluefin tuna fisheries.

Acceptance date: 11 January 2016
Available online:
http://www.sciencedirect.com/science/article/pii/S0079661116000070

Identifying copy number variation of the dominant virulence factor msa within genomes of the fish pathogen Renibacterium salmoninarum
Microbial Genomics
O. Brynildsrud, S. Gulla, E. J. Feil, S. F. Nørstebø, **L. D. Rhodes (NWFSC)**

- This paper suggests that two known dominant virulence factors for bacterial kidney disease in salmonids may be linked. Geographic origin seems to be a stronger predictor of expression of these genes than phylogeny.

Renibacterium salmoninarum is the causative agent of bacterial kidney disease (BKD), an important disease of farmed and wild salmonid fish worldwide. In spite of the wide spatiotemporal distribution for this disease and habitat pressures ranging from natural environment to aquaculture and rivers to marine environments, little variation has been observed in the *R. salmoninarum* genome. Here we use the coverage depth from genomic sequencing and real-time quantitative PCR to detect copy number variation (CNV) among the genes of *R. salmoninarum*. CNV was limited to the known dominant virulence factors *msa* and p22. Among 68 isolates representing the United Kingdom, Norway, and North America, the *msa* gene ranged from two to five identical copies and the *p22* gene ranged from one to five copies. CNV for these two genes co-occurred, suggesting they may be functionally linked. Isolates carrying CNV were phylogenetically restricted, and originated predominantly from sites in North America, rather than the United Kingdom or Norway. Although both phylogenetic relationship and geographic origin were found to correlate with CNV status, geographic origin was a much stronger predictor than phylogeny, suggesting a role for local selection pressures in the repeated emergence and maintenance of this trait.
Acceptance date: 17 March 2016
Available online:
http://mgen.microbiologyresearch.org/content/journal/mgen/10.1099/mgen.0.000055

Life history diversity of steelhead (Oncorhynchus mykiss) *in two coastal Washington watersheds*

Transactions of the American Fisheries Society (1.314)

J. E. Hall, P. Roni, T. R. Bennett, J. R. McMillan, **K. Hanson, G. R. Pess**, R. E. Moses, M. McHenry, W. Ehinger **(NMFS/NWFSC)**

- Life history diversity is an important, and often overlooked, factor that should be considered in developing Steelhead population management and recovery strategies.
- Our results revealed that migration timing matters given that adults were only produced by age-1 or older migrants, and that the production of migrants and age at migration were inversely related. In addition, our results suggest that the probability of expressing an age-0 migration timing is increasing over time.
- Therefore, management or recovery strategies that rely solely on migration production without considering migrant timing and subsequent return rates would be ill-advised in the study population.

Understanding the factors that influence *Oncorhynchus mykiss* life history diversity is of increasing importance given recent declines in anadromous life history types among Northeastern and Northwestern Pacific Ocean populations. To examine life history diversity and the factors that relate to the expression of life history trajectories, we used passive integrated transponder (PIT) tags implanted in juvenile *O. mykiss* to monitor the migration, growth, and survival of *O. mykiss* in two watersheds. We determined that East and West Twin *O. mykiss* populations were dominated by anadromous life history types with very little expression of resident life histories. While most migrants leave the river in their first fall or winter, these life history trajectories did not produce any adult returns during our study. Only fish that remained in the river for at least one year produced adults, with nearly all of the adults being produced by fish that reared for at least two or three years in the river. Our results indicate a positive relationship between fish length and the probability of survival to migration, but the probability of a fish remaining in the river for more than one year decreased with increasing length at tagging among fish that became migrants. This indicates the fish that achieve larger body sizes earlier in life are more likely to become migrants but the larger of these are more likely to leave the river in their first year and will ultimately have a lower chance of producing an adult. Our results also indicate river flow and temperatures may be related to observed patterns in survival and migration timing,

and that these are likely linked to observed variations in fish size that appear to be the strongest indicators for both survival to migration and migration timing.
Acceptance date: 21 March 2016

Pretty good multispecies yield
ICES Journal of Marine Science (2.525)
A. Rindorf, C. M. Dichmont, **P. S. Levin (NWFSC)**, P. M. Mace, S. Pascoe, R. Prellezo, A. E. Punt, D. Reid, R. Stephenson, C. Ulrich, M. Vinther, L. Worsoe Clausen

- "Pretty Good Mutltispecies Yield" provides a safe operating space for management that adheres to the principles of MSY while allowing the consideration of other aspects to be included in operational management advice in both data-rich and data-limited situations. PGMY also provides a way to integrate advice across stocks, avoiding clearly infeasible management combinations and hopefully increasing confidence in scientific advice.

MSY-principles for marine fisheries management reflect a focus on obtaining continuing high catches to provide food and livelihoods to humanity, while not compromising ecosystems. However, maintaining healthy stocks to provide the Maximum Sustainable Yield on a single species basis does not ensure that broader ecosystem, economic and social objectives are addressed. We investigate how the principles of a Pretty Good Yield range of fishing mortalities assumed to provide more than 95% of the average yield for a single stock can be expanded to a Pretty Good Multispecies Yield (PGMY) space and further to pretty good multidimensional yield to accommodate situations where the yield from a stock affects the ecosystem, economic and social benefits or sustainability. We demonstrate in a European example that PGMY is a practical concept that can address some ecosystem, economic and social trade-offs encountered in different parts of the PGMY space. As PGMY provides a safe operating space for management that adheres to the principles of MSY, it allows the consideration of other aspects to be included in operational management advice in both data-rich and data-limited situations. PGMY furthermore provides a way to integrate advice

across stocks, avoiding clearly infeasible management combinations and hopefully increasing confidence in scientific advice.
Acceptance date: 24 March 2016

A trans-Atlantic examination of haddock (Melanogrammus aeglefinus) *food habits*
Journal of Fish Biology (1.658)
J. C. Tam, **J. S. Link , S. I. Large**, B. Bogstad, A. Bundy, A. M. Cook, G. E. Dingsør, A. Dolgov, D. Howell, A. Kempf, J. K. Pinnegar, A. Rindorf, S. Schückel, A. F. Sell, **B. E. Smith (NMFS/NEFSC)**

- Haddock in North Atlantic ecosystems consistently consume echinoderms as part of their diet. In some ecosystems, echinoderms are a dominant food item for haddock.
- We discuss the energetic consequences of this prey choice, and also the possible reasons why haddock would choose a seemingly low energy prey.
- Research adds to knowledge of an important commercial fish in the North Atlantic.

Haddock (*Melanogrammus aeglefinus*) is a commercially and ecologically important gadoid in the food webs and economies of regional ecosystems across the North Atlantic. *Melanogrammus aeglefinus* is reported to be primarily piscivorous in some cases and primarily an echinoderm feeder in others. Often, the species exhibits ontogenetic dietary shifts, focusing on a specific prey at small sizes and on different prey at larger sizes. Here we explore and contrast the food habits of *M. aeglefinus* across multiple northeastern and northwestern Atlantic ecosystems, using databases that span multiple decades. The results show that, among all ecosystems, echinoderms are a consistent part of *M. aeglefinus* diet, but patterns do emerge regarding where and when *M. aeglefinus* primarily eat fishes versus echinoderms. *M. aeglefinus* does not regularly exhibit the increase in piscivory with ontogeny that other gadoids often show, in several ecosystems there is a lower occurrence of piscivory. There is an apparent inverse relationship between the consumption of fishes and echinoderms in *M. aeglefinus* over time, where certain years show high levels of one prey item and low levels of another. We view this apparent binary choice as part of a gradient of prey options, contingent upon a suite of factors external to *M. aeglefinus* dynamics. We discuss the energetic consequences of this prey choice, noting that in some instances it may not be a choice at all.

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Acceptance date: 18 March 2016

Monitoring Oregon coastal harmful algae: observations and implications of a harmful algal bloom-monitoring project
Harmful Algae (3.874)
S. M. McKibben, K. S. Watkins-Brandt, A. M. Wood, M. Hunter, Z. Hunter, A. Hopkins, X. Du, **B. T. Le Eberhart, B. T. Peterson** , and A. E. White
(NMFS/NWFSC)

- Increased knowledge on HAB species through monitoring
- Enhance ability to make decision based on early warning of HAB species

The planktonic biodiversity and metabolism of the upper ocean is modulated by local to basin-scale physical and chemical processes that occur over daily and weekly to inter-decadal timescales; these collective processes regulate phytoplankton community structure and bloom initiation, including harmful algal blooms (HABs). Here we summarize 5 years of Oregon coast HAB monitoring (2007-2012) and discuss the most significant HAB events during this period relative to potential causal factors. A 2009-2010 basin-scale warming event was associated with changes in local conditions and notable HAB events: coastwide shellfish harvesting closures due to saxitoxins (STX) in the fall of 2009 and closure of central Oregon coast shellfish harvesting due to elevated levels of domoic acid (DA) in the summer of 2010. The warming event began in the latter part of the 2009 upwelling season, enhancing late-summer conditions that often select for dinoflagellate growth. The warming persisted through June 2010, delaying the seasonal transition to upwelling-favorable conditions. We hypothesize that a delay in nutrient supply stressed the phytoplankton community, inducing DA production by *Pseudo-nitzschia* spp. In regards to HAB monitoring in upwelling regimes, we suggest that (1) water column concentrations of pDA > 10^3 ng L^{-1} can be used as a threshold for early-warning of shellfish DA toxicity and (2) approximately bi-weekly, or shorter, monitoring of *Alexandrium* in the surf zone and/or offshore can provide advance notice of STX contamination of shellfish. Both metrics are particularly useful if coupled with monitoring for onshore flow, which occurs during downwelling/relaxation events and facilitates interaction between offshore waters and shellfish.
Publication date: 11 November 2015
Available online:
http://www.sciencedirect.com/science/article/pii/S1568988315001390

NOAA SCIENTIFIC PUBLICATIONS REPORT
APRIL 11, 2016

Techniques for improving estimates of maturity ogives in groundfish using double-reads and measurement error models

Fisheries Research (1.903)

M. A. Head, G. L. Stokes, **J. T. Thorson, A. A. Keller (NMFS/NWFSC)**

- Accurate estimates of size and age at maturity are important to management models that estimate spawning biomass.
- Flexible models that incorporate multiple covariates and have the ability to account for reader precision will reduce uncertainty in our overall estimates.
- Double reads of fish ovary samples might not be essential to conduct routinely, it should be standard practice when training a new reader or beginning a new species. This had not been recorded in previous literature for histological ovarian reads, but is standard procedure for reading of fish otoliths.

The reproductive output of a population depends upon physiological factors, including maturation rates and fecundity –at-size and –at-age, as well as the rate at which post-maturation females fail to spawn (i.e. skipped spawning). These rates are increasingly included in stock assessment models, and are thought to change over time due to harvest and environmental factors. Thus, it is important to accurately estimate maturation and skipped spawning rates while also including information on imprecision. For this task, we developed a new double-read and measurement-error modeling protocol for estimating maturity that is based on the use of multiple histological reads of ovaries to account for reader error caused by poorly prepared slides, nuclear smear, and early yolk development. Application to three U.S. West Coast groundfishes (Pacific hake *Merluccius productus*, darkblotched rockfish *Sebastes crameri*, and canary rockfish *Sebastes pinniger*) indicates that reader uncertainty is strongly predictive of reader error rates. Results also show differences in rates of skipped spawning among species, which should be further investigated. We recommend that future maturity studies record reader certainty, use models that incorporate covariates into the analysis, and conduct an initial double reader analysis. If readers exhibit little variation, then double reads may not be necessary. In addition, slide quality should also be recorded, so that future studies do not confuse this with reader imprecision. This improved protocol will assist in estimating life history, as well as environmental, and anthropogenic effects on maturity.

Acceptance date: 2 March 2016

NOAA SCIENTIFIC PUBLICATIONS REPORT
APRIL 11, 2016

Assessment of sodium channel mutations in Makah Tribal members of the U.S. Pacific Northwest as a potential mechanism of resistance to paralytic shellfish poisoning

Harmful Algae (3.43)

N. G. Adams, A. Robertson, L. M. Grattan, S. Pendelton, S. Roberts, J. K. Tracy, **V. L. Trainer (NMFS/NWFSC)**

- Skeletal muscle sodium channel mutations that could confer resistance to paralytic shellfish toxins were not observed in a human population that historically consumed shellfish as a subsistence food item

The Makah Tribe of Neah Bay, Washington, has historically relied on the subsistence harvest of coastal seafood, including shellfish, which remains an important cultural and ceremonial resource. Tribal legend describes visitors from other tribes that died from eating shellfish collected on Makah lands. These deaths were believed to be caused by paralytic shellfish poisoning, a human illness caused by ingestion of shellfish contaminated with saxitoxins, which are produced by toxin-producing marine dinoflagellates on which the shellfish feed. These paralytic shellfish toxins include saxitoxin, a potent Na^+ channel antagonist that binds to the pore region of voltage gated Na^+ channels. Amino acid mutations in the Na^+ channel pore have been demonstrated to confer resistance to saxitoxin in softshell clam populations exposed to paralytic shellfish toxins present in their environment. Because of the notion of resistance to paralytic shellfish toxins, we aimed to determine if a resistance strategy was possible in humans with historical exposure to toxins in shellfish. We collected, extracted and purified DNA from buccal swabs of 83 volunteer Makah tribal members and sequenced the skeletal muscle Na^+ channel ($Na_v1.4$) at nine loci to characterize potential mutations in the relevant saxitoxin binding regions. No mutations of these specific regions were identified after comparison to a reference sequence. This study suggests that any resistance of Makah Tribal members to saxitoxin is not a function of $Na_v1.4$ modification but may be due to mutations in neuronal or cardiac sodium channels or some other mechanism unrelated to sodium channel function.

Acceptance date: 10 March 2016

Residency and movement of juvenile Chinook salmon at multiple spatial scales in a tidal marsh of the Columbia River estuary

Transactions of the American Fisheries Society (1.468)

R. A. McNatt, D. L. Bottom, S. A. Hinton (NMFS/NWFSC)

- This is the first study the authors know of that examines salmon estuarine residence time at multiple scales.
- Tidal marshes appear to be more important than was known for salmon growth and rearing.
- The authors found that juvenile salmon will move against tide to enter small channels for foraging.

Juvenile salmon use of the Columbia River estuary is garnering more attention as managers look to improve salmon survival through estuary restoration. Studies have shown that juvenile salmon are abundant in shallow-water habitats within the Columbia River estuary, but information regarding how juveniles exploit specific estuarine habitats is lacking. In this study we use a combination of physical marks and PIT-tag technology to record residence time, movement, and growth of juvenile Chinook Salmon within an emergent marsh of the Columbia River estuary during 2005, 2006, and 2008. We document marsh-scale residency and movement within the marsh complex and channel-scale residency and movement within two small secondary channels. Many juvenile Chinook Salmon remained in the marsh for two to four weeks and increased in size by 10–20 mm, with an average growth rate of 0.53 mm/d. Salmon entered secondary channels most frequently in late afternoon and occasionally against the tide. Our results indicate that subyearling Chinook Salmon take advantage of shallow estuarine habitat to a greater extent than previously documented in the Columbia River.

What influences the worldwide genetic structure of sperm whales (Physeter macrocephalus)*?*
Molecular Ecology (6.494)
A. Alexander, D. Steel, K. Hoekzema, **S. L. Mesnick (NMFS/SWFSC)**, D. Engelhaupt, I. Kerr, R. Payne, and C. S. Baker

- Global genetic analysis of sperm whale population structure reveals a worldwide population expansion followed by rapid assortment due to female social organization
- Sperm whales are both geographically and socially philopatric, but their relative importance differs by sex and ocean
- These data are useful in identifying units to conserve in highly mobile, long-lived, highly social, species with few barriers to dispersal

The interplay of natural selection and genetic drift, influenced by geographic isolation, mating systems, and population size, determines patterns of genetic

diversity within species. The sperm whale provides an interesting example of a long-lived species with few geographic barriers to dispersal. Worldwide mtDNA diversity is relatively low, but highly structured among geographic regions and social groups, attributed to female philopatry. However, it is unclear if this female philopatry is due to geographic regions or social groups, or how this might vary on a worldwide scale. To answer these questions, we combined mtDNA information for 1,091 previously published samples with 542 newly obtained DNA profiles (394 bp mtDNA, sex, 13 microsatellites) including the previously un-sampled Indian Ocean, and social group information for 541 individuals. We found low mtDNA diversity (π=0.430%) reflecting an expansion event <80,000 years bp, but strong differentiation by ocean, among regions within some oceans, and among social groups. In comparison, microsatellite differentiation was low at all levels, presumably due to male-mediated gene flow. A hierarchical AMOVA showed that regions were important for explaining mtDNA variance in the Indian Ocean, but not Pacific, with social group sampling in the Atlantic too limited to include in analyses. Social groups were important in partitioning mtDNA and microsatellite variance within both oceans. Therefore, both geographic and social philopatry influence genetic structure in the sperm whale, but their relative importance differs by sex and ocean, reflecting breeding behavior, geographic features, and perhaps a more recent origin of sperm whales in the Pacific. By investigating the interplay of evolutionary forces operating at different temporal and geographic scales, we show that sperm whales are perhaps a unique example of a worldwide population expansion followed by rapid assortment due to female social organization.
Published: 2 April 2016
Available online: http://www.ncbi.nlm.nih.gov/pubmed/27037911

Life history traits and effective population size in species with overlapping generations revisited: the importance of adult mortality
Heredity (3.805)
R. S. Waples (NMFS/NWFSC)

- Effective population size (Ne) affects the rates of all evolutionary processes
- Ne is complicated to calculate in species with overlapping generations (which comprise most of the species under NOAA stewardship)
- Shows how Ne and the ratio Ne/N can be estimated based on simple life history traits (the magnitude of adult mortality and age at maturity)

The relationship between life-history traits and the key eco-evolutionary parameters Ne and Ne/N is revisited for iteroparous species with overlapping generations, with a focus on the annual rate of adult mortality (d). Analytical methods based on populations with arbitrarily long adult lifespans are used to evaluate the influence of d on Ne, Ne/N, and the factors that determine these parameters: adult abundance (N), generation length (T), age at maturity (alpha), the ratio of variance to mean reproductive success in one season by individuals of the same age (phi), and lifetime variance in reproductive success of individuals in a cohort (Vk*). Although the resulting estimators of N, T, and are upwardly biased for species with short adult lifespans, the estimate of Ne/N is largely unbiased because biases in T are compensated for by biases in Vk* and N. For the first time, the contrasting effects of T and Vk* on Ne and Ne/N are jointly considered with respect to d and phi. A simple function of d and alpha based on the assumption of constant vital rates is shown to be a robust predictor (R2 = 0.78) of Ne/N in an empirical dataset of life tables for 63 animal and plant species with diverse life histories. Results presented here should provide important context for interpreting the surge of genetically-based estimates of Ne that has been fueled by the genomics revolution.
Acceptance date: 30 March 2016

OAR Publications

Using Citizen Science Reports to Evaluate Estimates of Surface Precipitation Type
Bulletin of the American Meteorological Society (11.57)
Sheng Chen, **Jonathan J. Gourley**, Yang Hong, Qing Cao, Nicholas Carr, Pierre-Emmanuel Kirstetter, **Jian Zhang**, Zac Flamig **(OAR/NSSL)**

- The Multi-Radar Multi-Sensor (MRMS) system provides precipitation rate and type products, including estimating precipitation rate at the surface.
- This is the first paper to comprehensively evaluate the MRMS rain-snow product using mPING crowd-sourced observations.
- Results indicate that the MRMS was slightly better at predicting rain than snow at the surface and that modification to the MRMS algorithm are needed.

Consistency in results from city to city give an indication that the citizen science reports of rain and snow from the meteorological Phenomena Identification Near the Ground app (mPING) provide useful information about the quality of the

MRMS precipitation type algorithm. The MRMS surface precipitation type algorithm has a slight propensity to produce too much rain where there is snow; this suggests some modifications are needed to the temperature thresholds and motivates probabilistic approaches.
Publication date: 14 March 2016
Available online: http://journals.ametsoc.org/doi/pdf/10.1175/BAMS-D-13-00247.1

Multifunction phased array radar for aircraft and weather surveillance
Proceedings of the IEEE (6.810)
J. Stailey, K. D. Hondl (OAR/NSSL)

- Multifunction Phased Array Radar (MPAR) is a multiagency initiative to investigate the feasibility of replacing aircraft surveillance and weather radar fleets in the United States with a network of phased array radars based on a single, scalable networked array architecture.

Multifunction phased array radar (MPAR) is a multiagency initiative to investigate the feasibility of replacing the aircraft surveillance and weather radar fleets in the US with a network of phased array radars based on a single, scalable architecture. The Federal Aviation Administration and the National Atmospheric and Oceanic Administration have been collaborating on MPAR risk reduction, which focuses on reducing cost, ensuring that the technology could accomplish all the missions within radar timelines, and developing dual polarization (dual pol) capability. The agencies have completed siting, cost, spectrum, dual pol, and back end studies, among others; have developed three dual pol architectures; and are building operational arrays to demonstrate that the technology can meet the basic needs of the agencies.
Publication date: March 2016
Available Online:
http://ieeexplore.ieee.org/xpl/articleDetails.jsp?arnumber=7393756

Project Sagebrush: revisiting the value of the horizontal plume spread parameter σy
Journal of Applied Meteorology and Climatology (2.099)

D. Finn, K. L. Clawson, R. M. Eckman, H. Liu, E. S. Russell, Z. Gao, S. Brooks **(OAR/ARL),**

- The most readily apparent and significant result from the study is that the horizontal plume spread was much greater than reported in many older tracer field experiments. The paper discusses how the cause of this is probably related, at least in part, to the modern tracer release and sampling schemes used in Project Sagebrush compared to many of the older experiments.

The first phase of an atmospheric tracer experiment program, designated Project Sagebrush, was conducted on the Idaho National Laboratory in October, 2013. The purpose was to re-evaluate the results of classical field experiments in short-range plume dispersion (e.g., Project Prairie Grass) using newer technologies available for measuring both turbulence levels and tracer concentrations. All releases were conducted during the daytime with atmospheric conditions ranging from neutral to unstable. The key finding was that the values of the horizontal plume spread parameter σy tended to be larger, by up to a factor of about two, than those measured in many previous field studies. The discrepancies tended to increase with downwind distance. The values of the ratio σy/σθ, where σθ is the standard deviation of the horizontal wind direction, also trend near the upper limit or above the range of values determined in earlier studies. There was also evidence to suggest that the value of σy began to behave independently of σθ for σθ >18o. It was also found that the commonly accepted range of values for σθ in different stability conditions might be limiting, at best, and possibly unrealistically low, especially at night in low wind speeds. The results raise questions about the commonly accepted magnitudes of σy derived from older studies. These are used in the parameterization and validation of both older stability class dispersion models as well as newer models based on Taylor's equation and modern PBL theory.

Publication date: 29 March 2016
Available online: http://journals.ametsoc.org/doi/10.1175/JAMC-D-15-0283.1

Is the melting Arctic changing midlatitude weather?
Physics Today (5.648)
J.E. Overland (OAR/PMEL)

- This article reviews recent work on the possible effects of Arctic warming and sea ice decline on mid-latitude jet stream circulation patterns, a topic of much debate in the climate science community.
- The author discusses whether jet stream variability and associated extreme cold events in the eastern US and Europe in recent years can be conclusively linked to Arctic warming.

This past year the average surface temperature of Arctic air was higher than it has ever been—about 2.5 °C above the value measured at the beginning of the 20th century. Global temperatures have also risen over the past century, but the upward trend has not been uniform. Since 1980 the Arctic's temperature rose at a rate more than double that of the Northern Hemisphere average—a relative increase referred to as Arctic amplification. Changes to the Arctic environment, driven by the warming of ocean and atmosphere, are stark and pervasive: thinning sea ice, retreating glaciers, thawing permafrost, and greening tundra are among the numerous trends that are apparent in today's Arctic. The region has lost two-thirds of its volume of sea ice during the past three decades. The Arctic snow cover in late spring has similarly suffered a large decline. As the sea ice continues to thin, it exposes an ever-growing area of open water to solar radiation. Because of the large difference in albedo between ice and water, less snow and ice covering the ocean during the Arctic's long summer days means that more sunlight is absorbed.
Published: March 2016
Available online:
http://scitation.aip.org/content/aip/magazine/physicstoday/article/69/3/10.1063/PT.3.3107

NOAA SCIENTIFIC PUBLICATIONS REPORT
APRIL 11, 2016

NWS Publications

Analysis of Ice-to-Liquid Ratios during Freezing Rain and the Development of an Ice Accumulation Model

Weather and Forecasting (1.860)

K. Sanders and B. Barjenbruch (NWS Topeka, KS)

- The authors determine mean and median ice-to-liquid ratios for 1,255 freezing rain events and develop a model to predict ice accumulations using other commonly predicted meteorological variables.
- For analyzed events, precipitation rate showed the strongest correlation to ice-to-liquid ratios, with heavier precipitation rates yielding lower ice-to-liquid ratios. The greatest icing efficiency occurred with wet-bulb temperatures just below freezing.

Significant freezing rain or drizzle occurs in about 24% of winter weather events in the continental United States. Proper preparation for these freezing rain events requires accurate forecasts of ice accumulation on various surfaces. The Automated Surface Observing System (ASOS) has become the primary surface weather observation system in the United States, and more than 650 ASOS sites have implemented an icing sensor as of March 2015. ASOS observations that included ice accumulation were examined from January 2013 through February 2015. The data chosen for this study consisted of 60-minute periods of continuous freezing rain with precipitation rates $\geq$ 0.5 mm h-1 (0.02 in h-1), and greater than a trace of ice accumulation, yielding a dataset of 1,255 hours of observations. Ice-to-liquid ratios were calculated for each 60-minute period and analyzed with 60-minute mean values of temperature, wet-bulb temperature, wind speed, and precipitation rate. The median ratio for elevated horizontal ice accumulation was 0.73:1, with a 25th percentile of 0.50:1 and 75th percentile of 1.0:1. Strong correlations were identified between ratio and precipitation rate, with correlations to wind speed and wet-bulb temperature also identified. These results were used to develop a multi-variable freezing rain accumulation model (FRAM) for use in predicting ice accumulation using commonly forecast input variables. FRAM performed superior to other commonly used forecast methods when tested on 20

randomly chosen icing events, with a mean absolute error (MAE) of 1.19 mm (0.047 in), and bias of -0.01 mm (-0.0004 in).
Publication date: 25 March 2016
Available online: http://journals.ametsoc.org/doi/abs/10.1175/WAF-D-15-0118.1

CROSS LINE OFFICE ARTICLES

A North American hourly assimilation and model forecast cycle: the rapid refresh
Monthly Weather Review (2.758)
Benjamin, S.G. (OAR/ESRL), Weygandt, S.S. (OAR/ESRL), Brown, J.M. (OAR/ESRL), Hu, M. (OAR/ESRL), Alexander, C. (OAR/ESRL), Smirnova, T.G. (OAR/ESRL), Olson, J.B. (OAR/ESRL), James, E. (OAR/ESRL), Dowell, D.C. (OAR/ESRL), Grell, G.A. (OAR/ESRL), Lin, H. (OAR/ESRL), Peckham, S.E. (OAR/ESRL), Smith, T.L. (OAR/ESRL), Moninger, W.R. (OAR/ESRL), Kenyon, J. (OAR/ESRL), Manikin, G.S. (NWS/NCEP)

- This is the first publication completely describing the operational NOAA RAP model.
- RAP meets the need for an effective hourly-updated assimilation and modeling system for the U.S. to support situational awareness and related decision-making for aviation and transportation, severe weather, and energy.
- The design of NOAA's newest severe weather model, the High Resolution Rapid Refresh (HRRR) is based on the RAP model and is discussed in this paper.

The Rapid Refresh (RAP), an hourly-updated assimilation and model forecast system, replaced the Rapid Update Cycle (RUC) as an operational regional analysis and forecast system among the suite of models at the NOAA National Centers for Environmental Prediction (NCEP) in 2012. The need for an effective hourly-updated assimilation and modeling system for the United States for situational awareness and related decision-making has continued to increase for various applications including aviation (and transportation in general), severe weather, and energy. The RAP is distinct from the previous RUC in three primary aspects: a larger geographical domain (covering North America); use of the community-based WRF-ARW (Weather Research and Forecasting – Advanced Research WRF) model replacing the RUC forecast model; and use of the Gridpoint Statistical Interpolation (GSI) assimilation instead of the RUC three-dimensional

variational (3DVar) assimilation. As part of the RAP development, modifications have been made to the community WRF-ARW model (especially in model physics) and GSI assimilation systems, some based on previous model and assimilation design innovations developed initially with the RUC. Upper-air comparison is included for forecast verification against both rawinsondes and aircraft reports, the latter allowing hourly verification. In general, the RAP produces superior forecasts to those from the RUC, and its skill has continued to increase from 2012 up to RAP version 3 as of 2015. In addition, the RAP can improve on persistence forecasts for the 1-3h forecast range for surface, upper-air, and ceiling forecasts.
Publication date: 21 December 2015
Available online: http://journals.ametsoc.org/doi/abs/10.1175/MWR-D-15-0242.1

OTHER REPORTS, BOOK CHAPTERS, AND INTERNAL PUBLICATIONS

Impacts of Climate Change on Human Health in the United States: A Scientific Assessment
OSTP Report
D. Easterling, K. Kunkel (NESDIS), M. Hawkins (NWS), J.Trtanj (OAR), T. Collier (NMFS), J. Jacobs (NOS), S. Moore (NMFS), K. Kunkel (NESDIS), J. Bell (NOAA/CDC affiliate), S. Herring, C. Schreck, K. Kunkel (NESDIS)

- This report provides policy makers and the public the most current science on how climate change affects human health. The two primary impacts are first, by changing the severity or frequency of health problems that are already affected by climate and weather factors; and second, by creating unprecedented or unanticipated health problems or health threats in places where they have not previously occurred.

On April 4, 2016, The Office of Science Technology and Policy (OSTP) is expected to release the "Impacts of Climate Change on Human Health in the United States: A Scientific Assessment." This scientific assessment was developed by the U.S. Global Change Research Program (USGCRP), as part of the ongoing efforts of USGCRP's sustained National Climate Assessment process and as called for under the President's Climate Action Plan.
The report provides a comprehensive, evidence-based, and, where possible, quantitative estimation of current and future impacts of climate change on public

health.

The report was lead under the auspices of the USGCRP Climate Change and Human Health Group (CCHHG) lead by NOAA, NIH and CDC, had over 100 authors (federal, contractor and grantee), engaged eight agencies and multiple departments therein. NOAA contributed leadership (CCHHG and Steering committee), Lead Authors, contributing authors, and critical support from the NOAA-funded Technical Support Unit. NOAA-funded research including from RISAs, the Ecological Forecasting Roadmap, and the former Oceans and Human Health Program, along with analysis of data and products from NCEI and NWS provided core science contributions to these findings.

This report provides policy makers and the public the most current science on how climate change affects human health. The two primary impacts are first, by changing the severity or frequency of health problems that are already affected by climate and weather factors; and second, by creating unprecedented or unanticipated health problems or health threats in places where they have not previously occurred.

OAR/CPO's Climate and Heat Health Lead Juli Trtanj was a lead author. CPO provided key leadership on the overall report through its CCHHG co-chair, and was lead author on the Water-Related Illness chapter--which fundamentally re-framed the water, health and climate change issue. Research from RISAs provided critical information.

Publication Date: 4 April 2016

Available online: https://health2016.globalchange.gov/