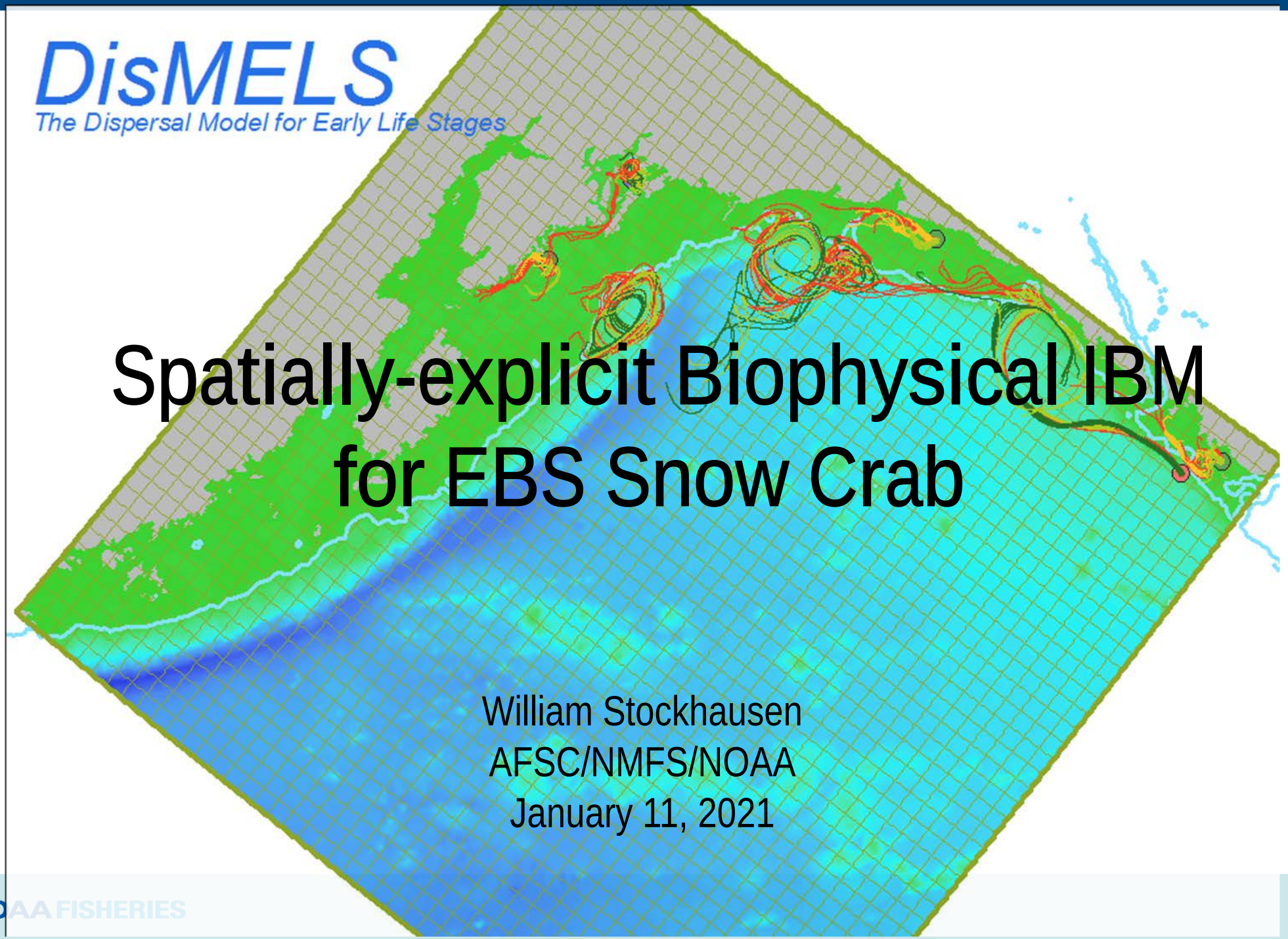
DisMELS

The Dispersal Model for Early Life Stages



Spatially-explicit Biophysical IBM for EBS Snow Crab

William Stockhausen
AFSC/NMFS/NOAA
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Overview

- General Intro to spatially-explicit, biophysical IBMs
- Overview of the snow crab IBM
- Results from ”hindcast” model runs
- In-progress and future work

What is an IBM?

- Population dynamics model (e.g., stock assessment model)
  - focus on population-level characteristics
  - ??
- IBM: Individual-based model
  - focus on individual characteristics, behavior, and variability
  - population-level dynamics and characteristics are result of “emergent” behavior
  - ??
- Spatially-explicit, biophysical IBM
  - embeds individuals within a time-varying, spatially-explicit, biophysical environment
  - physical environment: currents, temperature, salinity, pH, light, etc.
  - biological environment: prey fields, predator fields

Conceptual Model Configuration

IBM

S = Life Stage

S1

S2

S3

S4a

S4b

S5a

S5b

Biological Processes

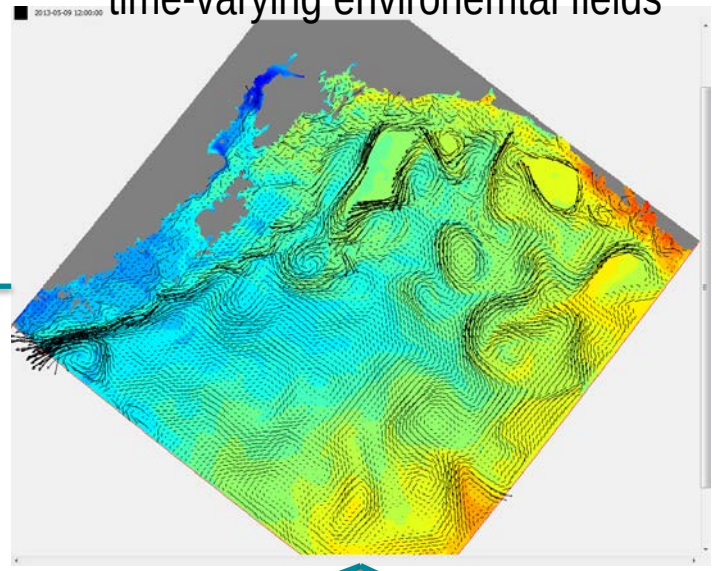
consumption

growth

movement

mortality

time-varying environemtal fields



Model Run

time

S1 S1 S1 S1 S2 S2 S2 S2 S3 S3 S3 S3 ....

S1 S1 S2 S2 S3 S3 S3 S3 S4a S4a S4a S4a ....

S1 S1 S1 S1 S2 S2 S2 S2 S3 S3 S3 S3 ....

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Why Spatially-explicit Biophysical IBMs in Fisheries Science?

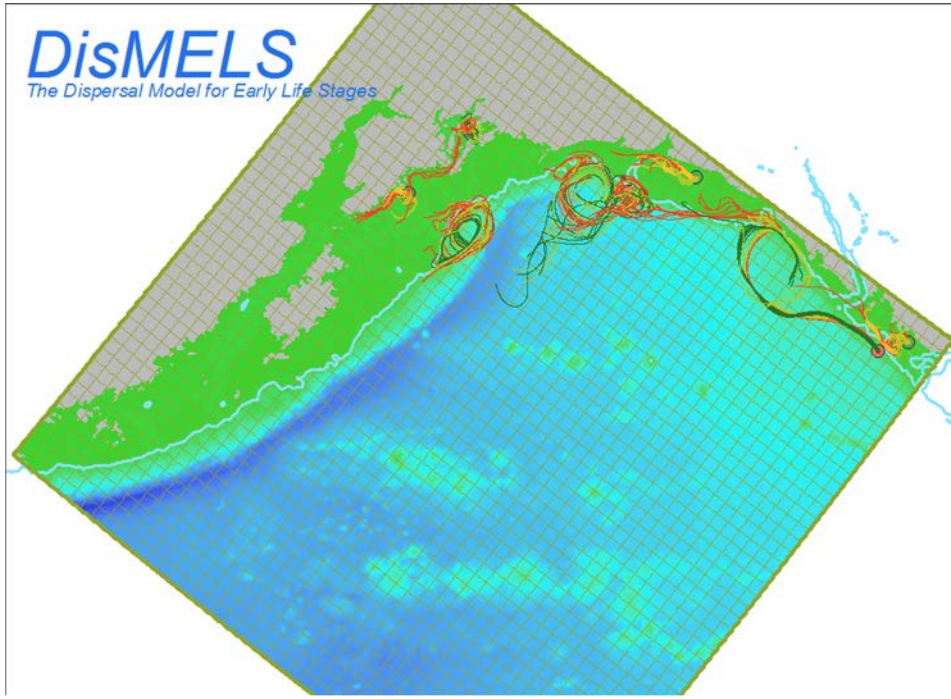
- Tools to investigate the linkages between the “environment” and population dynamics, with emphasis on early life stages

- Provide an “in situ” Lagrangian, integrative perspective on factors influencing biological processes
  - follow individuals in space and time
  - incorporate spatiotemporal variability in the environment
  - incorporate “best” mechanistic understanding of multiple biological processes

- Provide a relatively cheap testbed to
  - contrast consequences of different potential behaviors, processes
  - evaluate sensitivity to different parameterizations, environmental conditions
  - develop/test “intuition” regarding population pro

What is DisMELS (the Dispersal Model for Early Life Stages)?

- A framework for developing and running spatially-explicit, biophysically-coupled individual-based models (IBMs) for marine species
  - provides “plumbing” for species-specific IBMs to interact with the “environment”
  - species-specific IBMs are developed as separate modules and “plugged in”
  - ROMS model output files on “native” grid provide the “environment”
  - can follow 10,000’s of simulated individuals across space and time
- Framework and species-specific IBMs use
  - java object-oriented code
  - GUI interface
  - open-source libraries (e.g., Geotools, NetcdfTools)
  - Netbeans 8.2 modular framework for GUI and “pluggability”
  - input files: netcdf, xml, and csv files
  - output files: csv files
- Framework and species-specific IBMs hosted on GitHub[1]

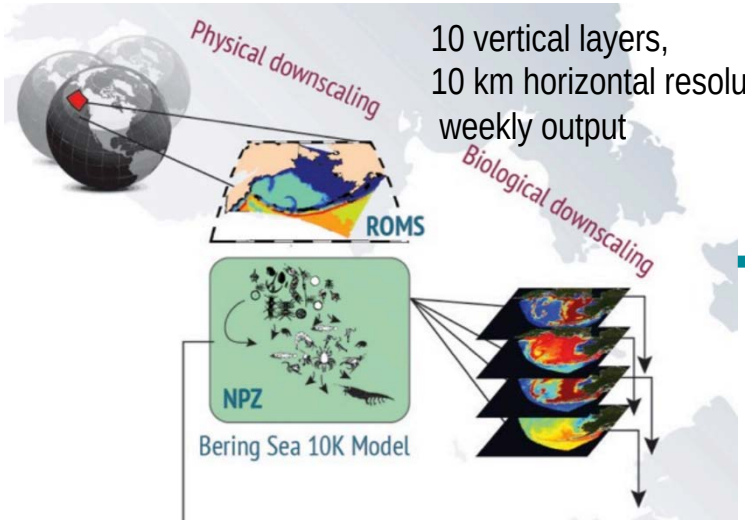


[1]https://github.com/wStockhausen/DisMELS/tree/DisMELS_2.2NoROMS2D

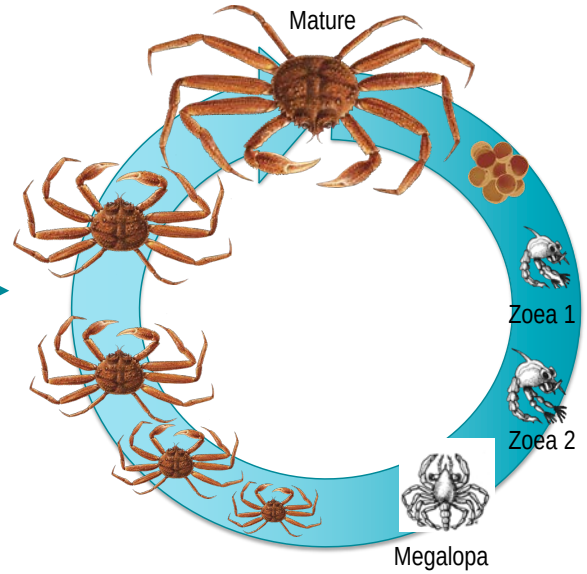
Publications using DisMELS

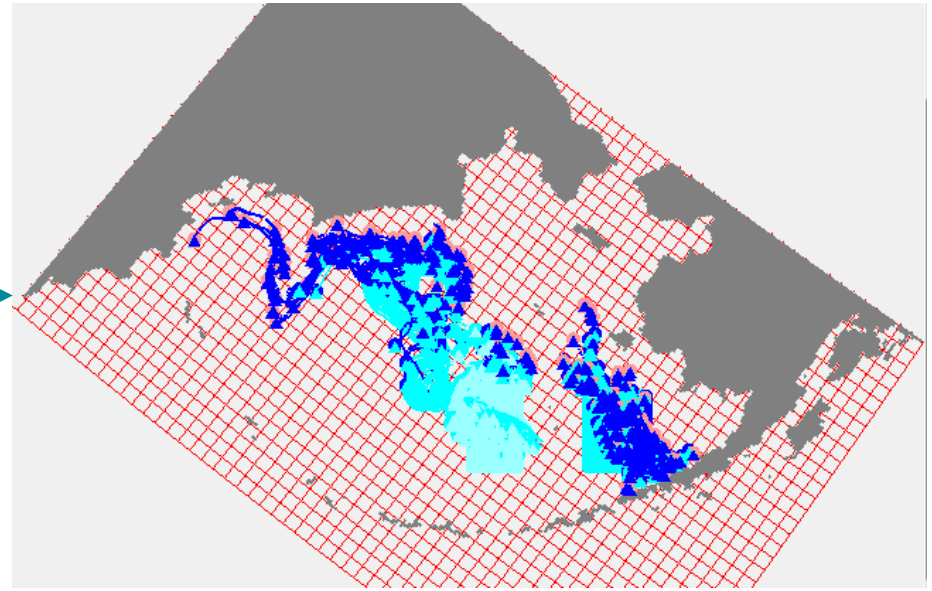
- Stockhausen et al., 2019a. DSRII. Arrowtooth flounder.
- Stockhausen et al., 2019b. DSRII. Pacific ocean perch.
- Gibson et al., 2019. DSRII. Sablefish.
- Hinckley et al., 2019. DSRII. Pacific cod.
- Goldstein et al., 2019. L&O. Arrowtooth flounder.
- Kim et al., 2019. KJMS. Chub mackerel.
- McGowan et al., 2020. MEPS. Capelin.
- Sadorus et al., 2020. Fish. Oc. Pacific halibut.
- Torre et al., submitted. DSRII. Snow crab.

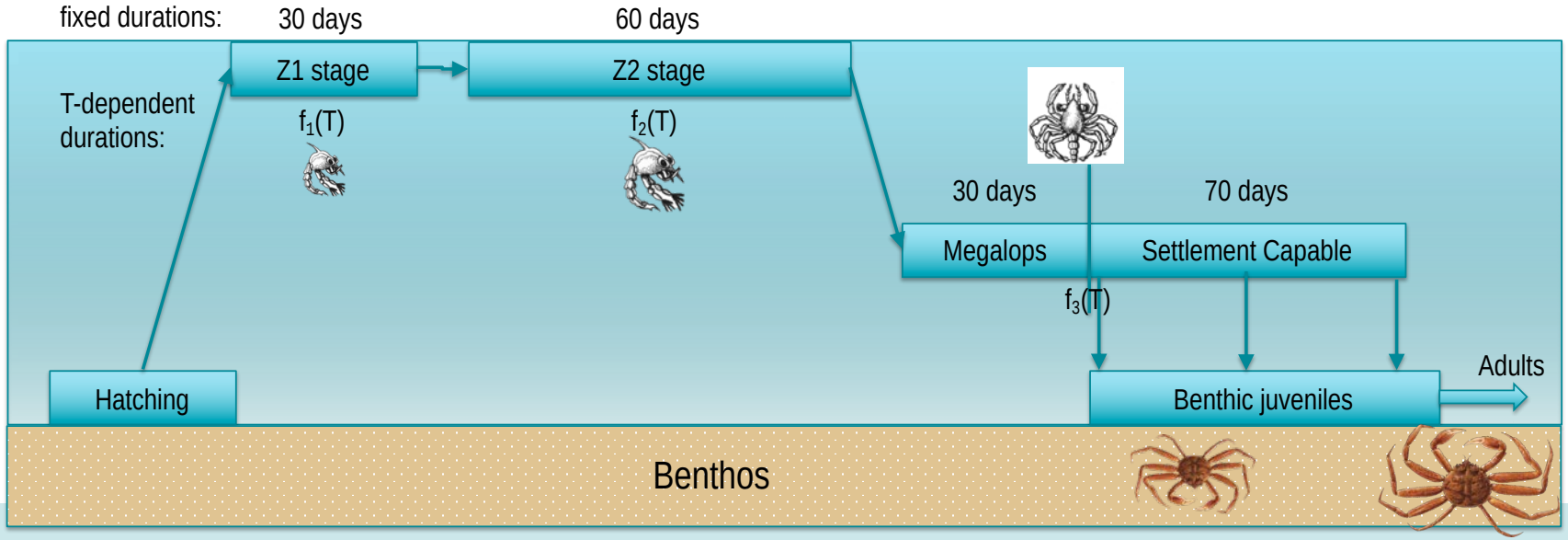
Snow crab IBM



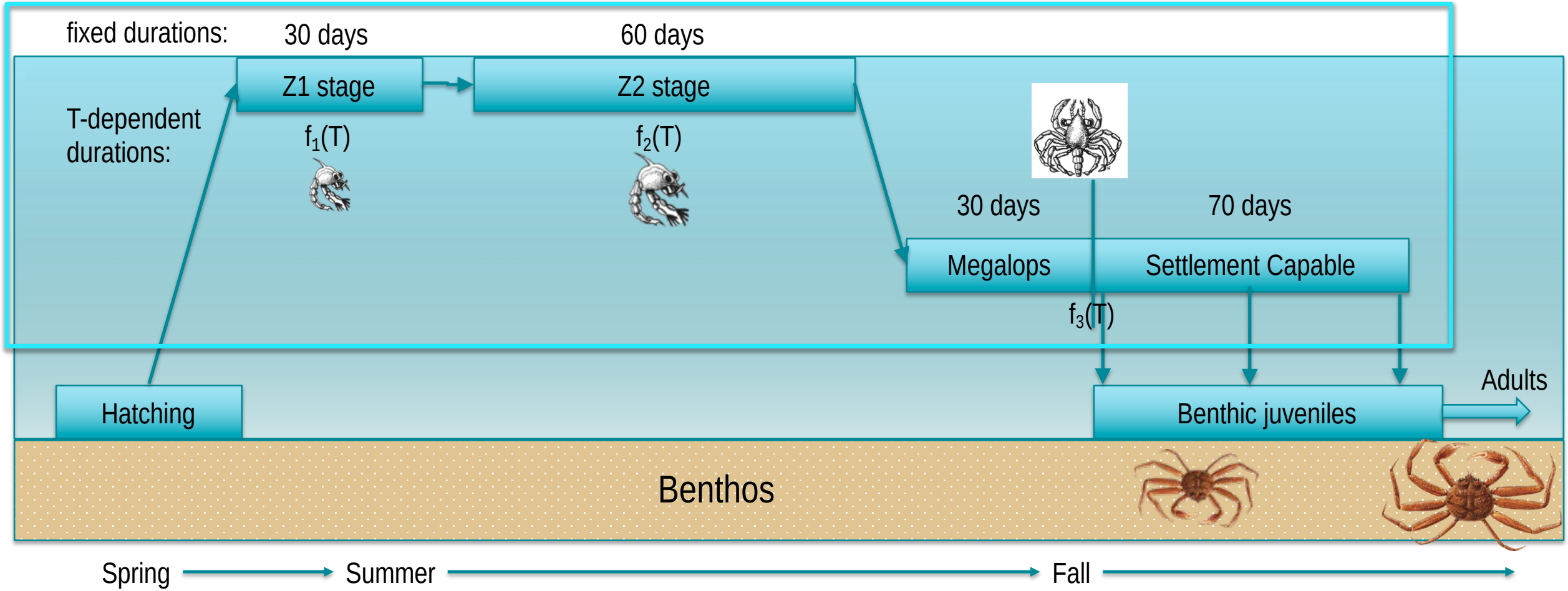
10 vertical layers,
10 km horizontal resolution
weekly output







The conceptual model



Model details

	IBM Stage	Life stage	Biological processes
	Z1	1st zooeal stage	TD-IMD or F-IMD, vertical swimming, advection
	Z2	2nd zooeal stage	TD-IMD or F-IMD, vertical swimming, advection
	M1, M2	megalopal stage (2 sub-stages)	TD-IMD or F-IMD, vertical swimming, advection, settlement
	C1M, C1F	1st benthic instar (sex-specific)	TD IMD
	C2M, C2F – C7M, C7F	2nd-7th benthic instars (sex-specific)	TD IMD
	pubertal stages	(sex-specific)	TBD
	adult stages	(sex-specific)	TBD

TD-IMD: temperature-dependent intermolt duration

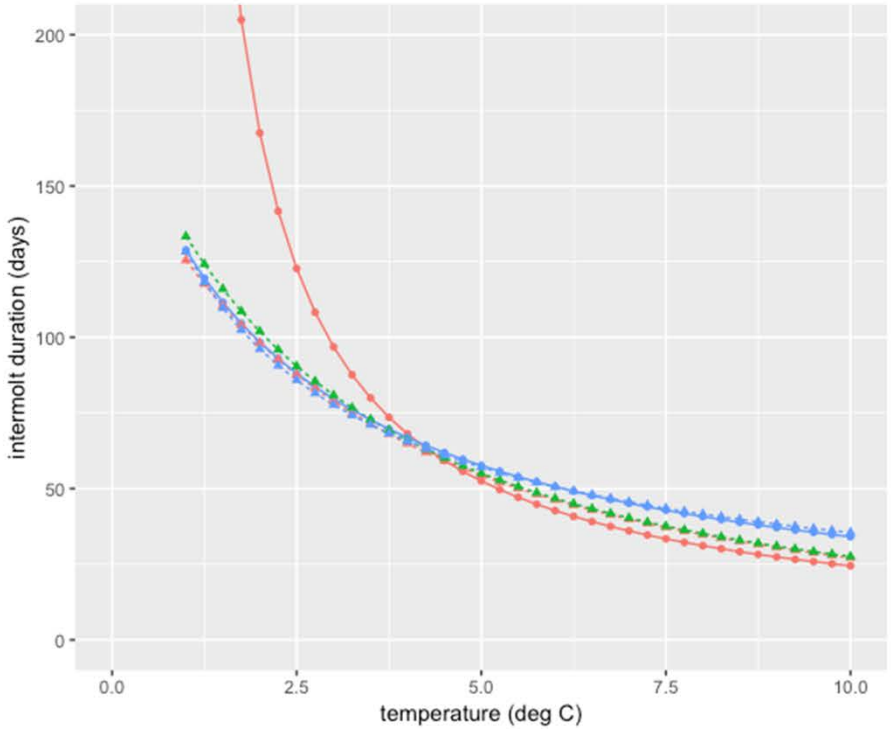
F-IMD: fixed intermolt duration

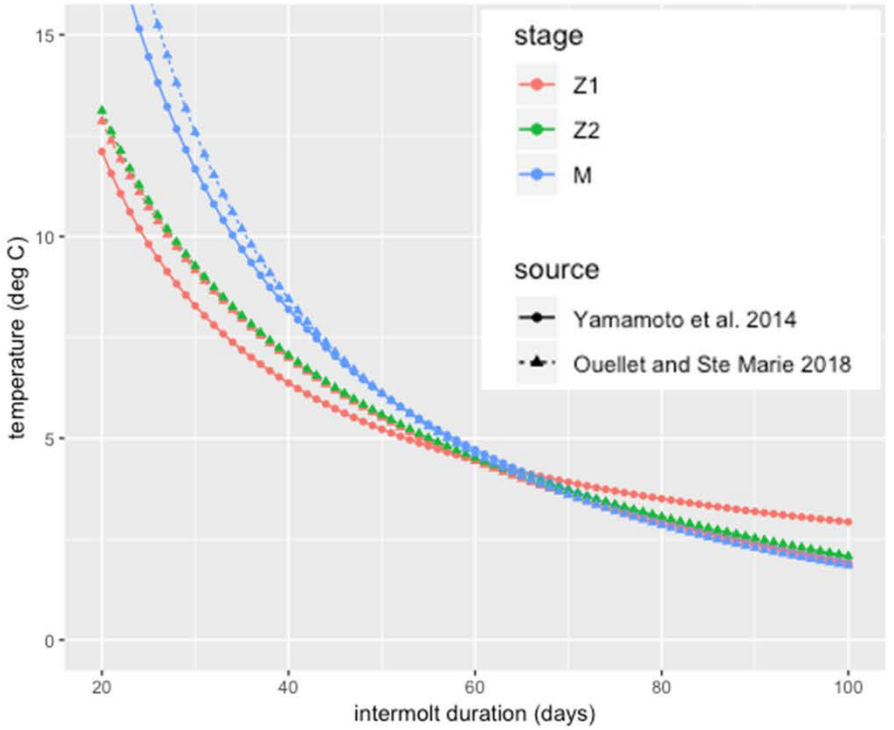
IMD: Intermolt duration

Fixed IMD

Stage	Duration (d)
Z1	30
Z2	60
M1	10
M2	20

Temperature-dependent IMD





Vertical migration behavior



Stage	VMB1	VMB2
Z1	upper 20 m	upper 20 m
Z2	upper 20 m	upper 20 m
M1	within 50 m of bottom (150 m max depth)	upper 20 m
M2	same as M1	within 50 m of bottom (150 m max depth)

Based on

- Zooea:
  - Incze et al. (1987)
  - Parada et al. (2010)
- Megalopae:
  - Kon et al. (2003)
  - Yamamoto et al. (2015)
  - Ouellet and Saint-Marie (2018)

Simulation details

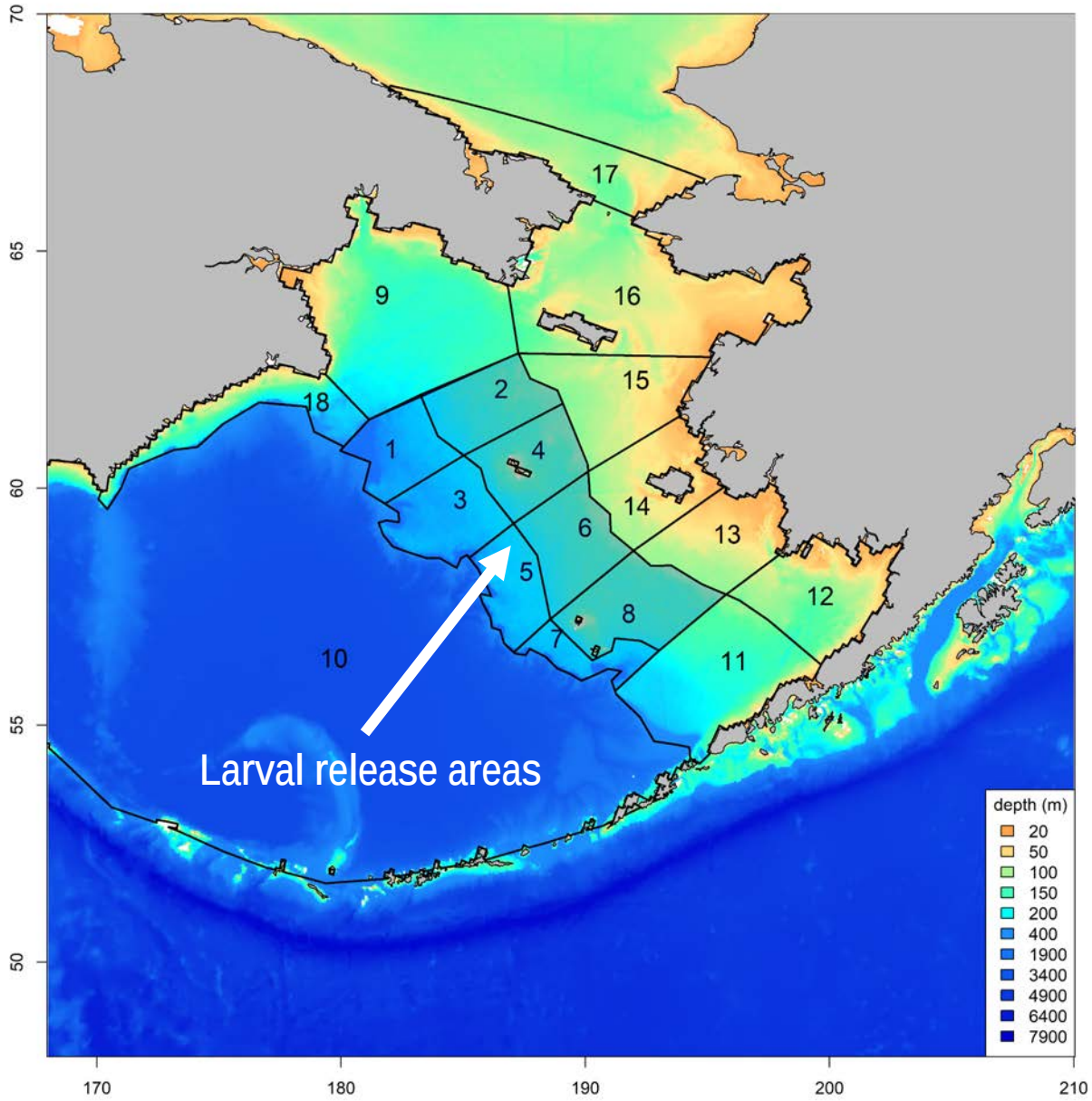
- fully crossed experimental design
  - 2 IMD scenarios
    - fixed duration (F-IMD)
    - temperature-dependent (TD-IMD)
  - 2 VMB scenarios for megalopae
    - descend to near-bottom immediately
    - remain in upper water column for initial 1/3 of stage
- used 10-layer ROMS model for EBS
  - 10-km horizontal resolution
  - weekly-averaged output
  - 1971-2004

- 11,000+ Z1's released on May 1
- integrated using 20-min time step
- individual attributes recorded daily
  - life stage, location, *in situ* temperature
- "successful" individuals settled in benthic nursery habitat (25-150 m depths) as C1's
- "unsuccessful" individuals
  - were M2's which did not metamorphose to C1 within 70 days after becoming M2
  - or were advected beyond the ROMS grid
  - or had not settled by the end of the simulation

Initialization

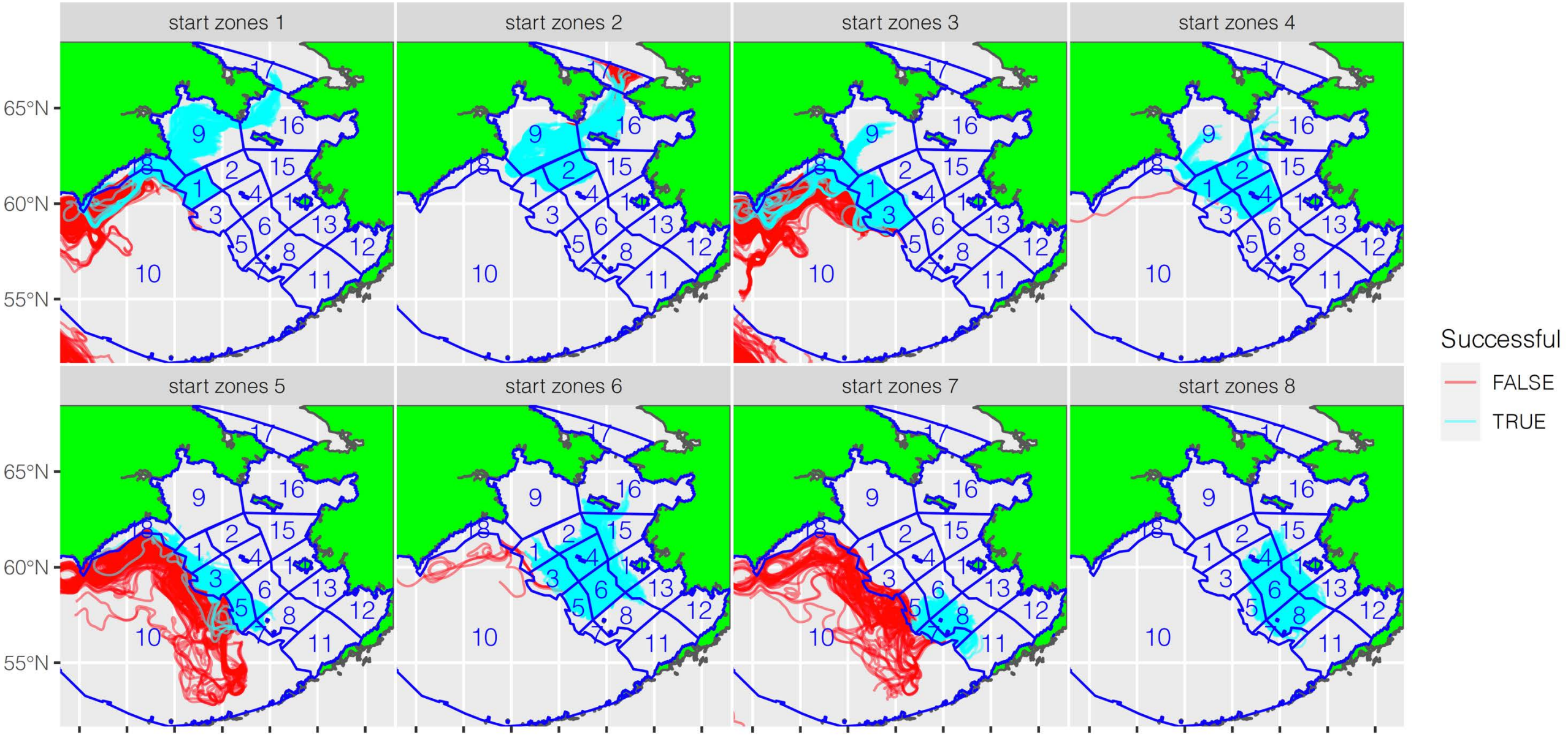
~11,000 equally-spaced individuals released as Z1's

- on May 1 each year 1971-2004
- just above bottom in Zones 1-8 at depths < 250 m

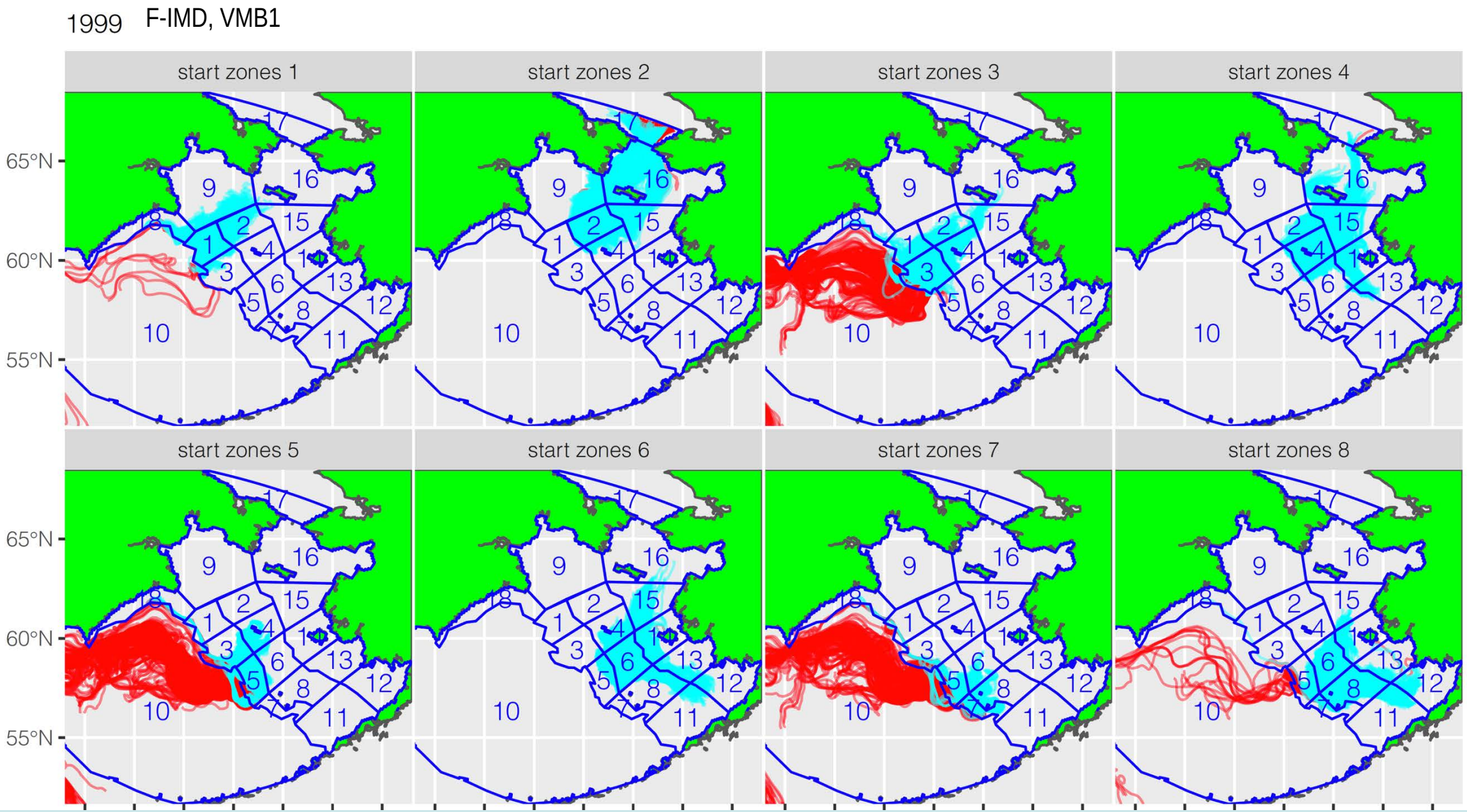


Results: Individual trajectories

1993 F-IMD, VMB1

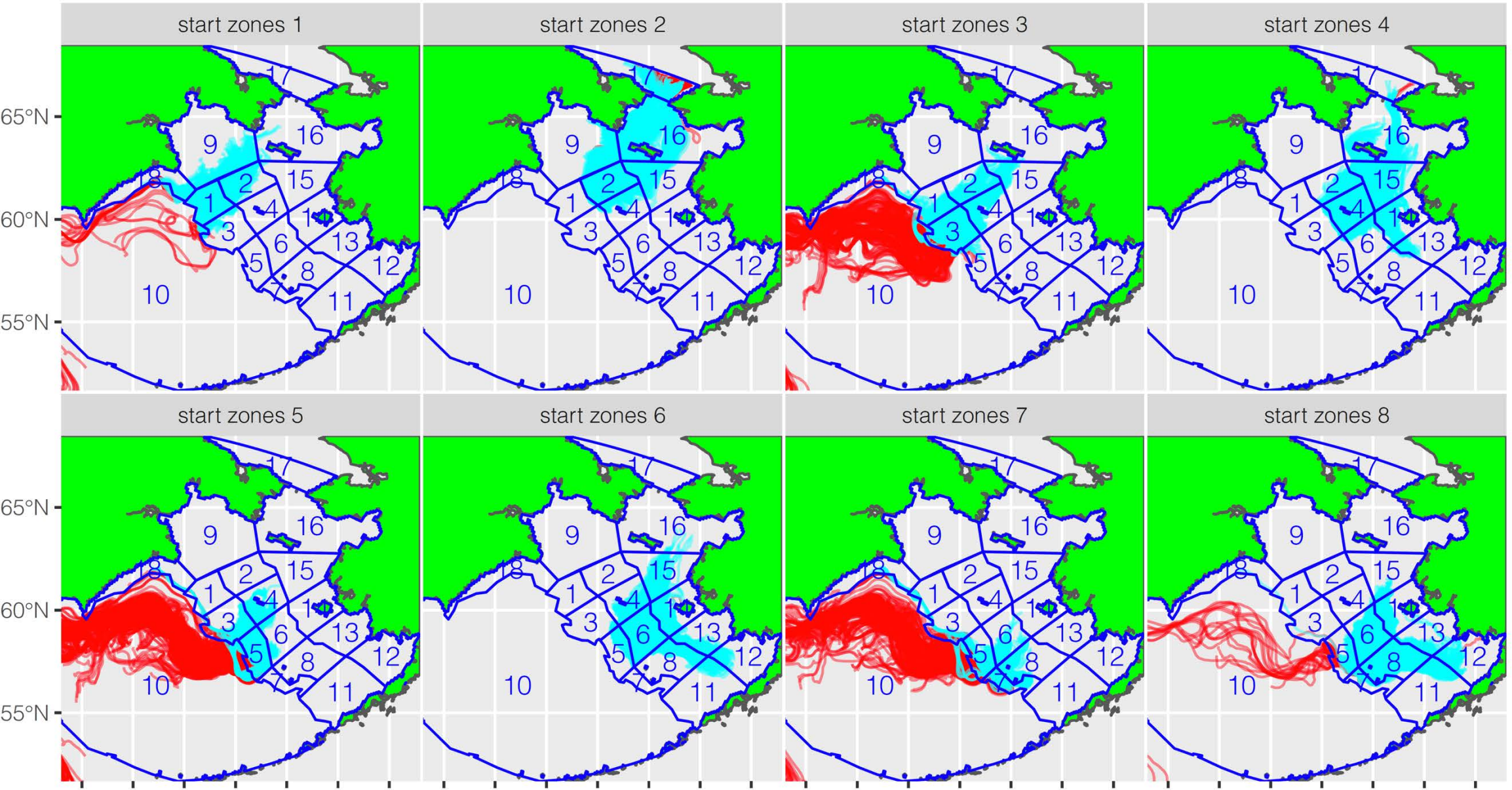


Results: Individual trajectories



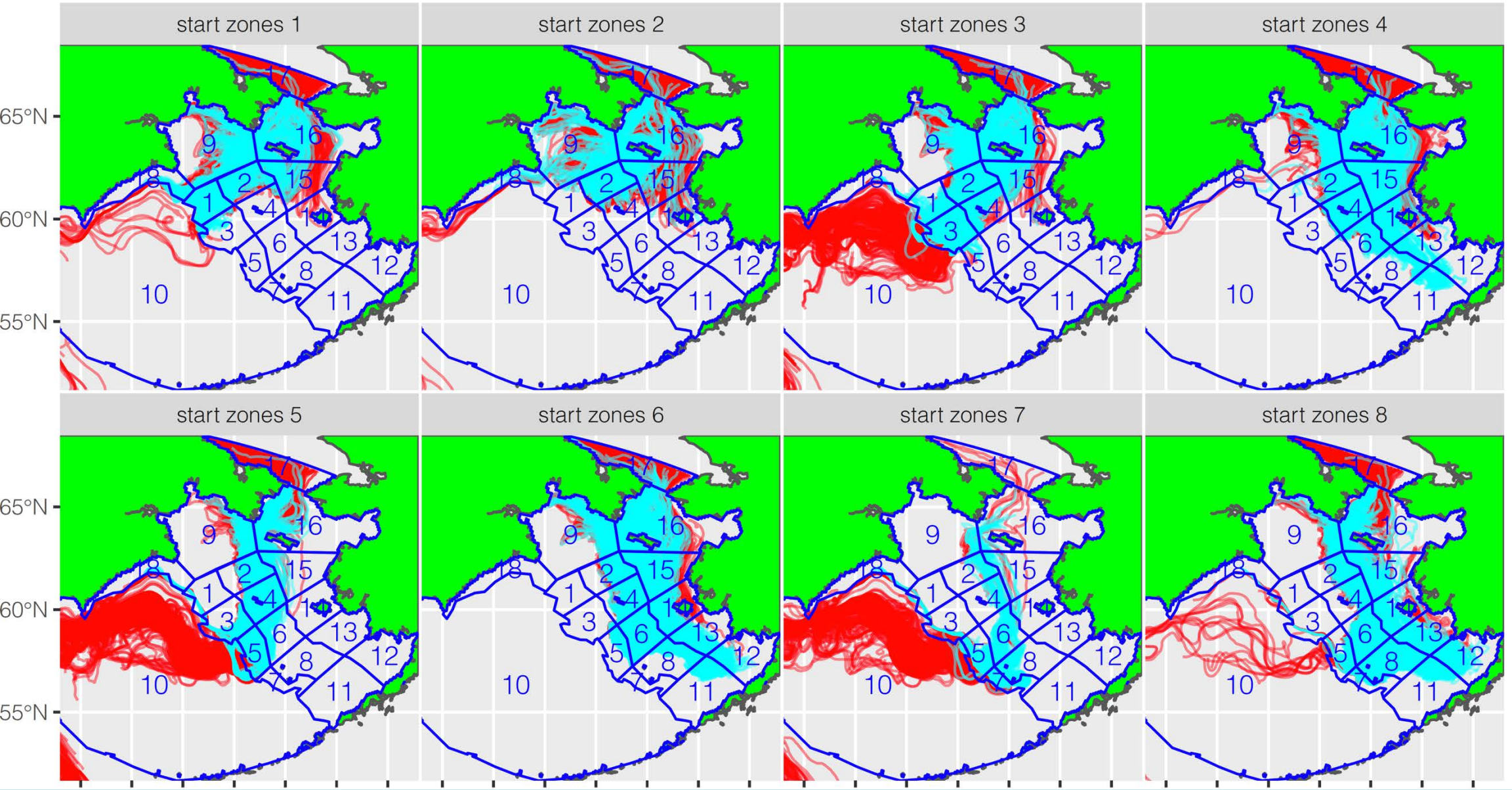
Results: Individual trajectories

1999 F-IMD, VMB2



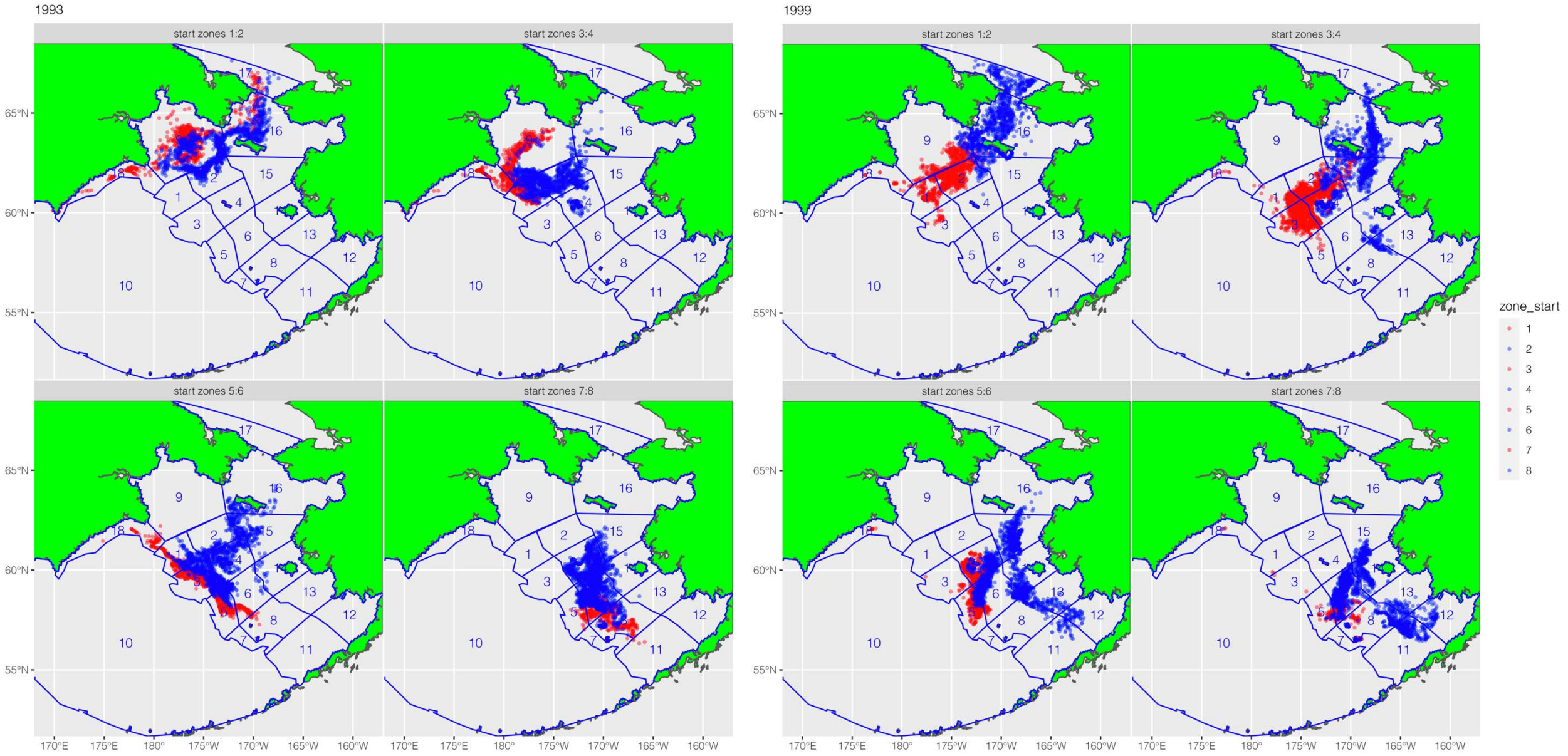
Results: Individual trajectories

1999 TD-IMD, VMB1



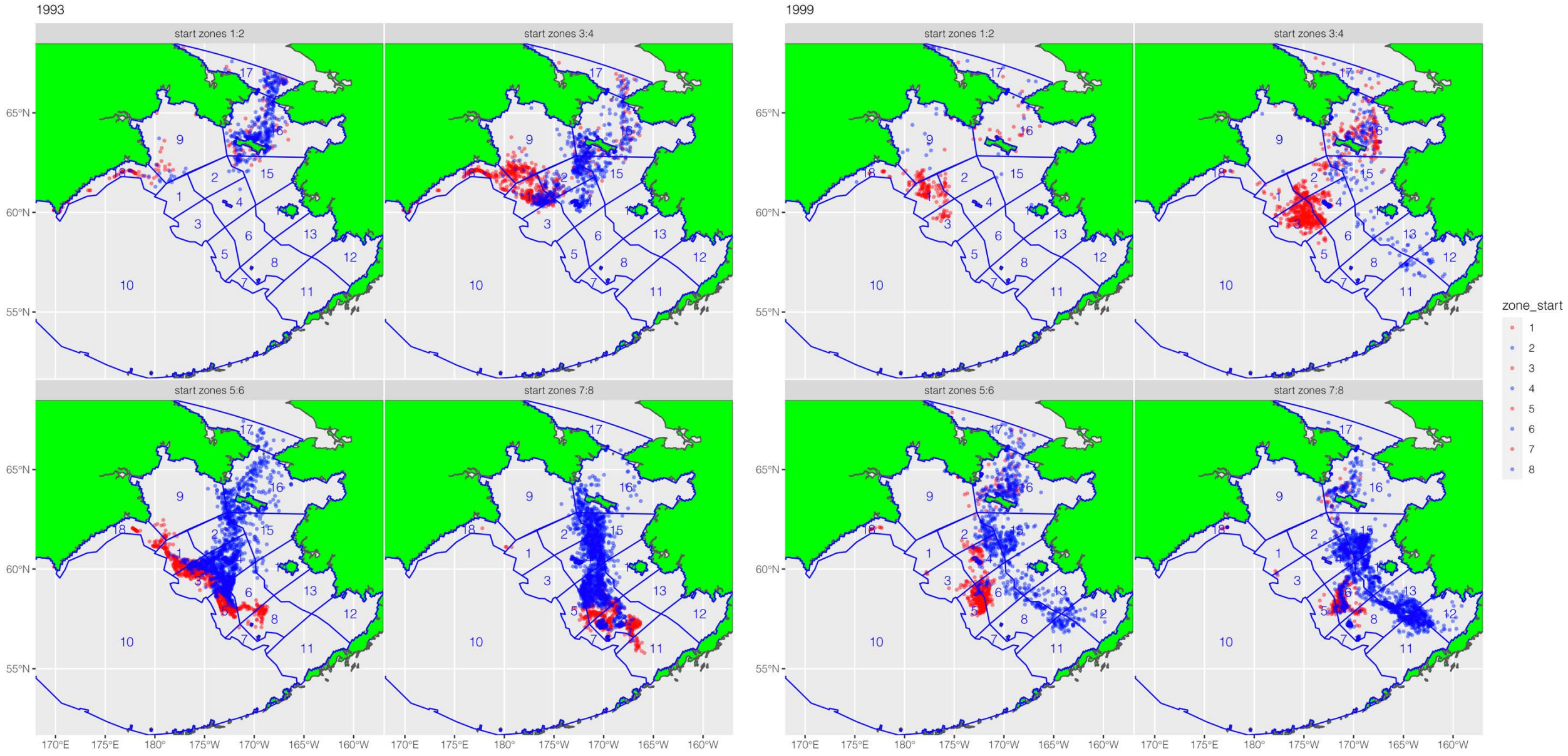
Results: Settlement patterns

F-IMD, VMB1



Results: Settlement patterns

TD-IMD, VMB1



Results: Connectivity

- "Successful" individuals
  - Settle at end of M2 stage

- Connectivity between zones defined as

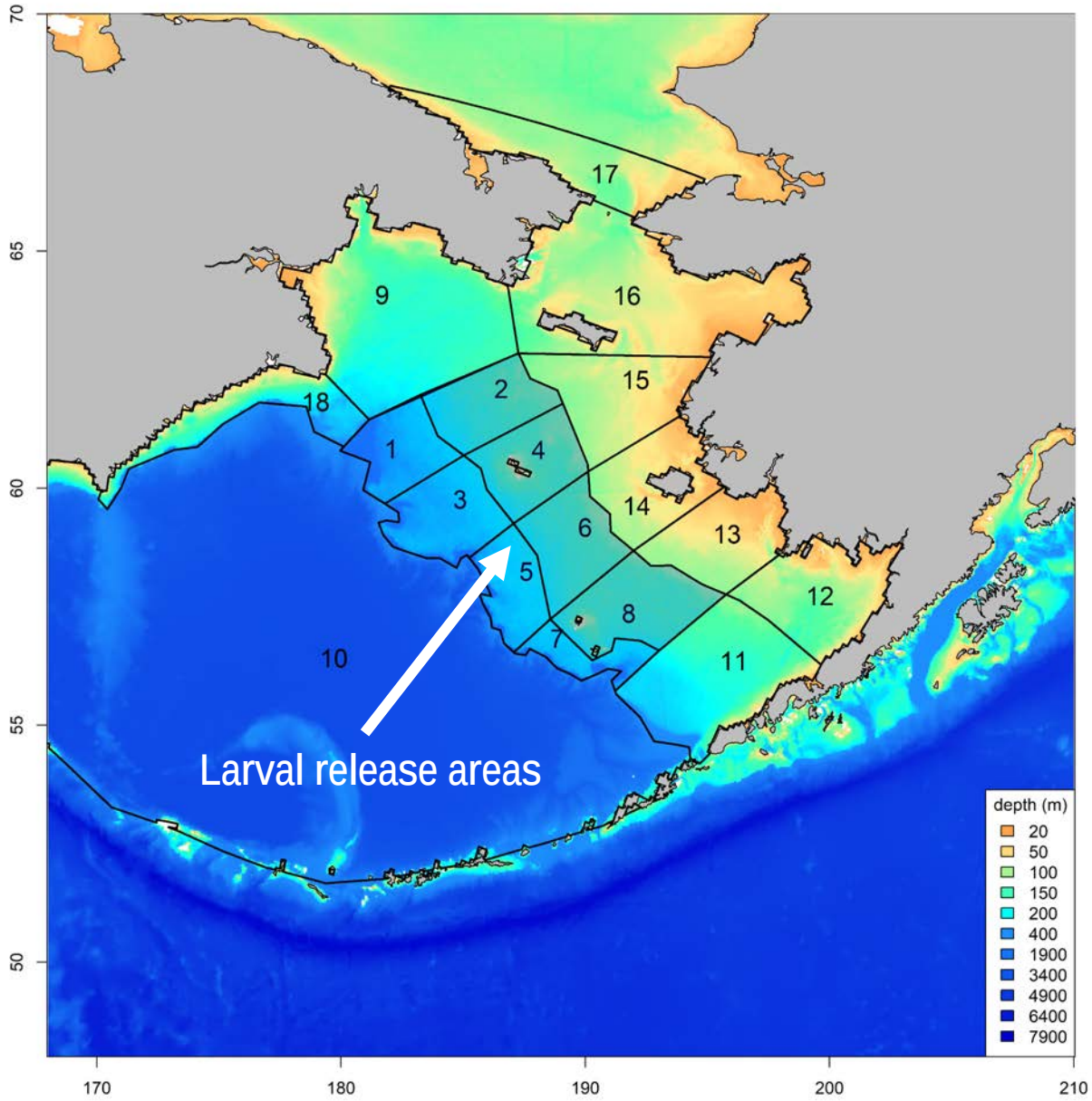
$$C_{i,j} = \frac{S_{i,j}}{N_j}$$

  - N_j = number hatched in zone *j*
  - $S_{i,j}$ = number settling in zone *i* hatched in zone *j*

- Connectivity is "maximum potential"
  - does not include mortality
  - "unsuccessful" individuals either

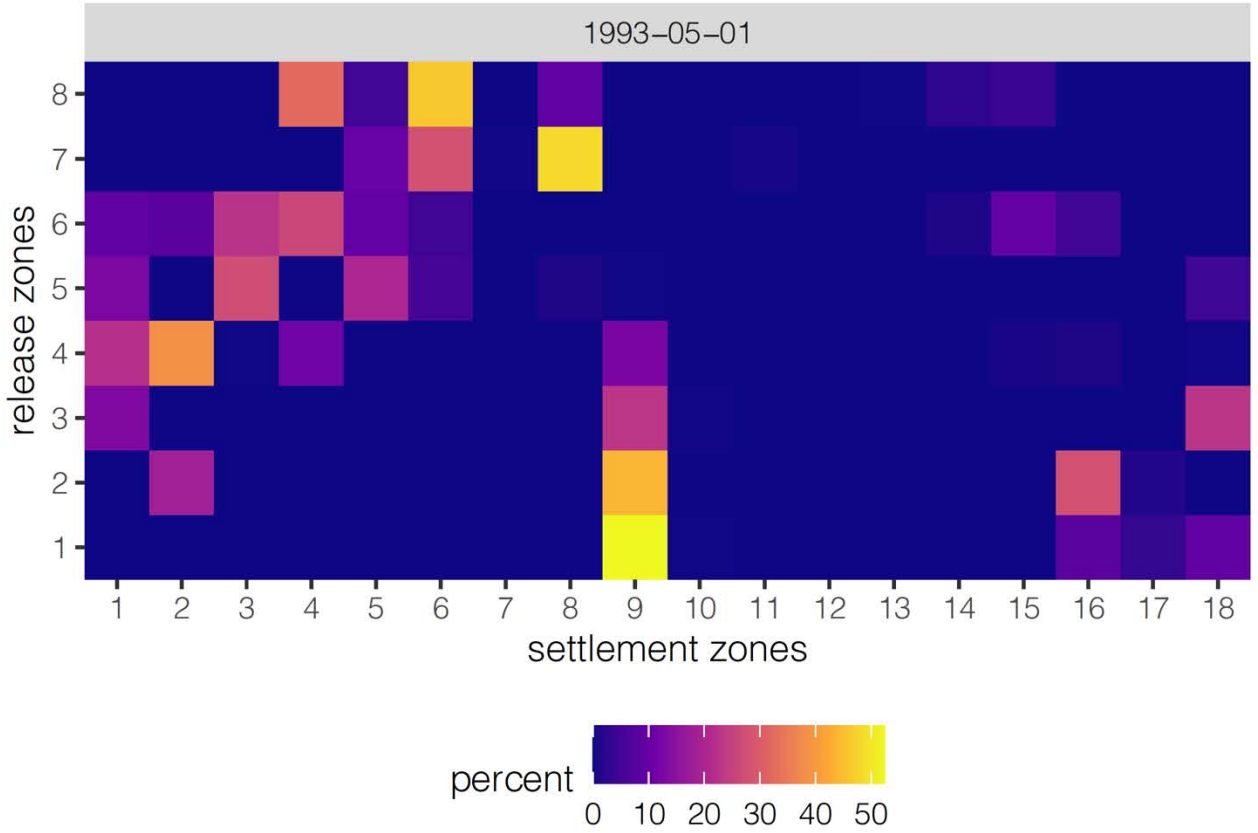
    a) move over unsuitable habitat or off the grid

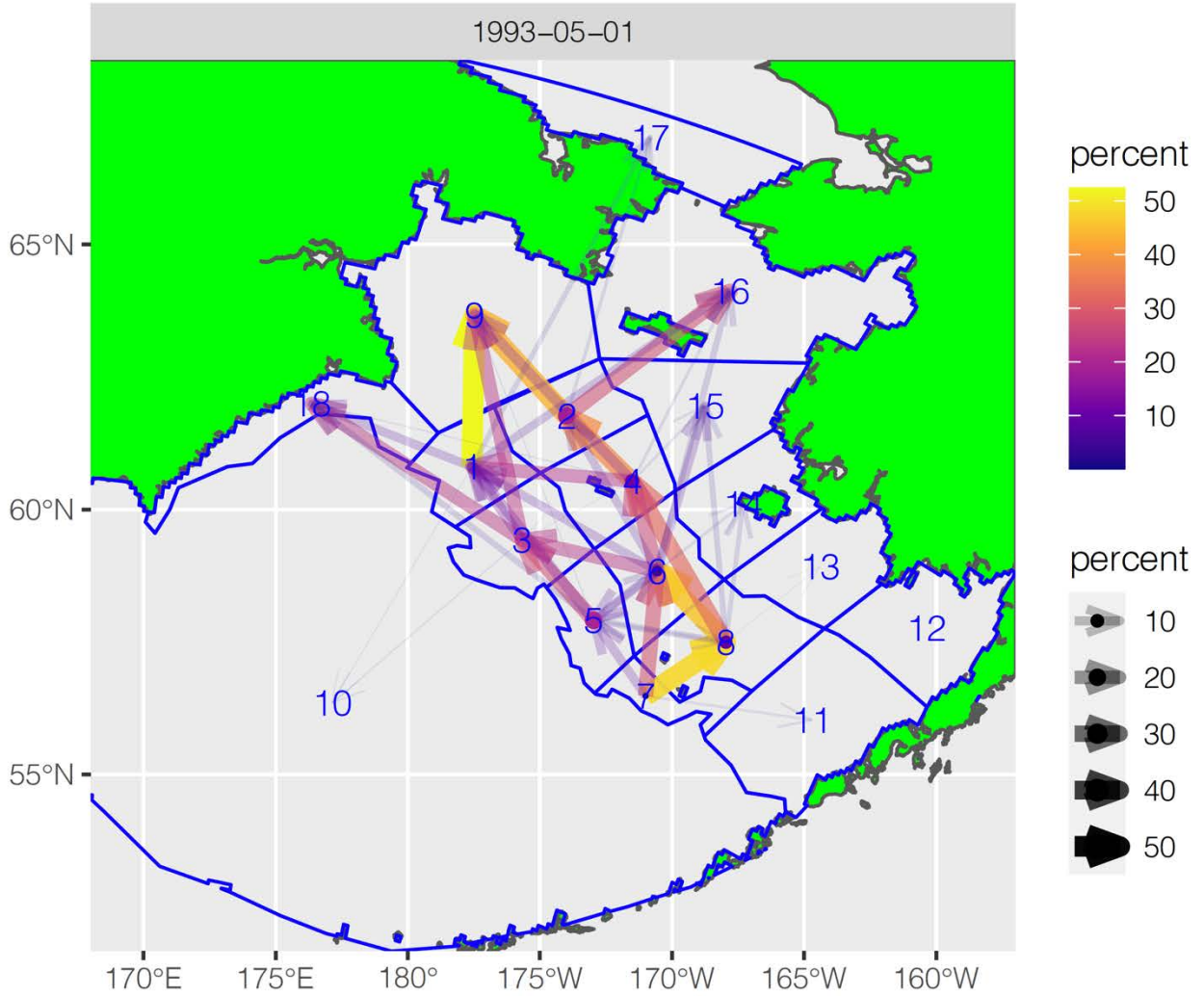
    b) move into cold water and fail to metamorphose into next stage



Results: Connectivity

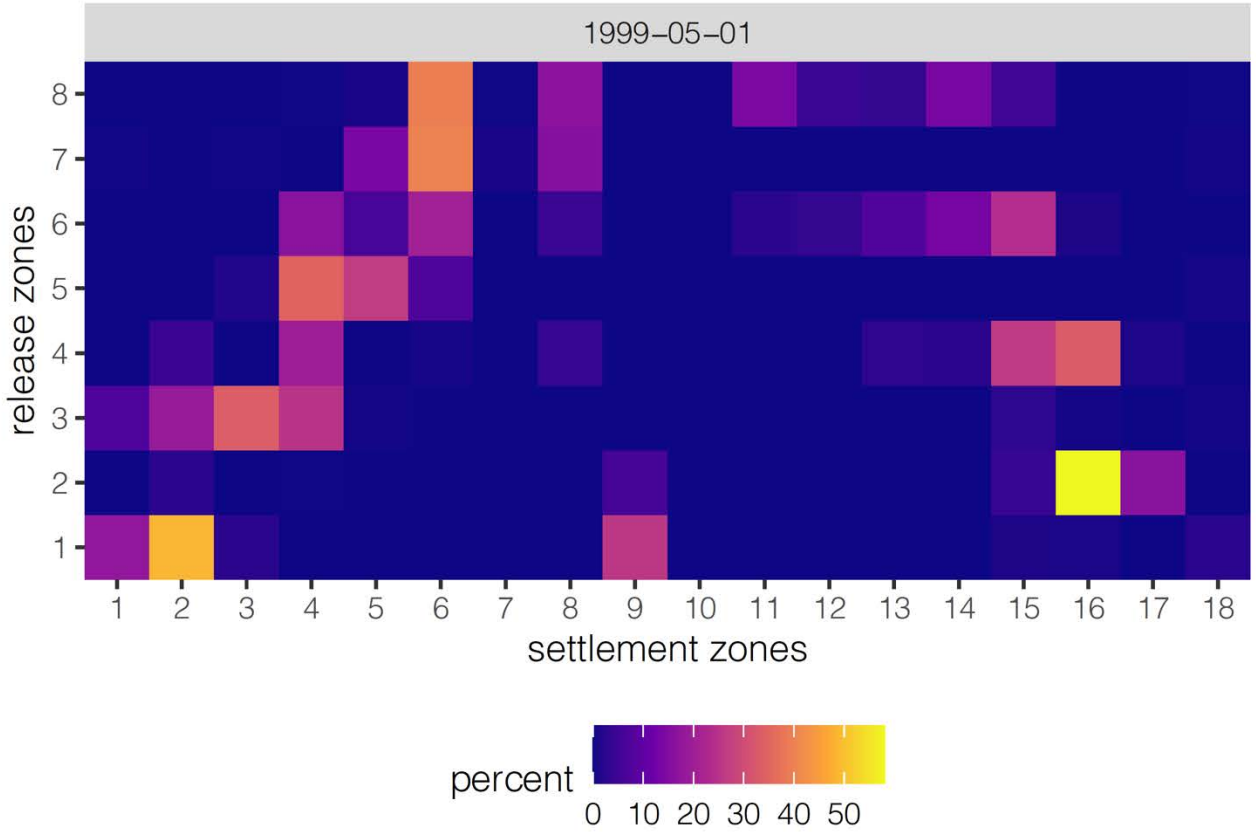
F-IMD, VMB1

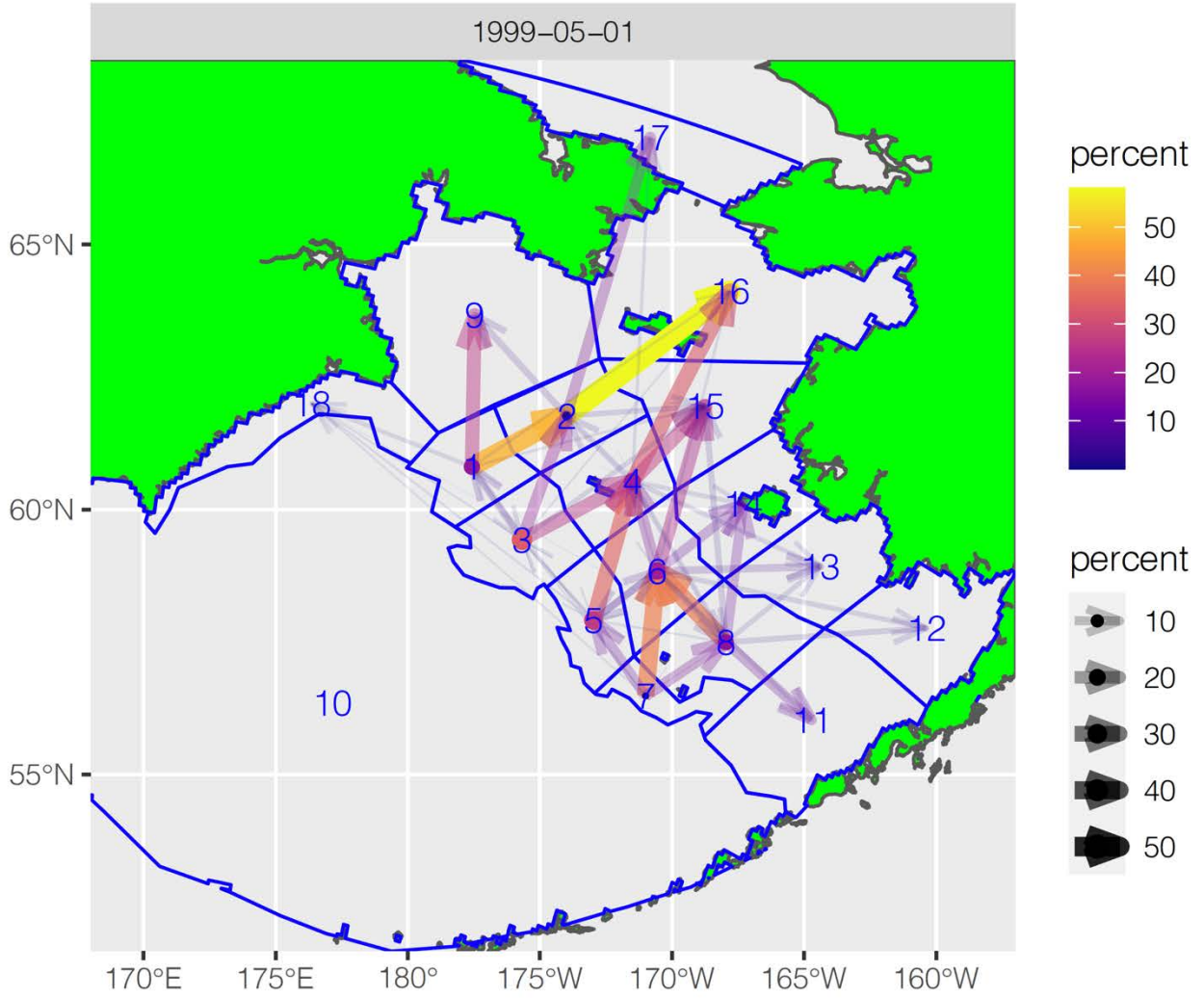




Results: Connectivity

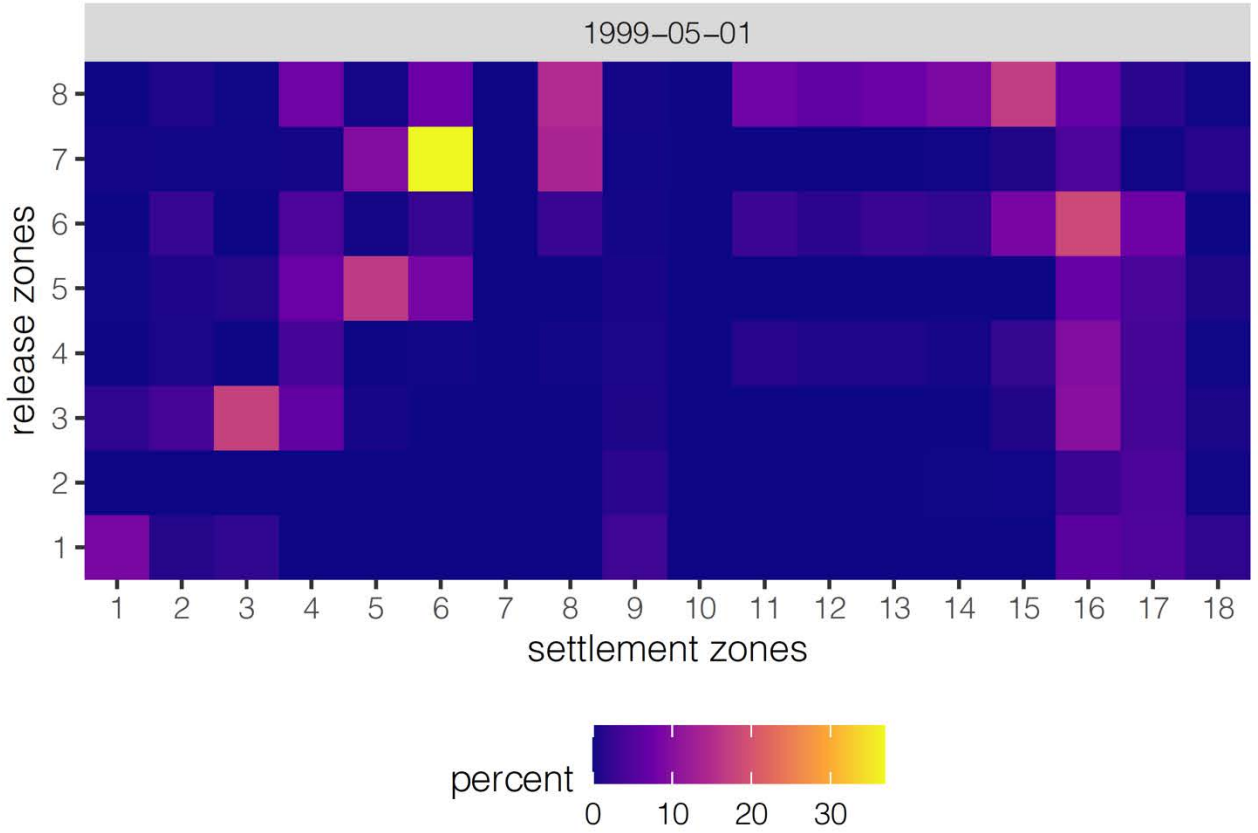
F-IMD, VMB1

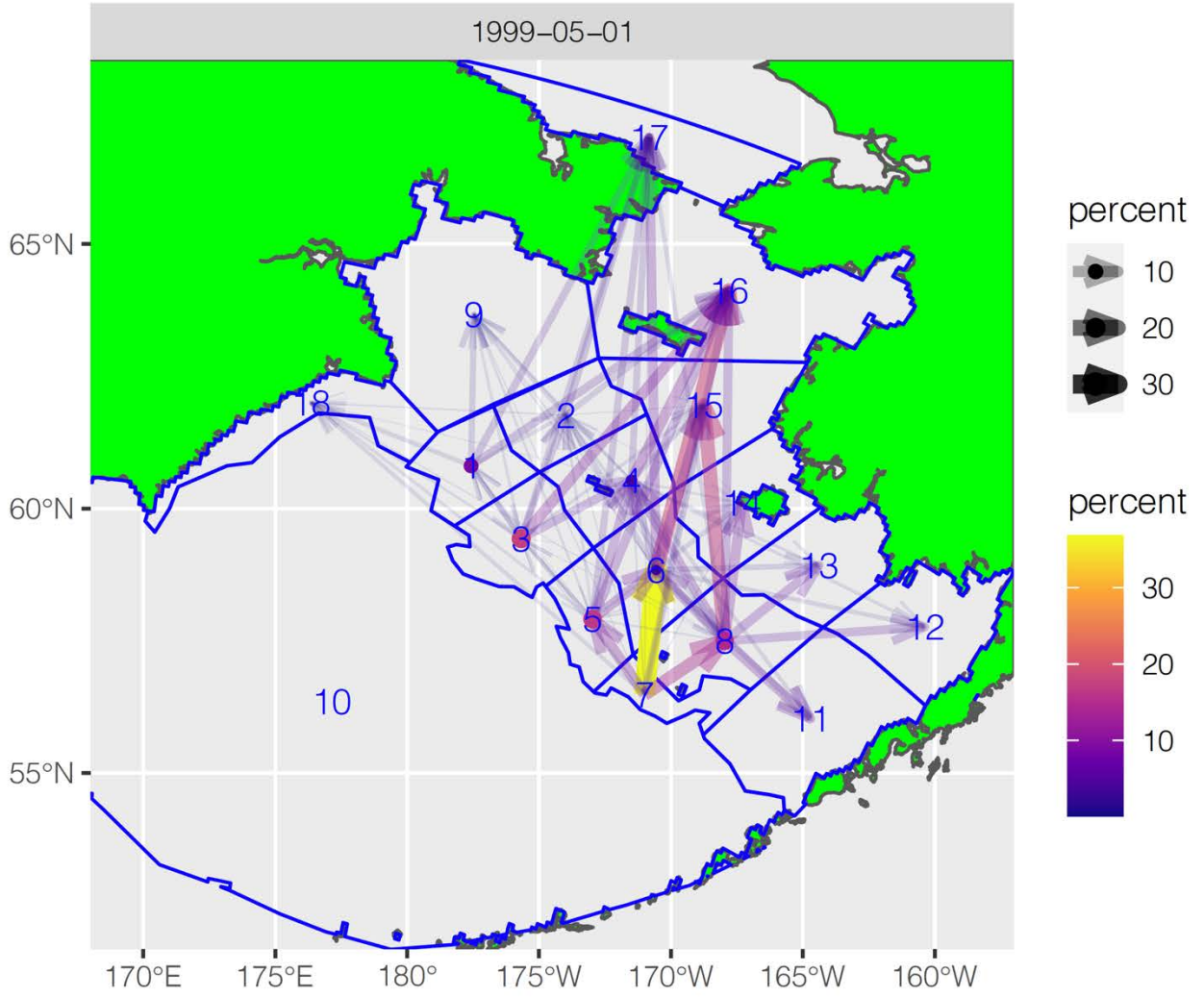




Results: Connectivity

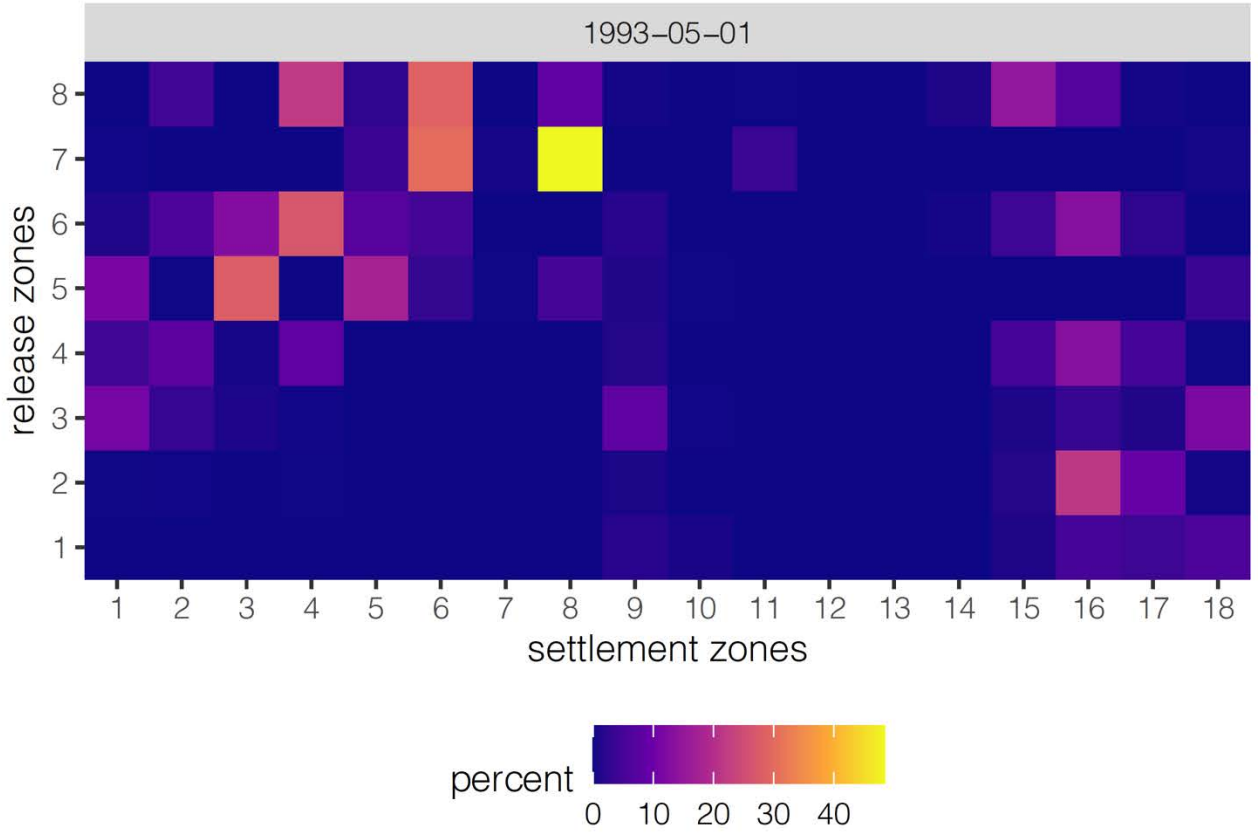
TD-IMD, VMB1

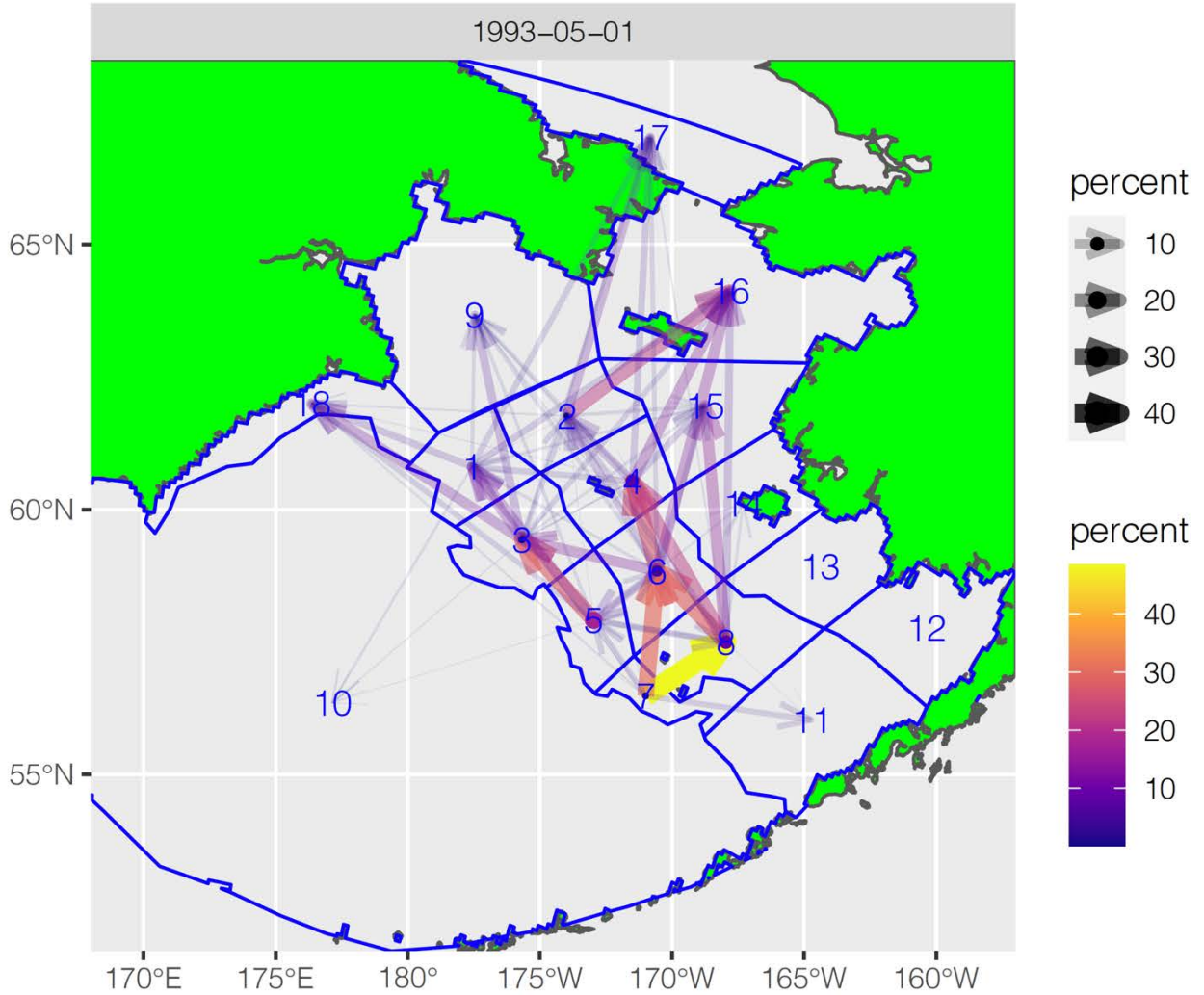




Results: Connectivity

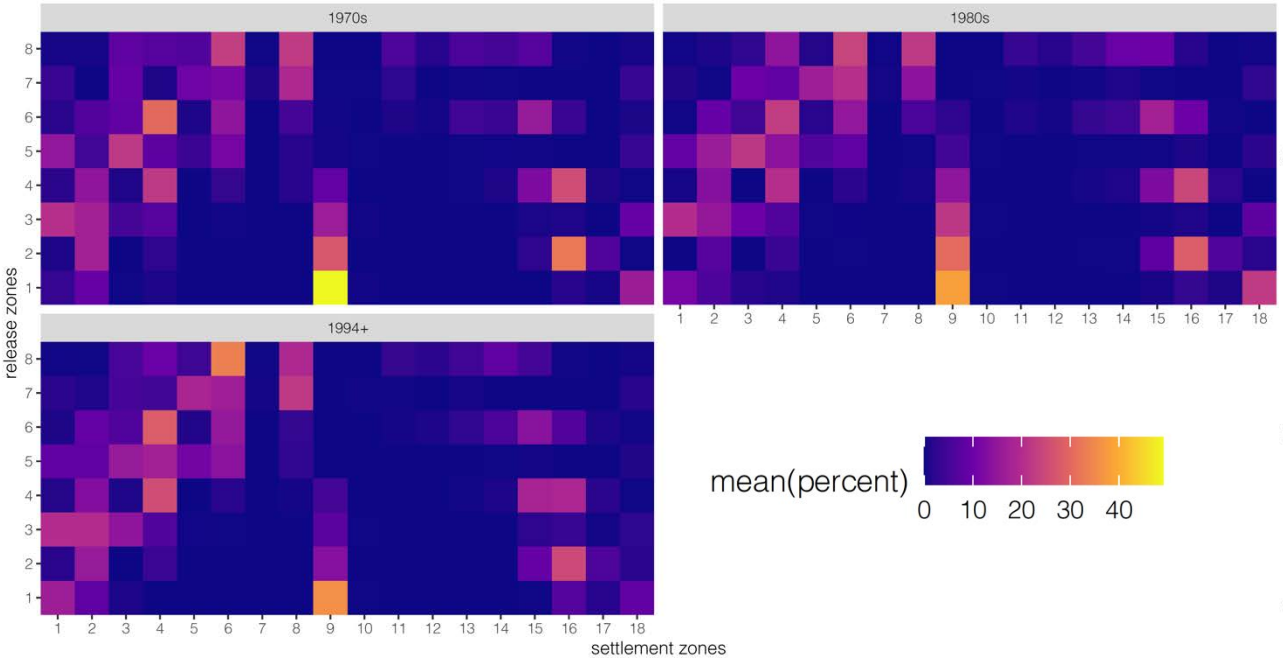
TD-IMD, VMB1

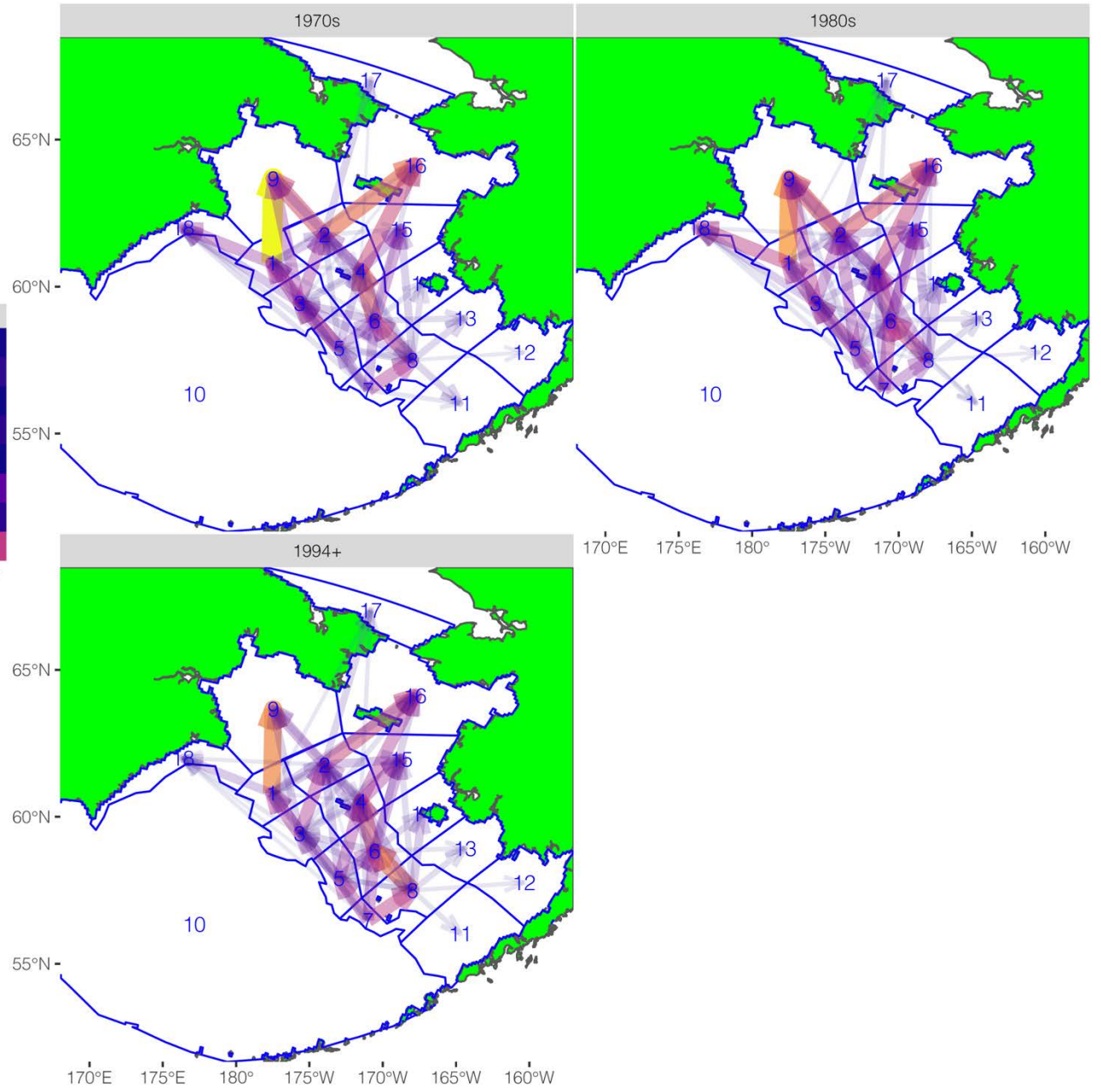




Results: Mean connectivity

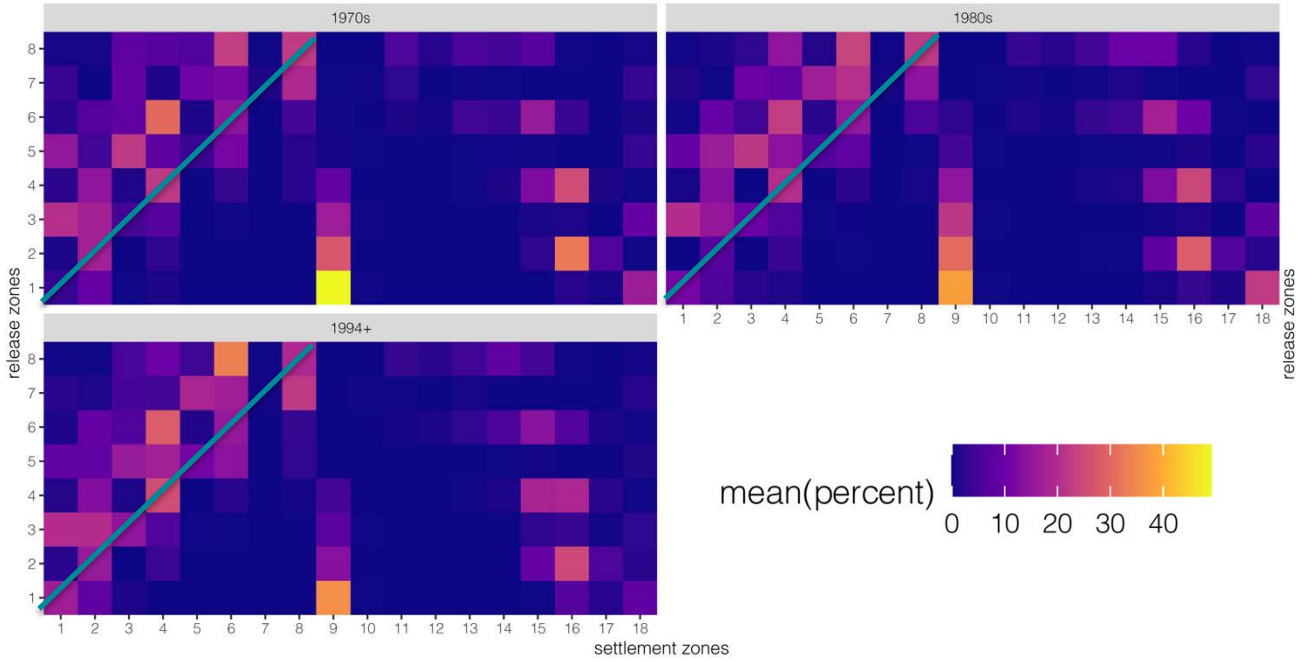
F-IMD, VMB1



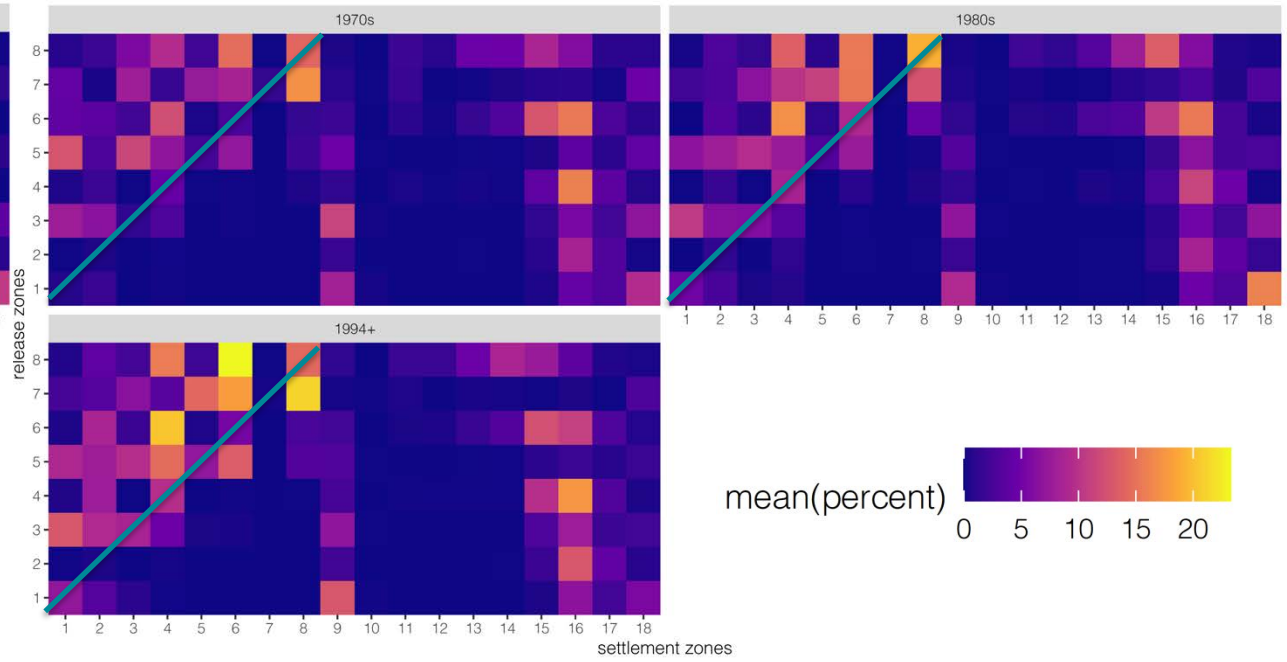


Results: Mean connectivity

F-IMD, VMB1



TD-IMD, VMB1



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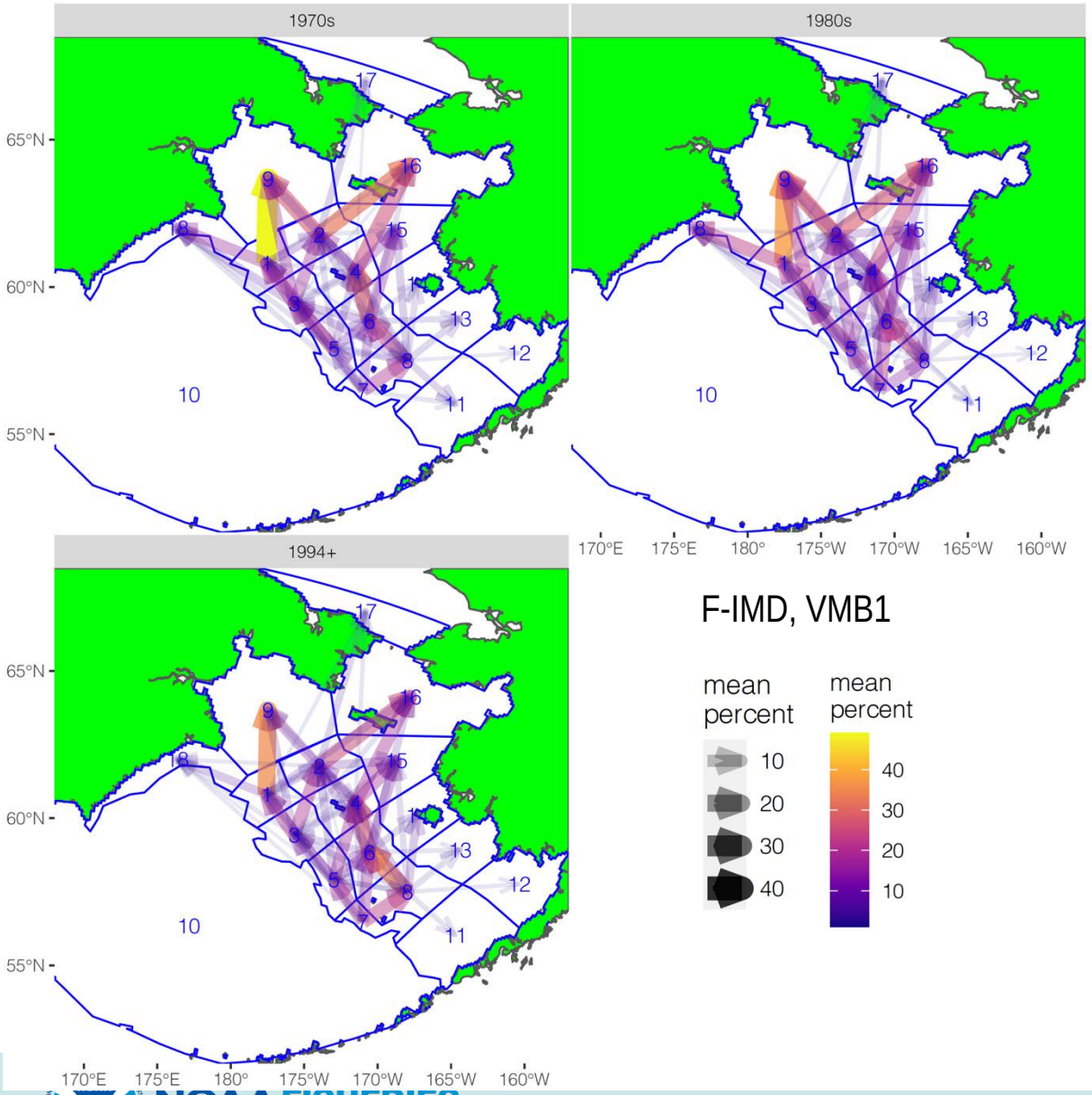
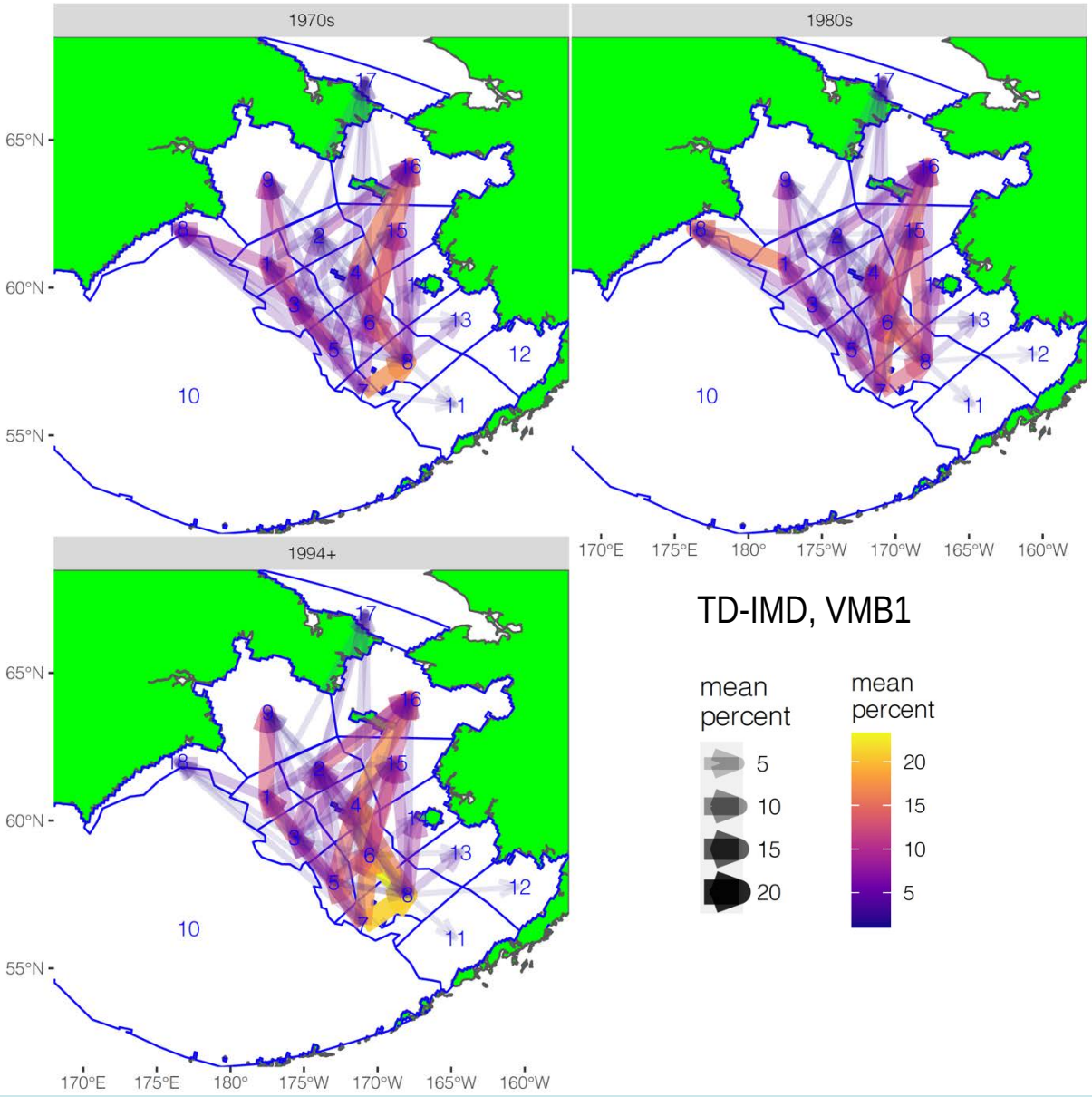
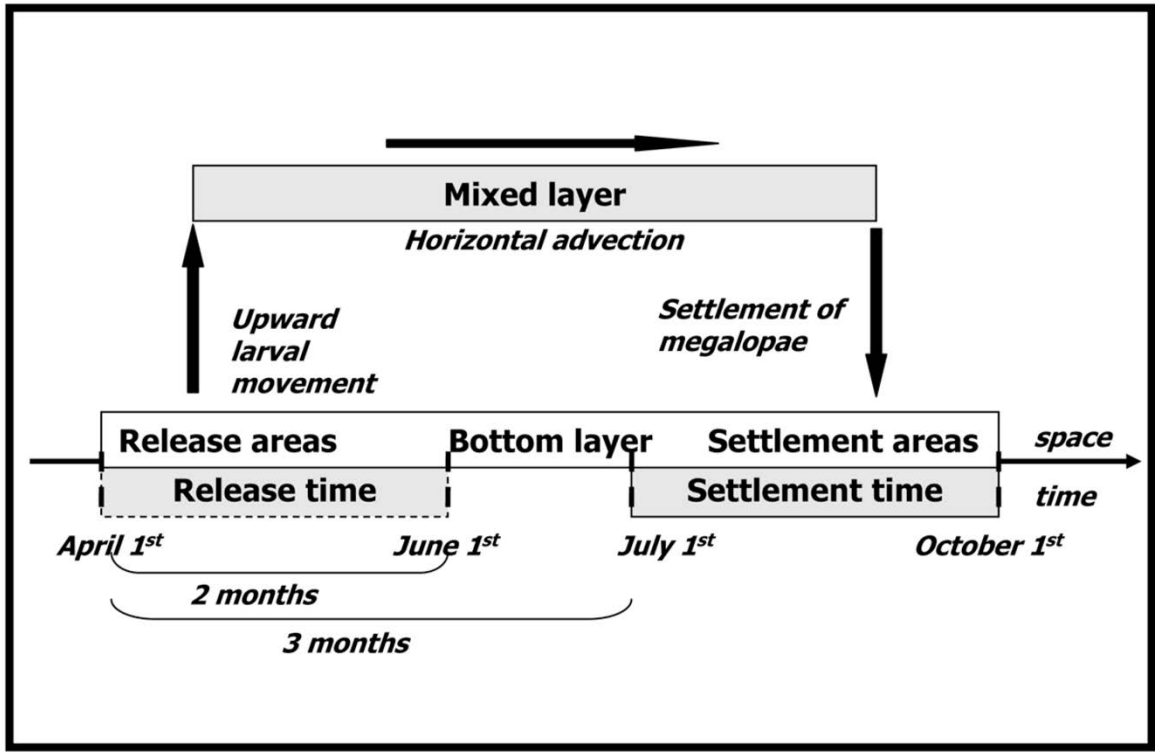




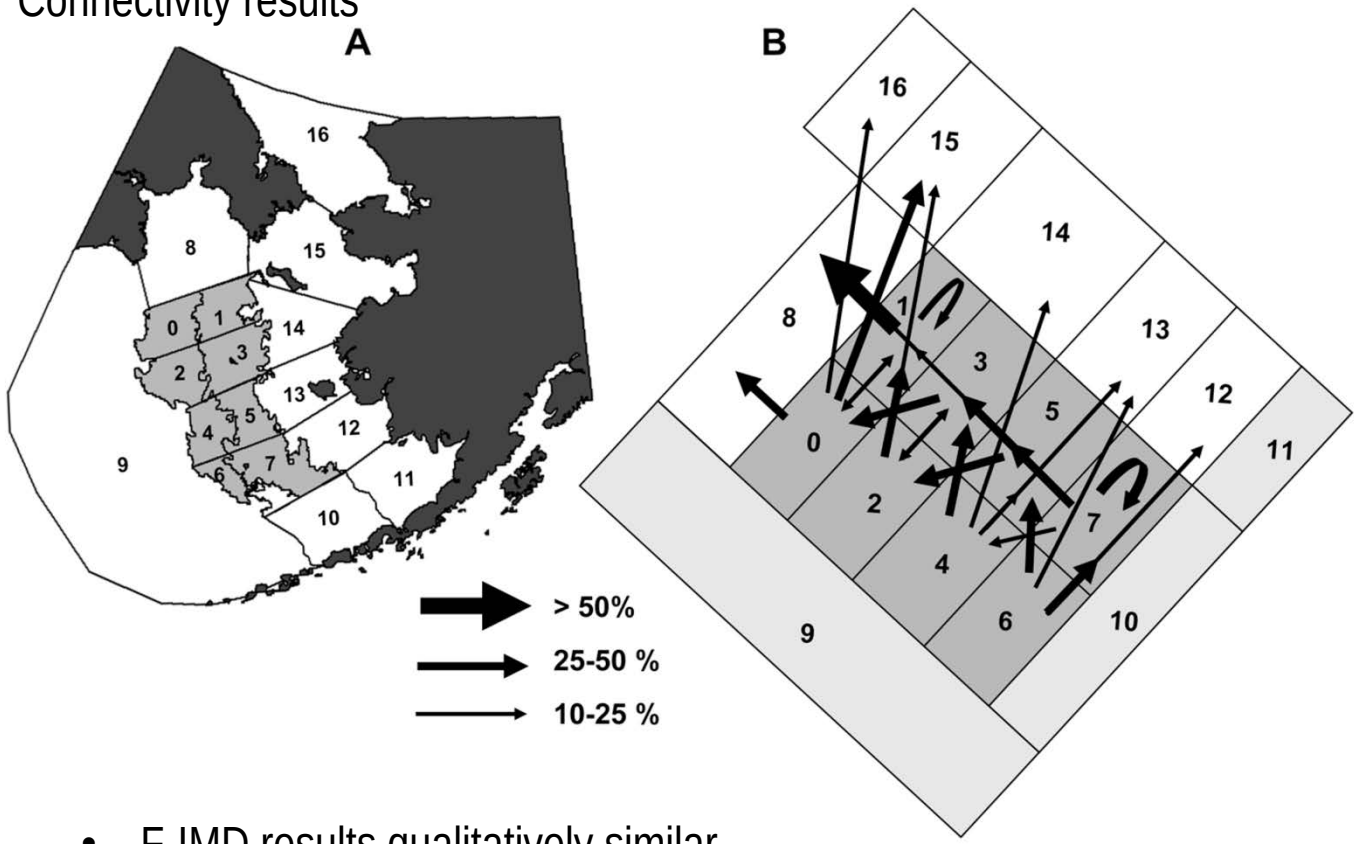
Previous work: Parada et al. (2010)

[note: zones 0 to 16 match our 1 to 17]

Conceptual model



Connectivity results



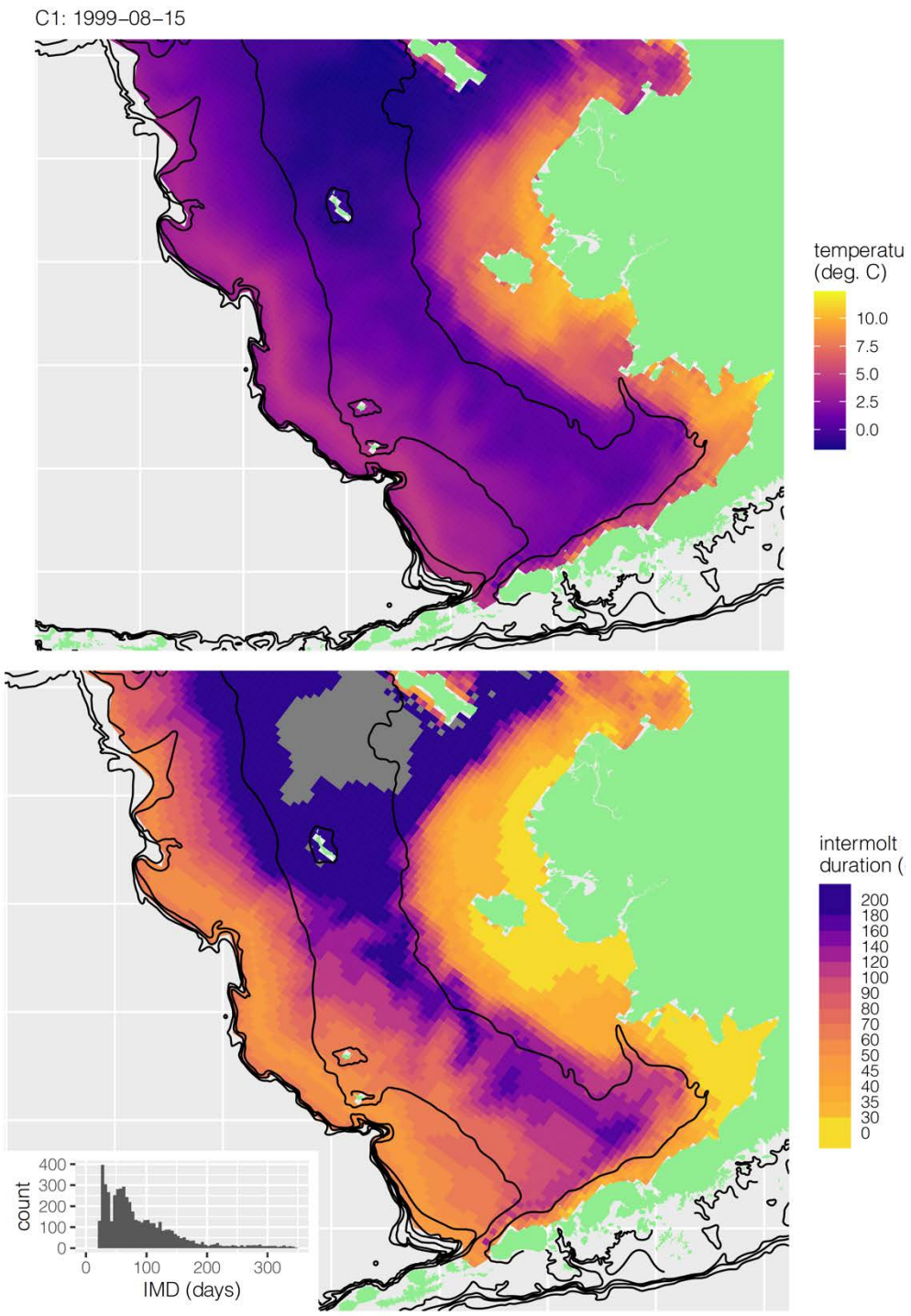
- zooea tracked for 90 days
- fixed stage durations
- settlement evaluated at beginning of megalopal stage

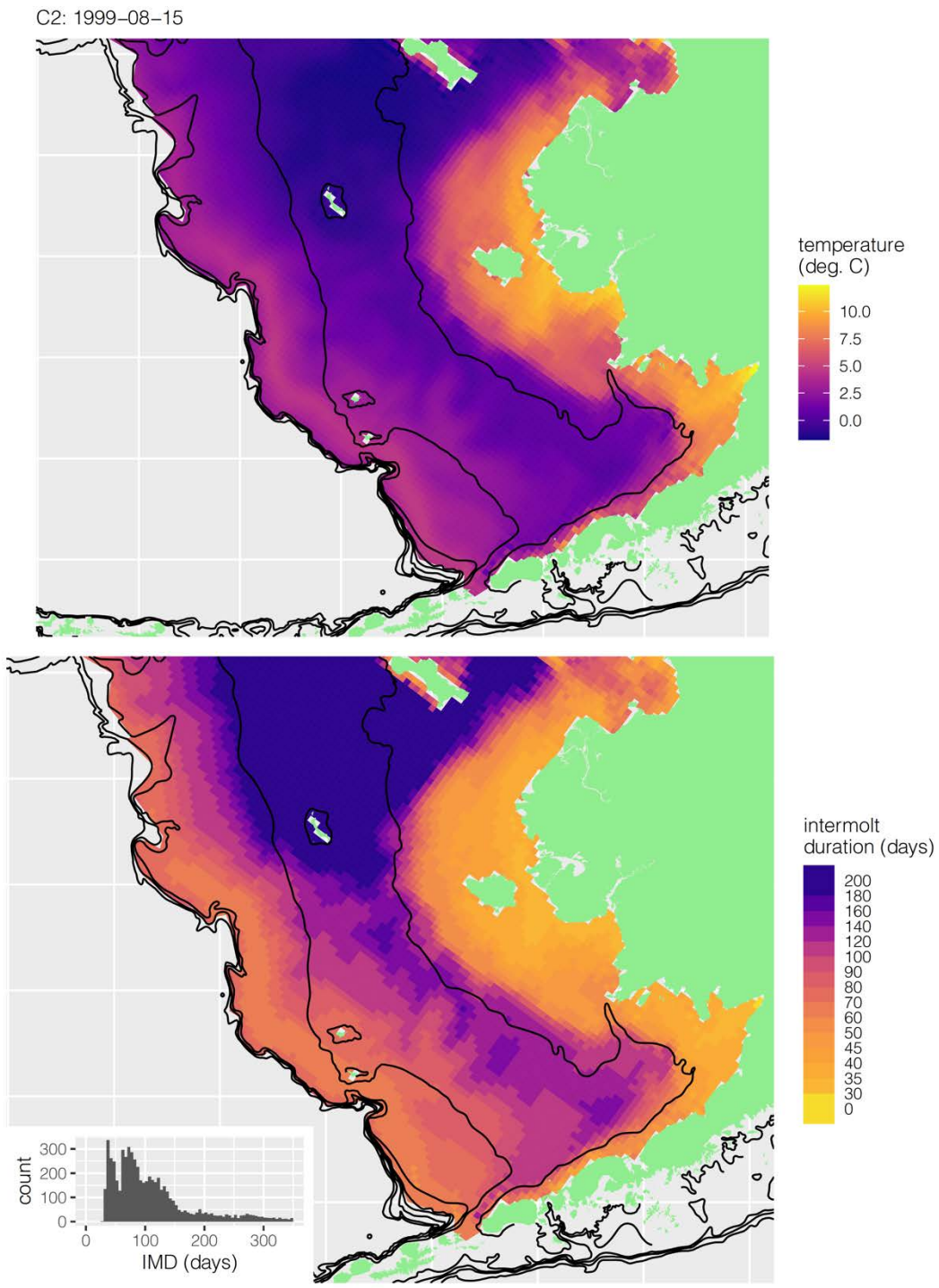
- F-IMD results qualitatively similar
  - different ROMS models
  - different settlement “windows”

In-process/future work (1)

- Forecast changes in connectivity using downscaled CMIP6 ROMS models
- Integrate spatial patterns of primiparous and multiparous females into connectivity calculations to predict benthic settlement patterns
- Simulate TD-IMD trends for early benthic instars C1-C7 to predict/estimate annual mixtures of cohorts “recruiting” to assessment model
  - possible ESP contribution?

TD-IMDs for Early-Benthic Instars





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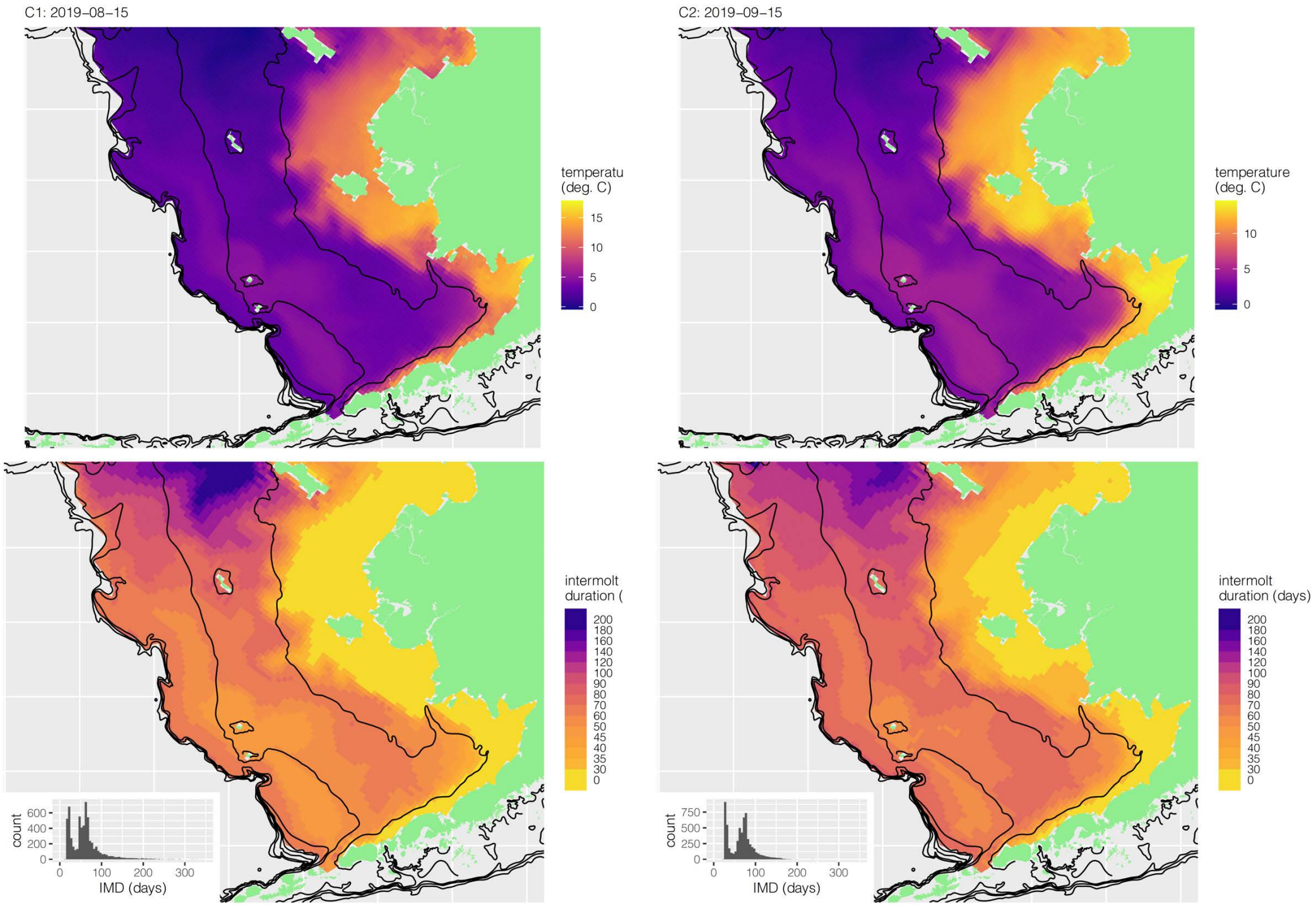
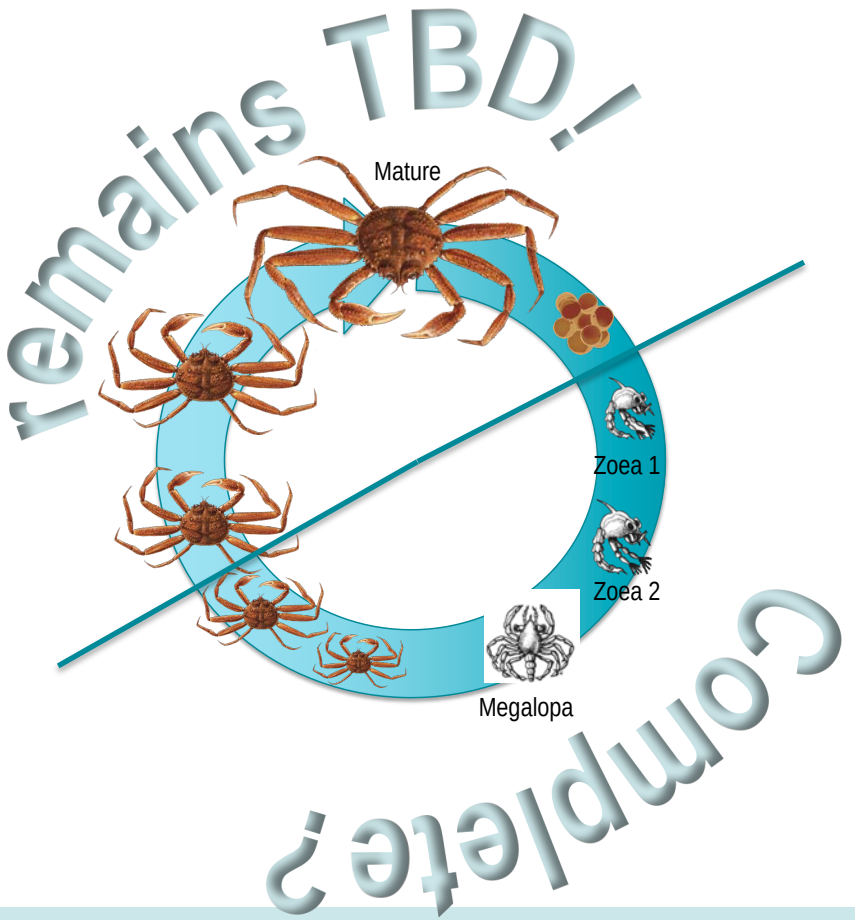
TD-IMDs for Early-Benthic Instars



In-process/future work (2)

- Add bioenergetics
- Add mortality
- Interface with spatially-explicit snow crab assessment model

- Close the life cycle



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    - NOAA FATE
    - NPRB GOA IERP, GOA IERP Synthesis
  - Snow Crab IBM
    - NMFS Magnuson-Stevens Research Funds
- Contributors
  - Postdocs: Michael Torre, Christine Stawitz
  - ROMS model output: ACLIM 1.0, 2.0
    - Al Hermann, Wei Cheng, Kelly Kearney
  - Others: Cody Szuwalski, Robert Foy, Kirstin Holsman, Anne Holllowed