

Understanding the life cycle of North Sea brown shrimp *Crangon crangon*: a simulation model approach

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Marine Ecology Progress Series 584: 119–143 (2017)

Table S1: Settings and parameters of previous model versions. Most settings of standard run (SR) I in the present study were identical to the final standard run (V4) of Rückert (2011), however, four modifications were applied: (1) we simulated a population with males and females instead of modelling only females. (2) Mortality between the larval and the adult life-stage was interpolated smoothly instead of assuming a stepwise decrease. (3) We used the moulting function of Hufnagl & Temming (2011) and (4) changed the implementation of growth variability between cohorts.

Parameter/Setting	Author		Temming & Damm 2002	Lütke 2002	ICES 2003	Rückert 2011	Temming & Hufnagl 2015
	Version number	Name and further specification	V1	V2	V3	V4	V5
		Unit					
Sex		-	female only	see V1	see V1	female + males	see V4
Spawning index (monthly)			0.86;0.50;0.43;0.76;1.18;1.44; 1.69;1.26;0.50;0.38;1.01;1.17	see V1	see V1	1.01; 1.07; 0.37; 0.91; 1.46; 1.92; 2.28; 1.01; 0.41; 0.32; 0.52; 0.73	0.89;0.64;0.78;1.12;1.78;2.37; 1.88;1.11;0.31;0.22;0.53;0.74
Growth variability parameters			-	s: standard deviation, life-stage dependent ; r: random number with mean = 0 and sd = 1;	see V2	see V2	vG: life-stage independent cohort specific number; drawn from a normal distribution with mean =1 and sd=0.3
Growth Rate	D; egg dev.time	(d)	D = 1031.34 * T ^{-1.354} (Redant 1978)	D = (1031.34 + s*r) * T ^{-1.354} , s= 48.7;	not specified	see V2	D = (1031.34 * T ^{-1.354})* vG
	D; larval dev. time	(d)	D = (5.5/0.00584) * T ^{-1.347} (Crales & Anger 1986)	D = (5.5/0.00584) * T ^(-1.347 + s*r) , s = 0.037;	not specified	see V2	D = ((5.5/0.00584) * T ^{-1.347}) * vG
	GR; growth rate	(mm*d ⁻¹)	GR = 0.1625 +0.01025*T - 0.00403 *L (Kuipers & Dapper 1984)	Three variants: (1): GR = 0.1625 +0.01025*T - 0.00403 * (1+s*r) *L; (2): GR = 0.25 +0.014*T - 0.0042 * (1+s*r) *L; (3): GR = 0.038*T - 0.0017 * e ^{0.087*T} * (1+s*r) *L; s = 0.3;	see V2, variant (3)	splitted in female and male	see V4

	GR _{fem} ; female growth rate	(mm*d ⁻¹)	-	-	-	GR _{fem} = 0.03946*T - 0.00177 * e ^{0.0951*T} * (1+s*r) * L; s = 0.3;	GR _{fem} = (0.04028 * T - 0.00193 * e ^{0.0878 * T} * L) * vG (Hufnagl & Temming (2011))
	GR _{male} ; male growth rate	(mm*d ⁻¹)	-	-	-	GR _{male} = 0.03238*T - 0.00187 * e ^{0.0951*T} * (1+s*r) * L; s = 0.3;	GR _{male} = (0.03424 * T - 0.00187 * e ^{0.0878 * T} * L) * vG (Hufnagl & Temming 2011)
Length:Weight relationship	WW; wet weight	(g)	-	WW = 0.375*10 ⁻⁶ *L ^{3.186} (van Lissa 1977)	<i>see V2</i>	WW = 4.625*10 ⁻⁶ *L ^{3.084} (Hufnagl et al. 2010)	<i>see V4</i>
	DW; dry weight	(g)	-	DW = WW*0.25	<i>see V2</i>	DW = WW *0.2585 (Hufnagl et al. 2010)	<i>see V4</i>
Length:Weight relationship of zoea stages (ZS)	DW _{ZS} ; dry weight	(kg)	-	DW _{ZS} = e ^{2.7+0.222 * ZS} * 10 ⁶ (Criales 1985)	<i>see V2</i>	<i>see V2</i>	<i>see V2</i>
	WW _{ZS} ; wet weight	(kg)	-	WW _{ZS} = DW _{ZS} *0.25 ⁻¹	<i>see V2</i>	<i>see V2</i>	<i>see V2</i>
Natural mortality	M _{egg} ; egg mortality	(y ⁻¹)	-	M _{adu}	<i>see V2</i>	<i>see V2</i>	<i>see V2</i>
	M _{larvae} ; larval mortality	(y ⁻¹)	-	M _{larvae} = 365* 1.22*0.0423* WW _{ZS} ^{-0.25} (Peterson & Wroblewski 1984)	M _{larvae} (Life-stage average) = 17.7; (Source: M _{larvae} = 0.65* WW _{ZS} ^{-0.37} ; Banse & Mosher 1980)	M _{larvae} (Life-stage average) = 26.6; (Source: M _{larvae} =1.22*1.5768* DW _{ZS} ^{-0.25} ; Peterson & Wroblewski 1984)	M _{larvae} = 1.22*1.5768* DW _{ZS} ^{-0.25} (Peterson & Wroblewski 1984)
	M _{juv} ; juvenile mortality	(y ⁻¹)	-	M _{juv} = 365* 1.22*0.0423*WW ^{-0.25} (Peterson & Wroblewski 1984)	M _{juv1} (Life-stage average; 6 - 20mm) = 10.2; M _{juv2} (Life-stage average; 20- 50mm) = 4.5 (Source: M _{juv} = 0.65* WW ^{-0.37} ; Banse & Mosher 1980)	M _{juv1} (Life-stage average; 6 - 20 mm) = 9.9; M _{juv2} (Life-stage average; 20- 50 mm) = 4.8 (Source: M _{juv} = 1.22*1.5768*DW ^{-0.25} ; Peterson & Wroblewski 1984)	interpolated from M ₆ (6 mm, ZS 6) = 23.5 to M _{adu} ; M = exp((log(M ₆) + (log(L) - log(6)) * (log(M _{adu}) - log(M ₆)) / (log(50) - log(6))))
	M _{adu} ; adult mortality	(y ⁻¹)	-	3.83	3.2	3.3	variable
Seasonal mortality index (monthly)	sM _{larvae}	-	-	0.23;0.23;0.27;0.28;0.56;1.13; 1.69;2.26;2.26;1.69;1.13;0.28	<i>see V2</i>	<i>see V2</i>	<i>see V2</i>
	sM _{juv1} (5-20mm)	-	-	0.30;0.30;0.34;0.39;0.44;0.54; 0.69;1.97;2.46;2.46;1.67;0.44	<i>see V2</i>	0.22;0.22;0.27;0.28;0.57;1.13; 1.69;2.26;2.26;1.69;1.12;0.28	0.26;0.26;0.28;0.30;0.51;1.10; 1.65;2.19;2.21;1.75;1.17;0.33

	sM _{juv2} (20-50mm)	-	-	0.56;0.61;0.67;0.67;0.89;0.89; 1.12;1.12;1.34;1.79;1.56;0.78	see V2	0.25;0.25;0.29;0.29;0.50;1.08; 1.64;2.20;2.24;1.78;1.16;0.33	sM _{juv1}
	sM _{adu} (> 50mm)	-	-	0.35;0.35;0.35;0.35;1.41;1.41; 1.41;1.41;1.41;2.12;1.06;0.35	see V2	0.33;0.33;0.33;0.33;0.33;0.96; 1.50;2.02;2.14;2.02;1.26;0.45	see V4
Fishing Mortality		(y ⁻¹)	-	1.91	1.6	2.2	Variable
Fishing effort index (monthly)		-	-	0.04;0.04;0.31;1.41;1.41;1.41; 1.41;1.41;1.41;1.41;1.41;0.31	0.06;0.06;0.32;1.40;1.40;1.40; 40; 1.40;1.40;1.40;1.40;1.40;0.32	eq.V2	0.16;0.20;0.80;1.65;1.47;1.28; 1.17;1.23;1.28;1.23;1.03;0.48 (ICES hp-days at sea (Germany); 2002-2010)
Z (total mortality)		(y ⁻¹)	-	5.75	4.8	5.5	Variable
Moult	MF; moulting frequency	(d)	Polynom function of temperature and female length (see Temming & Damm 2002)	see VI	see VI	see VI	-
Spawn age min		(d)	-	-	-	185	-
Temperature	T _{larvae}	(°C)	German Run (Helgoland Roads): 1986, 1992, 1993, mean (1960-1995); Dutch run (Texel lightship, Fonds 1978): 1986, 1992, 1993, mean (1960-62, 64)	see VI	see VI	Texel lightship: mean (1960-62, 64) (Fonds 1978)	not specified
	T _{others}	(°C)	German Run: warmer T of T _{larvae} or Büsum Harbour (1986, 1992, 1993, mean (1960-1995)); Dutch run: warmer T of T _{larvae} Or Wadden Sea (1986, 1992, 1993, mean (1960-62, 64)) (Fonds 1978)	see VI	see VI	warmer T of Helgoland Roads (1960-1995) or Büsum Harbour (1960-1995)	not specified

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for (start_day in 1:1095) { # Loop 1: simulate for 3 years
length_mat = 47.5 + (1/0.244) * log(P_mat / (99.5*0.076-0.076* P_mat)) #define cohort specific length at first maturity (equation 13)

  for (daily_cohort in 1:30) { # Loop 2: number of daily cohorts

    # define start conditions for each daily cohort
    D_egg = 0 # state of egg development; 0=start (at age 0), 1=egg stage completed; if D_egg > 1 larval development starts
    D_larvae = 0 # state of larval development; 0=start (at age 0), 1=larval stage completed; if D_larvae > 1 juvenile growth starts
    Length_female = 6 # female length starts with 6 mm
    Length_male = 6 # male length starts with 6 mm
    Abund_female = start_number * spawn_index[start_day]/2 # Initial cohort size as a function of season (females)
    Abund_male = start_number * spawn_index[start_day]/2 # Initial cohort size as a function of season (males)

    for (age in 1:730) { # Loop 3: age (days) of a daily cohort

      real_day <- start_day + age-1 # helper variable (to use input data (e.g. temperature) of the particular day)

      # take values of the last time step (for „length“ see first gender condition)
      i_Abund_f = Abund_female
      i_Abund_m = Abund_male
      i_Devel_egg = D_egg
      i_Devel_larv = D_larvae

      D_egg = 1/((1031.44*T_others[real_day]-1.354)) # daily fraction of egg development (equation 4)
      D_larvae = 1/((5.0/0.00584*T_larvae[real_day]-1.347)) # daily fraction of larval development (equation 5)

      for (gender in 1:2) { # gender 1 = female, gender 2 = male

        if (gender == 1) { # female
          i_Length = Length_female # take length of the last time step
          length_increment = 0.04028 * T_others[real_day]-0.00193 * exp(0.08777 * T_others[real_day])*i_Length
          # daily length increment (equation 8)
        } else if (gender == 2) { # male
          i_Length = Length_male # take length of the last time step
          length_increment = 0.03424 * T_others[real_day]-0.002 * exp(0.08777 * T_others[real_day])*i_Length
          # daily length increment (equation 8)
        } # end of „gender“ - condition

        # Add variability to development and growth of daily cohorts
        D_egg = D_egg * vG[daily_cohort]
        D_larvae = D_larvae * vG[daily_cohort]
        length_increment = length_increment * vG[daily_cohort]

        if (i_Devel_egg < 1) {
          i_Devel_egg = i_Devel_egg + D_egg # add fraction of egg development if cohort is in egg stage
        } else if (i_Devel_egg > 1 & i_Devel_larv < 1) {
          i_Devel_larv = i_Devel_larv + D_larvae # add fraction of larval development if cohort is in larval stage
        } else if (i_Devel_larv > 1) { # add daily length growth interval if daily_cohort is in juvenile/adult stage
          i_Length = i_Length + length_increment # add length increment if cohort is in juv./adult stage
        } # end of condition for adding development fraction / length increment

        # natural mortality – larval stage
        ZS = 1 + floor(i_Devel_larv/20) # floor: rounding down
        # ZS: Zoea stage estimated by larvae development state
        # 0-20, 20-40, 40-60, 60-80 & 80-100% of total development
        # corresponds to ZS I, II, III, IV & V
        DW_ZS = 0.000001*exp(2.7+0.222*i_Devel_larv) # dry weight of ZS (equation 10)
        M_larvae = 1.22*1.5768* DW_ZS^0.25 # size dependent mortality of larvae (equation 9)
        M_larvae = M_larvae * sM_larvae[real_day] # size dependent and seasonal mortality for larvae

        # natural mortality – juvenile stage
        DW_ZS_V = 0.000001*exp(2.7+0.222*(5)) # dry weight of ZS V (equation 10)
        M_6 = 1.22*1.5768* DW_ZS_V^0.25 # M of ZS V / start of juv. Stage (equation 9)
        M_juv = exp(log(M_6) + (log(i_Length)-log(6)) * (log(M)-log(M_6))/(log(50)-log(6)))
        # size dependent mortality for juveniles (equation 11)
        M_juv1 = M_juv * sM_juv1[real_day] # size dependent and seasonal mortality for juveniles of 6-20 mm
        M_juv2 = M_juv * sM_juv2[real_day] # size dependent and seasonal mortality for juveniles of 20-50 mm
        M_adu = M * sM_adu[real_day] # size dependent and seasonal mortality for adult shrimp

        # fishing mortality
        F = F*sF[real_day] # seasonal fishing mortality

        # total mortality
        if (i_Devel_egg < 1) {
          Z = M_adu + F # natural and fishing mortality of adult stage if cohort is in egg stage
        } else if (i_Devel_egg > 1 & i_Devel_larv < 1) {
          Z = M_larvae # natural mortality of larvae if cohort is in larval stage
        } else if (i_Devel_larv > 1 & i_Length < 20) {
          Z = M_juv1 # natural mortality of small juveniles if cohort has finished larval stage and is smaller 20 mm
        } else if (i_Length > 20 & i_Length < 50) {
          Z = M_juv2 # natural mortality of large juveniles if cohort has finished larval stage and is smaller 50 mm
        } else if (i_Length > 50) {
          Z = M_adu + F # natural and fishing mortality of adult shrimps
        } # end of condition for total mortality
      }
    }
  }
}

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GROWTH

MORTALITY

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if (start_day > 730){ # only for the last year of simulation

  if (gender == 1) { # females
    if (age > age_min_spawn & i_Length > length_mat) { # spawn if min. spawning age and
      # length of maturation is reached
      share_moult = 1/(5.7066 * i_Length^0.7364 * exp(-0.09363 * T_others [real_day]))
      # inverse of intermoult period (equation 3)
      EF = 0.001805 * i_Length^3.539 # eggs per female (equation 2)
      i_egg = i_Abund_f * share_moult * EF # number of spawned eggs
    } # end of spawn conditions
  }

  i_n_landings = i_Abund_f * (1 - exp(-F * (1/365))) # landings in numbers (females)
  i_landings = i_n_landings * 4.625 * 0.000001 * i_Length^3.084 # landings in g (equation 14)
  i_n_bio = i_Abund_f # number in the population (females)
  i_bio = i_n_bio * 4.625 * 0.000001 * i_Length^3.084 # biomass (equation 14)
  # also stored but not shown here: length frequency distribution of females (biomass & landings)

  if (i_Length == 15) {
    i_rec = i_Abund_f # number of 15 mm recruits (females)
  } # end of „recruit length“ condition

  } else if (gender == 2) { # males

    i_n_landings = i_Abund_m * (1 - exp(-F * (1/365))) # landings in numbers (males)
    i_landings = i_n_landings * 4.625 * 0.000001 * i_Length^3.084 # landings in g (equation 14)
    i_n_bio = i_Abund_m # number in the population (males)
    i_bio = i_n_bio * 4.625 * 0.000001 * i_Length^3.084 # biomass (equation 14)
    # also stored but not shown here: length frequency distribution of females (biomass & landings)

    if (i_Length == 15) {
      i_rec = i_Abund_m # number of 15 mm recruits (males)
    } # end of „recruit length“ condition

  } # end of gender condition

  # add both genders and add on monthly basis;
  # store results of for this age of the corresponding cohort
  # "month" is a helper variable that gives the corresponding month at a specific start_day
  landings_age [month] = landings_age [month] + sum(i_landings) * 0.000001 # total landings (t)
  neggs_age [month] = neggs_age [month] + sum(i_egg); # number of produced eggs
  biomass_age [month] = biomass_age [month] + sum(i_bio) * 0.000001 # cumulative biomass (t)
  rec_age [month] = rec_age [month] + sum(i_rec) # number of recruits
  # also stored but not shown here: length frequency distribution of females (biomass & landings)

} # end of last year condition

D_egg = i_Devel_egg
D_larvae = i_Devel_larv
if (gender == 1) { # female
  Abund_female = i_Abund_f * (exp(-Z * (1/365))) # Reduce cohort size (equation 12)
  Length_female = i_Length
} else if (gender == 2) { # male
  Abund_male = i_Abund_m * (exp(-Z * (1/365))) # Reduce cohort size (equation 12)
  Length_male = i_Length
} # if-else condition gender

} # close gender loop
} # close Loop 3 (age)

# store results for each daily cohort
landings_cohorts [month] = landings_cohorts [month] + landings_age [month]
neggs_cohorts [month] = neggs_cohorts [month] + neggs_age [month]
biomass_cohorts [month] = biomass_cohorts [month] + biomass_age [month]
rec_cohorts [month] = rec_cohorts [month] + rec_age [month]
# also stored but not shown here: length frequency distribution of females (biomass & landings)

} # close Loop 2 (daily cohort)

# store results for each start_day
landings [month] = landings [month] + landings_cohorts [month]
neggs [month] = neggs [month] + neggs_cohorts [month]
biomass [month] = biomass [month] + biomass_cohorts [month]
rec [month] = rec [month] + rec_cohorts [month]
# also stored but not shown here: length frequency distribution of females (biomass & landings)

} # close Loop 1 (start_day)

biomass = biomass / monthlength # calculate average monthly biomass

```

Figure S1: Modified extract of the model programmed in “R” to illustrate program structure. To increase comprehensibility only important features were selected. The original code (not shown here) uses a matrix algebra to increase calculation speed

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