SUPPLEMENTARY FIGURES AND TABLES

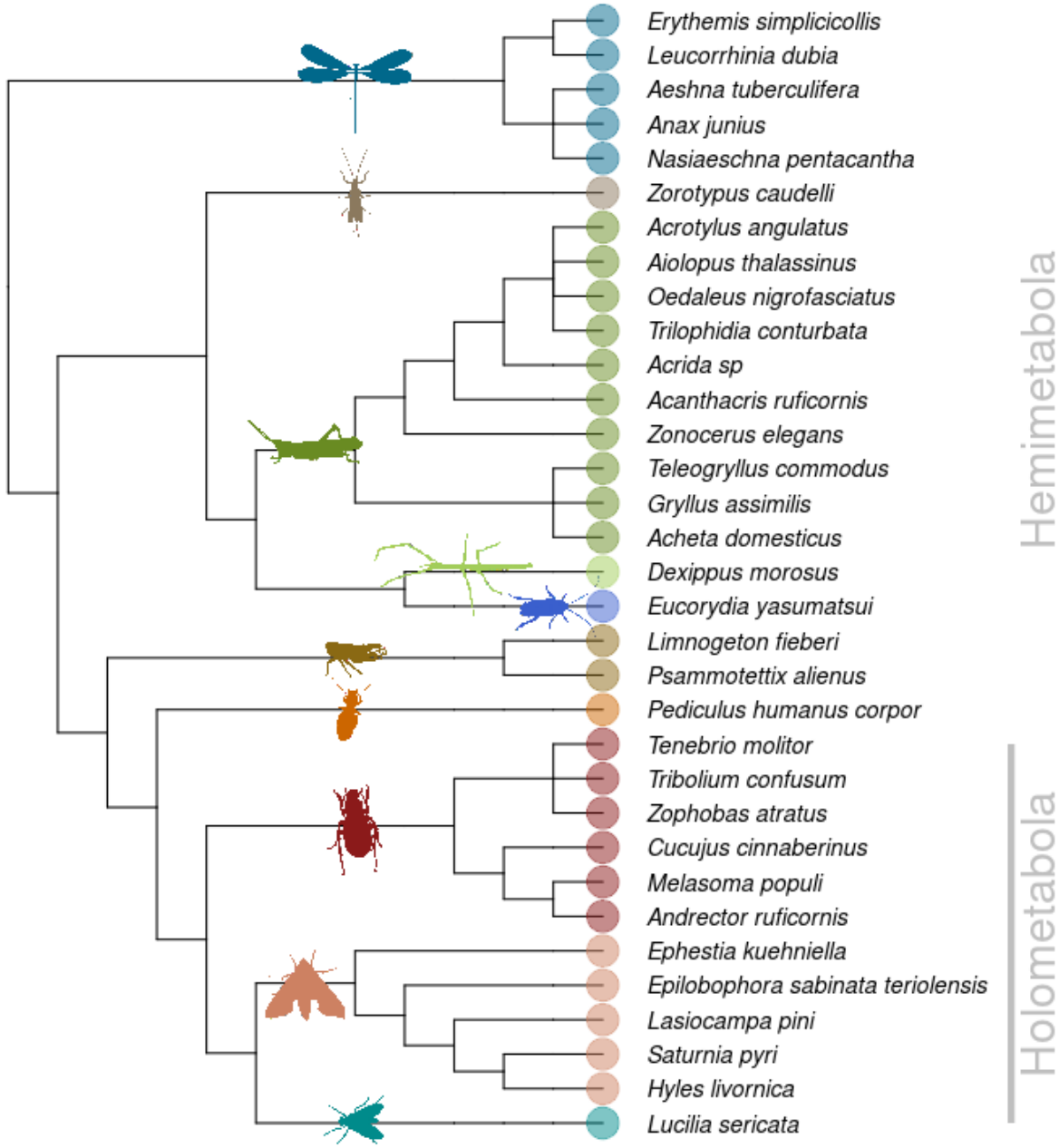
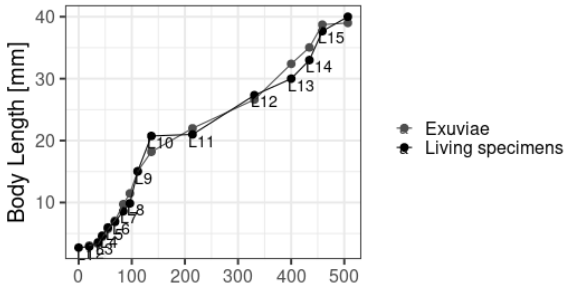


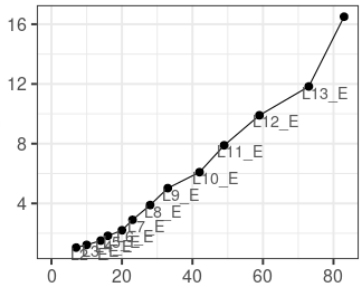
Figure S1: **Phylogeny of the insect species included in our comparative study of growth rates.** Our analysis includes 21 hemimetabolous and 12 holometabolous insects. The Hemimetabola cover seven orders (Odonata, Zoraptera, Orthoptera, Phasmatodea, Blattodea, Hemiptera and Psocodea) and the Holometabola three (Coleoptera, Lepidoptera, and Diptera). The growth trajectories for each species can be found in the supplementary material.

Odonata

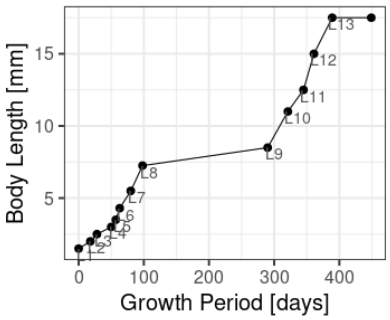
Aeshna tuberculifera



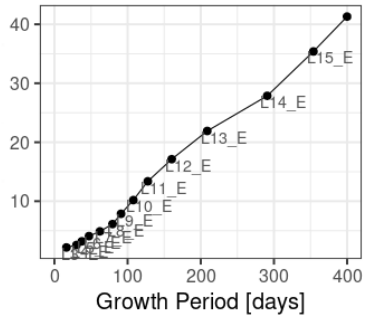
Erythemis simplicicolli



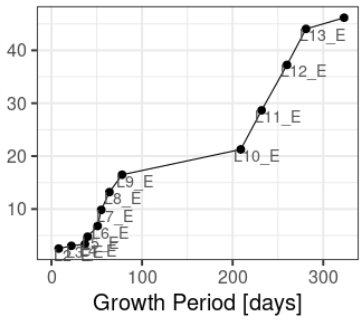
Leucorrhinia dubia



Nasiaeschna pentacantha

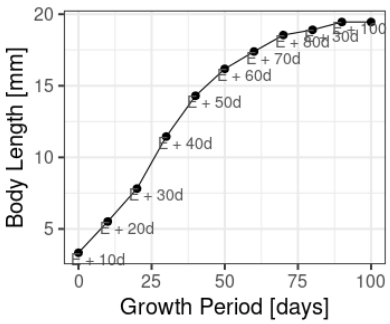


Anax junius

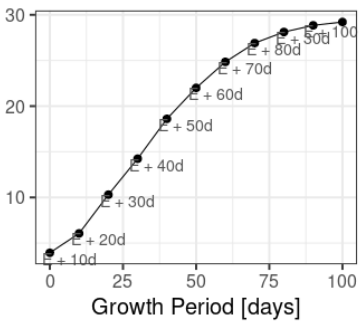


Orthoptera

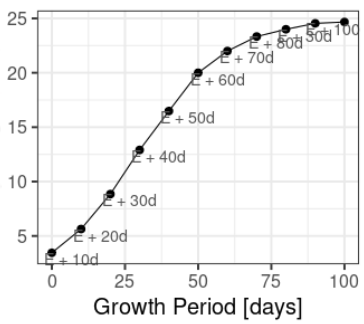
Acheta domesticus



Gryllus assimilis

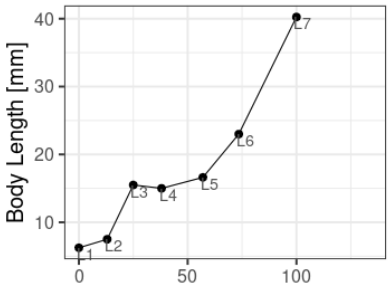


Teleogryllus commodus

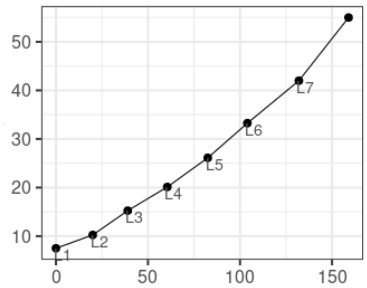


Orthoptera

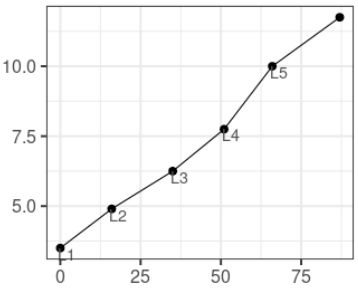
Acanthacris ruficornis



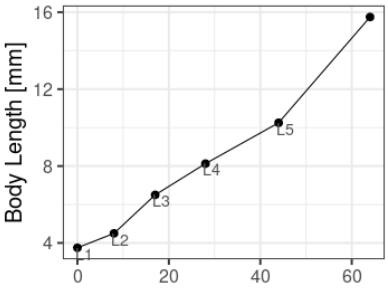
Acrida sp.



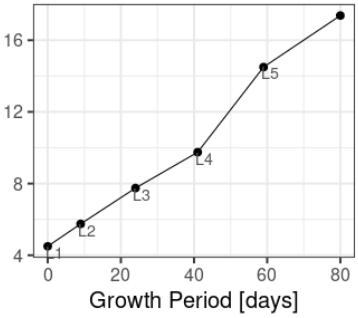
Acrotylus angulatus



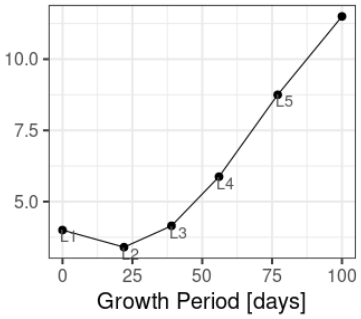
Aiolopus thalassinus



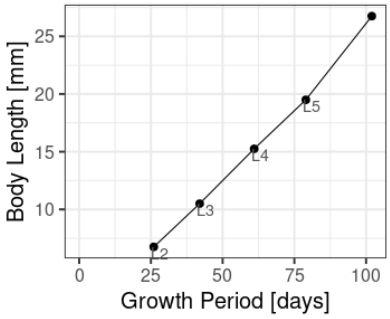
Oedaleus nigrofasciatus



Trilophidia conturbata

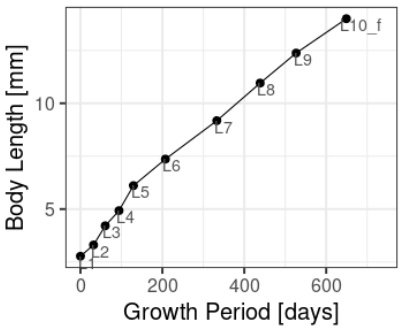


Zonocerus elegans



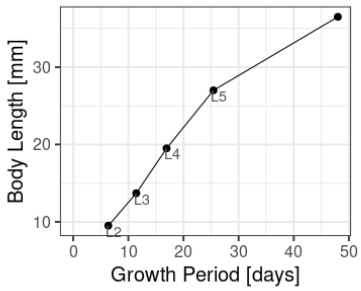
Blattodea

Eucorydia yasumatsui

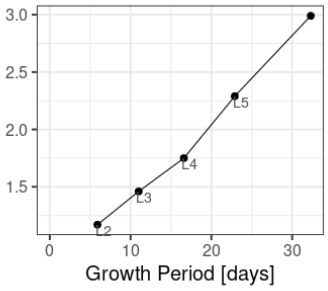


Hemiptera

Limnogeton fieberi

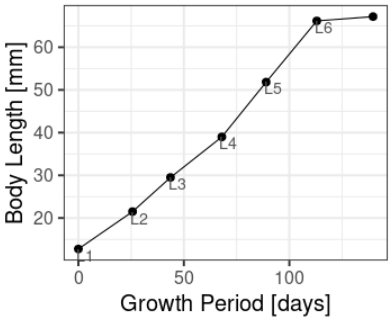


Psammotettix alienus



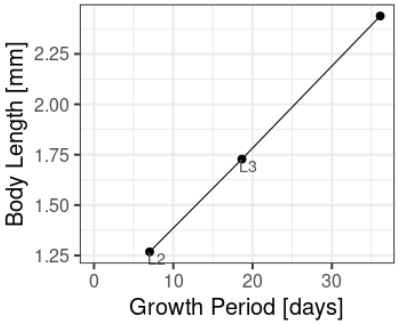
Phasmatodea

Dixippus morosus



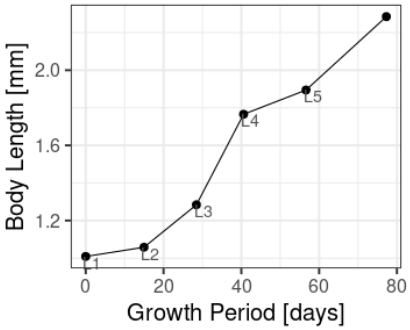
Psocodea

Pediculus humanus corpor



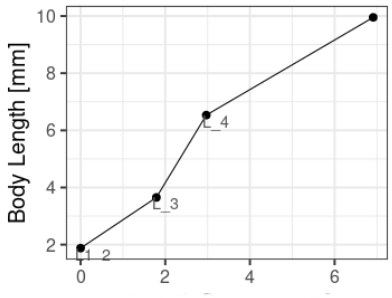
Zoraptera

Zorotypus caudelli

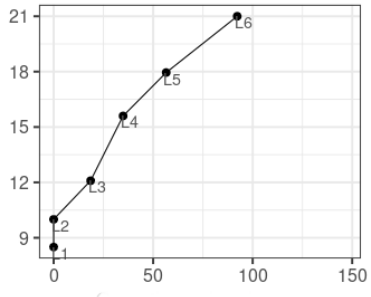


Coleoptera

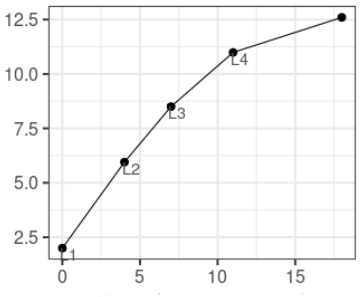
Andrector ruficornis



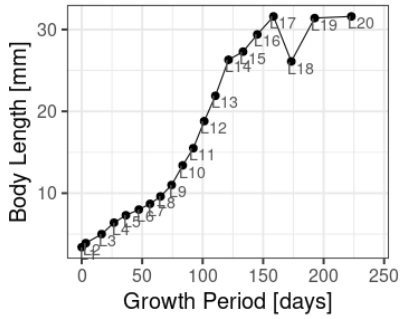
Cucujus cinnaberinus



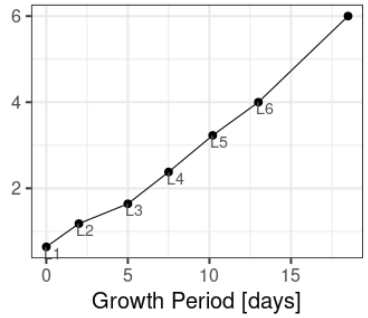
Melasoma populi



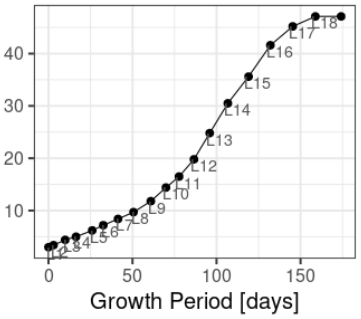
Tenebrio molitor



Tribolium confusum

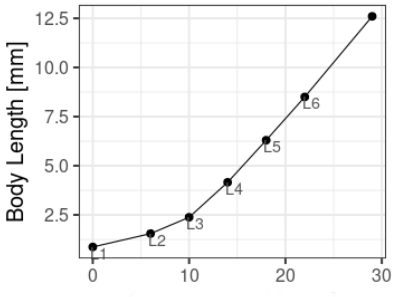


Zophobas atratus

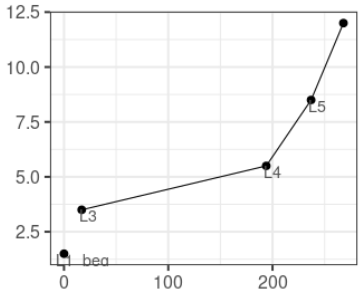


Lepidoptera

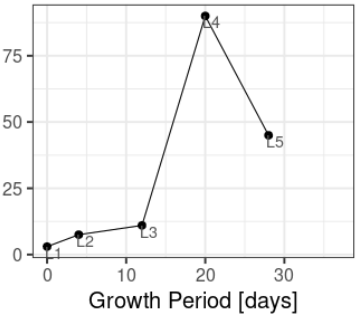
Ephestia kuehniella



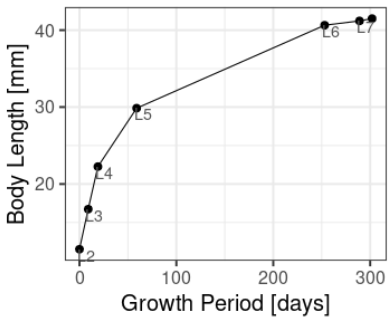
Epilobophora sabinata teriolensis



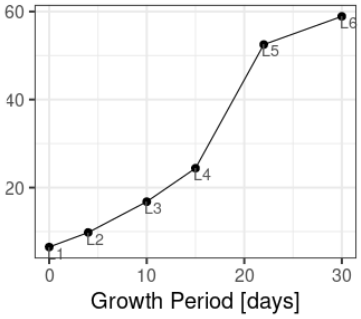
Hyles livornica



Lasiocampa pini



Saturnia pyri



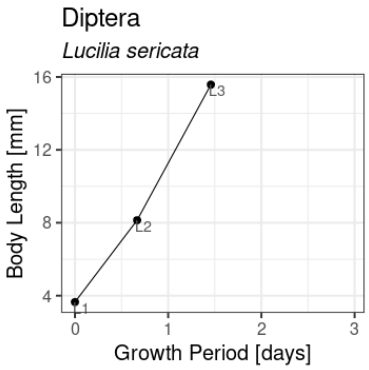


Figure S2: The growth trajectories of all insect species, ordered by insect order, included in the comparative analysis (mean relative growth rates per immature stage).

Table S1: Keywords used to search ZOBODAT for literature on insect growth. Also shown are the number of publications of the initial and final search (all criteria met) and the number of insects we used for the final dataset.

	Search terms		No. of publications (initial search)	No. of publication that fit all criteria	Species number
	Keywords (from Misof et al, 2014)	German names and synonyms			
Hemimetabola	Archaeognatha	Felsenspringer	18	0	0
	Zygentoma	Fischchen	10	0	0
	Odonata	Libelle; Wasserjungfer	928	5	5
	Ephemeoptera	Eintagsfliege	80	0	0
	Zoraptera	Bodenlaus	4	1	1
	Dermaptera	Ohrwurm	50	0	0
	Plecoptera	Steinfliege	546	0	0
	Orthoptera	Heuschrecke	538	2	10
	Mantophasmatodea	Gladiatorschrecke; Gladiator; Fersenläufer	4	0	0
	Grylloblattodea	Grillenschabe; Notoptera	0	0	0
	Embioptera	Tarsenspinner; Fersenspinner	4	0	0
	Phasmatodea	Gespenstschrecke; Phasmida; Phasmiden	37	1	1
	Mantodea	Fangschrecke; Gottesanbeterin	104	0	0
	Blattodea	Schabe; Blatteria	61	1	1
	Isoptera	Termiten	143	0	0
	Thysanoptera	Fransenflügler; Thrips; Blasenfüße; Gewittertierchen; Gewitterwürmer	76	0	0
	Hemiptera	Schnabelkerfe; Rhynchota	584	2	2
	Psocodea	Staublaus; Psocoptera	7	1	1
	Hymenoptera	Hautflügler	3526	0	0
	Raphidioptera	Kamelhalsfliege	112	0	0
	Megaloptera	Großflügler; Schlammfliege	40	0	0
	Neurotera	Netzflügler; Planipennia	292	0	0
	Strepsiptera	Fächeflügler	41	0	0

	Search terms		No. of publications (initial search)	No. of publication that fit all criteria	Species number
	Keywords (from Misof et al, 2014)	German names and synonyms			
Holometabola	Coleoptera	Käfer	5478	6	6
	Trichoptera	Köcherfliege	678	0	0
	Lepidopera	Schmetterling	4791	5	5
	Siphonaptera	Flöhe	68	0	0
	Mecoptera	Schnabelfliege; Schnabelhafte	5	0	0
	Diptera	Zweiflügler	2014	1	1

Table S2: Results of the regression analyses controlled for phylogeny (multivariate linear mixed-effects models) testing differences in *RGR* between hemi- and holometabolous insects.

Model		Estimate	SE	T-value	Df	P-value	Lower CI	Upper CI	
(1) Intercept model	Intercept	0.023	0.003	7.156	32	<.0001	0.016	0.029	***
(2) Model looking at contrast between the groups	Intercept	0.019	0.004	4.737	31	<.0001	0.011	0.027	***
	Hemi Holo	0.018	0.008	2.286	31	0.0293	0.002	0.035	*
(3) Modelling heteroscadasticity	Intercept	0.0178	0.0023	7.9218	31	<.0001	0.0132	0.0224	***
	Hemi_Holo	0.0548	0.0215	2.5482	31	0.0160	0.0109	0.0986	*

Table S3: The regression analysis results controlled for phylogeny testing differences in RGR between hemi- and holometabolous insects for the reduced dataset without the three Gryllidae species measured in ten-day intervals (multivariate linear mixed-effects models with specified variance structure by modelling heteroscedasticity).

Growth estimate		Estimate	SE	T-value	Df	P-value	Lower CI	Upper CI	
(3) Modelling heteroscadasticity	Intercept	0.0179	0.0026	6.8023	28	<.0001	0.0125	0.0233	***
	Hemi_Holo	0.0547	0.0215	2.5414	28	0.0169	0.0106	0.0988	*

Table S4: Results of the Breusch-Pagan test for heteroscedasticity (heterogeneity of variances) using the *ncvTest* function from the R package car and the percentage of total variation due to heterogeneity from the phylogenetic intercept models using the *i2_ml function* from the orchaRd package.

Growth estimate	Breusch-Pegan test				Extent of heterogeneity (I^2)		
	X^2	Df	P-value		Total I^2 [%]	I^2 due to phylogeny [%]	I^2 due to species ID [%]
RGR	28.572	1	9.0266e-08	***	96.57	48.28	48.28

Table S5: Table of results for the visualised models showing the plotted group estimates with their respective confidence intervals (CI) and prediction intervals (PR).

Visualised model	Growth	Estimate	Lower CI	Upper CI	Lower PR	Upper PR
Heteroscadasticity model for RGR	Hemimetabola	0.018	0.013	0.022	-0.001	0.037
	Holometabola	0.073	0.029	0.116	-0.067	0.213

Table S6: Listed are the insect species with a variable number of instars. Their pupation (Holometabola) and adult eclosion (Hemimetabola) rates were used to calculate weighted RGR.

	Insect	No. of instars	Rate [%]
Hemi.	*Eucorydia yasumatsui*	8	27.27
		9	68.18
		10	4.55
Holometabola	*Tenebrio molitor*	14	5.63
		15	19.39
		16	21.98
		17	28.32
		18	15.05
		19	6.29
		20	2.5
	Zophobas atratus	13	2.86
		14	11.43
		15	17.14
		16	25.71
		17	25.71
		18	17.14
	Lasiocampa pini	4	7.14
		5	69.05
		6	19.05
		7	4.76

Table S7: Mean RGR estimates for each species with standard errors ascending ordered within Hemimetabola and Holometabola, respectively.

	Order	Species	Instars		RGR	RGR SE	Weighted
			No	Used			
Hemimetabola	Phasmatodea	*Dixippus morosus*	6	6	0.003	0.002	No
	Blattodea	*Eucorydia yasumatsui*	10	10	0.004	0.001	Yes
	Odonata	*Aeshna tuberculifera*	30	29	0.011	0.002	No
	Zoraptera	*Zorotypus caudelli*	5	5	0.011	0.004	No
	Orthoptera	*Trilophidia conturbata*	5	5	0.011	0.005	No
	Odonata	*Leucorrhinia dubia*	13	13	0.013	0.003	No
	Odonata	*Nasiaeschna pentacantha*	15	13	0.013	0.002	No
	Orthoptera	*Acrida sp.*	7	7	0.013	0.002	No
	Orthoptera	*Acrotylus angulatus*	5	5	0.014	0.002	No
	Orthoptera	*Acheta domesticus*	10	10	0.018	0.006	No
	Orthoptera	*Oedaleus nigrofasciatus*	5	5	0.018	0.003	No
	Orthoptera	*Zonocerus elegans*	5	4	0.019	0.003	No
	Orthoptera	*Teleogryllus commodus*	10	10	0.020	0.006	No

	Orthoptera	*Gryllus assimilis*	10	10	0.020	0.006	No
	Orthoptera	*Acanthacris ruficornis*	7	6	0.020	0.009	No
	Psocodea	*Pediculus humanus corpor*	3	2	0.023	0.003	No
	Orthoptera	*Aiolopus thalassinus*	5	5	0.024	0.004	No
	Odonata	*Anax junius*	13	12	0.029	0.011	No
	Hemiptera	*Psammotettix alienus*	5	4	0.037	0.004	No
	Odonata	*Erythemis simplicicollis*	13	12	0.048	0.007	No
	Hemiptera	*Limnogeton fieberi*	5	4	0.047	0.013	No
Holometabola	Lepidoptera	*Epilobophora sabinata teriolensis*	5	3	0.008	0.003	No
	Coleoptera	*Cucujus cinnaberinus*	6	5	0.009	0.002	No
	Coleoptera	*Tenebrio molitor*	20	19	0.015	0.003	Yes
	Lepidoptera	*Lasiocampa pini*	7	6	0.019	0.007	Yes
	Coleoptera	*Zophobas atratus*	18	18	0.021	0.002	Yes
	Lepidoptera	*Saturnia pyri*	6	5	0.088	0.022	No
	Lepidoptera	*Ephestia kuehniella*	6	6	0.096	0.012	No
	Coleoptera	*Melasoma populi*	4	4	0.089	0.046	No
	Lepidoptera	*Hyles livornica*	5	3	0.111	0.063	No
	Coleoptera	*Tribolium confusum*	6	6	0.138	0.035	No
	Coleoptera	*Andrector ruficornis*	3	3	0.263	0.081	No
	Diptera	*Lucilia sericata*	3	2	1.012	0.192	No

Table S8: *Listed is the per species information about the rearing temperature, where the study was conducted (field or laboratory), and whether living specimens or exuviae were measured.*

	Order	Species	Laboratory / Field	Temp	living insect
Hemimetabola	Blattodea	*Eucorydia yasumatsui*	Laboratory	18-24	living
	Hemiptera	*Limnogeton fieberi*	Laboratory	28	living
		Psammotettix alienus	Laboratory	>20	living
	Odonata	*Aeshna tuberculifera*	Laboratory	RT	exuvie and living
		Anax junius	Laboratory	10 - 31.6	exuvie
		Nasiaeschna pentacantha	Laboratory	RT	exuvie
		Erythemis simplicicollis	Laboratory	RT	exuvie
		Leucorrhinia dubia	Field	RT	living
	Orthoptera	*Acanthacris ruficornis*	Laboratory	Africa	living
		Acrida sp.	Laboratory	Africa	living
		Acrotylus angulatus	Laboratory	Africa	living
		Aiolopus thalassinus	Laboratory	Africa	living
		Oedaleus nigrofasciatus	Laboratory	Africa	living
		Trilophidia conturbata	Laboratory	Africa	living
		Acheta domesticus	Laboratory	25	living
		Gryllus assimilis	Laboratory	25	living
		Teleogryllus commodus	Laboratory	25	living
		Zonocerus elegans	Laboratory	Africa	living
	Phasmatodea	*Dixippus morosus*	Laboratory	20	living
	Psocodea	*Pediculus humanus corpor*	Laboratory	RT	living
		Pediculus humanus corpor	Laboratory	RT	living

Holometabola	Zoraptera	*Zorotypus caudelli*	Laboratory	26	living
	Coleoptera	*Andrector ruficornis*	Laboratory	28	living
		Melasoma populi	Laboratory	RT	living
		Cucujus cinnaberinus	Laboratory	22	living
		Tenebrio molitor	Laboratory	25	living
		Tribolium confusum	Laboratory	30	living
		Zophobas atratus	Laboratory	25	living
	Diptera	*Lucilia sericata*	Laboratory	25	living
	Lepidoptera	*Epilobophora sabinata teriolensis*	Field	shady and cool	living
		Lasiocampa pini	Lab. / Field	RT	living
		Ephestia kuehniella	Laboratory	30	living
		Saturnia pyri	Laboratory	RT	living
		Hyles livornica	Laboratory	<20	living

Table S9: References for the growth data.

		Species	Author	Title	Journal	Vol, No., pp.	Year	Language
Hemimetabola	Blattodea	*Eucorydia yasumatsui*	Fujita Mari, Ryuichiro Machida	Reproductive biology and postembryonic development of a polyphagid cockroach Eucorydia yasumatsui Asahina (Blattodea: Polyphagidae)	Arthropod Systematics & Phylogeny	72, 2, 193-211	2014	English
	Hemiptera	*Limnogeton fieberi*	J. Voelker	Untersuchungen zu Ernährung, Fortpflanzungsbiologie und Entwicklung von Limnogeton fieberi Mayr (Belostomatidae, Hemiptera) als Beitrag zur Kenntnis von natürlichen Feinden tropischer Wasserschnecken	Entomologische Mitteilungen aus dem Zoologischesn Staatsinstitut u. Zoologischen Museum Hamburg	3,60	1968	German
		Psammotettix alienus	Binari Manurung, Werner Witsack, Egon Fuchs, Silke Mehner	Zur Embryonal-und Larvalentwicklung der Zikade Psammotettix alienus (DAHLBOM, 1851):(Hemiptera, Auchenorrhyncha)	Cicadina	4, 49-58	2001	German
	Odonata	*Aeshna tuberculifera*	Elsie Lincoln	Growth in Aeshna Tuberculifera (Odonata)	Proceedings of the American Philosophical Society	83, 5, 589-605	1940	English
		Anax junius	Philip P. Calvert	The Rates of Growth, Larval Development and Seasonal Distribution of Dragonflies of the Genus Anax (Odonata: Æshnidæ)	Proceedings of the American Philosophical Society	73, 1, 1-70	1934	English
		Nasiaeschna pentacantha	S.W. Dunkle	Larval growth in Nasiaeschna pentacantha (Rambur)(Anisoptera: Aeshnidae)	Odonatologica	14, 1, 29-35	1985	English
		Erythemis simplicicollis	George H. Bick	Life-history of the dragofly, Erythemis simplicicollis (Say)	Annals of the Entomological Society of America	34, 1, 215-230	1941	English
		Leucorrhinia dubia	Fritz Prenn	Aus der Nordtiroler Libellenfauna	Buch; Verlag: K.k.zoologisch-		1929	German

				botanische Gesellschaft, Wien			
Orthoptera	*Acanthacris ruficornis* *Acrida sp.* *Acrotylus angulatus* *Aiolopus thalassinus* *Oedaleus nigrofasciatus* *Trilophidia conturbata* *Zonocerus elegans*	Julia Chesler	Observations on the biology of some South African Acrididae (Orthoptera)	Transactions of the Royal Entomological Society of London	87, 14, 313-351	1938	English
	Acheta domesticus *Gryllus assimilis* *Teleogryllus commodus*	Robert Sturm	Längen- und Gewichtsentwicklung der Larven verschiedener Grillenarten (Orthoptera: Gryllidae) vom Zeitpunkt des Ausschlüpfens bis zur Adulthäutung	Linzer biologische Beiträge	35, 1, 487-498	2003	German
Phasmatodea	*Dixippus morosus*	Eidmann	Untersuchungen über Wachstum und Häutung der Insekten	Zeitschrift für Morphologie und Ökologie der Tiere	2, 3-4, 567-610	1924	German
Psocodea	*Pediculus humanus corpor*	P.A. Buxton	Studies on the growth of Pediculus (Anoplura)	Parasitology	30,1, 65-84	1938	English
	Pediculus humanus corpor	P.A. Buxton	The biology of the body louse (Pediculus humanus corporis: Anoplura) under experimental conditions	Parasitology	32, 3, 303-312	1940	English
Zoraptera	*Zorotypus caudelli*	Yuta Mashimo, Rolf G. Beutel, Romano Dallai, Chow-Yang Lee, Ryuichiro Machida	Postembryonic development of the ground louse Zorotypus caudelli Karny (Insecta: Zoraptera: Zorotypidae)	Arthropod Systematics & Phylogeny	72, 1, 55-71	2014	English
Holometabola Coleoptera	*Andrector ruficornis*	Wolfgang Heyer, Maria Luisa Chiang Lok, Bienvenido Cruz	Zum Einfluss der Temperatur und Wirtspflanze auf die Entwicklung von Andrector ruficornis (Oliv.) (Coleoptera: Chrysomelidae)	Beiträge zur Entomologie	38, 1, 183-188	1988	German
	Melasoma populi	A. Willer	Beobachtungen zur Biologie von Melasoma populi L.	Zeitschrift für wissenschaftliche Insektenbiologie	15, 65-73	1919	German
	Cucujus cinnaberinus	Ulrich Straka	Zur Biologie des Scharlachkäfers Cucujus cinnaberinus (Scopoli, 1763)	Beiträge zur Entomofaunistik	8, 11-26	2008	German
	Tenebrio molitor	Jong Bin Park, Won Ho Choi, Seong Hyun Kim, Hyo Jung Jin, Yeon Soo Han, Yong Seok Lee, Nam Jung Kim	Developmental characteristics of Tenebrio molitor larvae (Coleoptera: Tenebrionidae) in different instars	International Journal of Industrial Entomology	28, 1, 5-9	2014	English
	Tribolium confusum	Tom A. Brindley	The Growth and Development of Ephestia Kuehniella Zeller (Lepidoptera) and Tri-Bolium Confusum Duval (Coleoptera) under	Annals of the Entomological Society of America	23, 4, 741-757	1930	English

			Controlled Conditions of Temperature and Relative Humidity				
	Zophobas atratus	Sun Young Kim, Hong Geun Kim, Sung Ho Song, Nam Jung Kim	Developmental characteristics of Zophobas atratus (Coleoptera: Tenebrionidae) larvae in different instars	International Journal of Industrial Entomology	30, 2, 45-49	2015	English
Diptera	*Lucilia sericata*	Martin Grassberger, Christian Reiter	Effect of temperature on Lucilia sericata (Diptera: Calliphoridae) development with special reference to the isomegalen-and isomorphen-diagram	Forensic Science International	120, 1-2, 32-36	2001	English
Lepidoptera	*Epilobophora sabinata teriolensis*	Wilhelm Mack	Die Entwicklung von Nothopteryx (Lobophora) sabinata H.-Schäf.f von teriolensis Kitt	Zeitschrift des Wienerr Entomologen-Vereins	27, 16-22	1942	German
	Lasiocampa pini	Karl Eckstein	Beiträge zur Kenntnis des Kiefernspinners Lasiocampa (Gastropacha, Dendrolimus) pini L.	Zoologische Jahrbücher, Abteilung für Systematik, Geographie und Biologie der Tiere	31, 59-164	1911	German
	Ephestia kuehniella	Tom A. Brindley	The Growth and Development of Ephestia Kuehniella Zeller (Lepidoptera) and Tri-Bolium Confusum Duval (Coleoptera) under Controlled Conditions of Temperature and Relative Humidity	Annals of the Entomological Society of America	23, 4, 741-757	1930	English
	Saturnia pyri	Oliver Eitschberger	Die Biologie und Metamorphose des Wiener Nachtpfauenauges Saturnia pyri ([Denis & Schiffermüller], 1775)	Neue Entomologische Nachrichten	148-171	2010	German
	Hyles livornica	M. Gillmer	Ein Beitrag zur Entwicklungsgeschichte von Phryxus livornica, Esp.	Entomologische Zeitschrift	70-72	1904	German

Table S10: Model parameters and descriptions

Symbol	Description
L_T	Asymptotic size
k	Baseline rate of growth in size
t	Age at the end of the period of growth in size
v	Hypothetical age at which size would be zero
Δ	Age at the end of the period of differentiation
μ_G	Rate of mortality during the growth phase
F	Fertility, defined as the product of growth in size and differentiation at the end of each respective phase ($F = L_t D_\Delta$)
R_0	Net reproductive number across both the growth and differentiation phase
r_1	Allocation of resources towards growth in size

Symbol	Description
L_T	Asymptotic size
r_2	Allocation of resources towards differentiation during the growth phase
r_3	Allocation of resources towards differentiation in the final phase

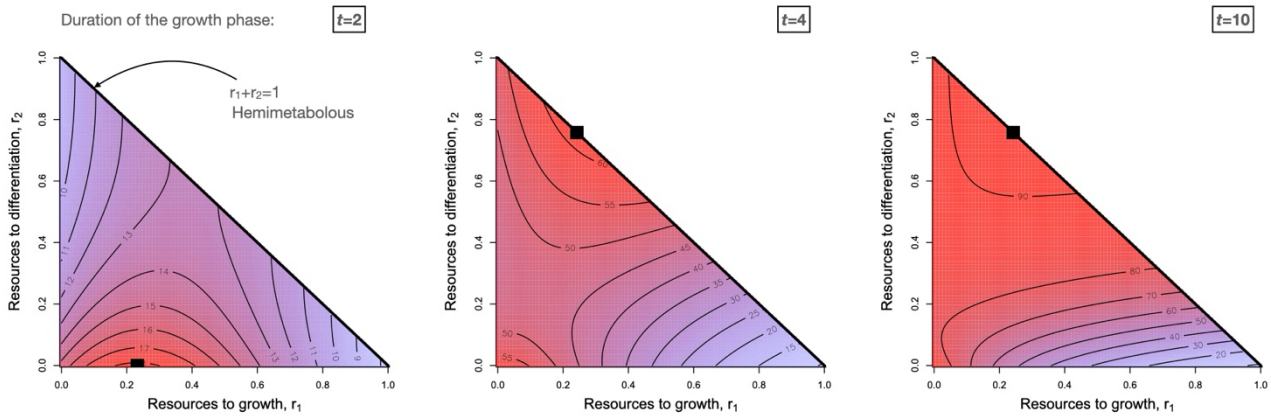


Figure S3: Fitness landscapes showing the magnitude of R_0 (contours, colours, with red corresponding to maximum fitness) across resource allocation parameters (r_1, x axis, and r_2, y axis) for three values of the duration of the growth phase (*t*, panel titles). The combination of r_1 and r_2 where R_0 is maximal is indicated by a square. On the diagonal (solid black line) $r_1 + r_2 = 1$, and thus allocation towards differentiation after the growth period, r_3, is zero, indicating that in this example, a hemimetabolous life cycle is selected at higher values of *t*. Other parameters are k=0.5, L_t=10, v=1, and μ_G =0.01.

R-Scripts

Phylogenetic model

```
library(tidyverse)
library(ape)
library(metafor)
library(orchaRd)
library(ape)
library(phytools)
library(tidyverse)



##############################################
# Import DF
##############################################


ALL_GR_summarySE <- read.csv("TableS7.csv", header = TRUE, dec=",", sep="\t", na.strings =
"na")



##############################################
# Make Phylogeny
##############################################

text.string<- "((Odonata(Aeshnidae(Aeshna_tuberculifera,Anax_junius,Nasiaeschna_pentacantha),
Libellulidae(Erythemis_simplicicollis,Leucorrhinia_dubia))),(((Zoraptera(Zorotypidae(Zorotypus_c
audelli))),((Orthoptera((Acrididae(Cyrtacanthacridinae(Acanthacris_ruficornis),
(Acridinae(Acrida_sp), Oedipodinae(Trilophidia_conturbata, Oedaleus_nigrofasciatus,
Aiolopus_thalassinus, Acrotylus_angulatus))), Pyrgomorphidae(Zonocerus_elegans)),
Gryllidae(Acheta_domesticus, Gryllus_assimilis,
Teleogryllus_commodus))),((Phasmatodea(Phasmatidae(Dixippus_morosus))),(Blattodea(Polyphagi
dae(Eucorydia_yasumatsui)))))),((Hemiptera(Belostomatidae(Limnogeton_fieberi),Cicadellidae_Jas
```

sidae(Psammotettix_alienus))),((Psocodea(Pediculidae(Pediculus_humanus_corpor))),((Coleoptera(
Tenebrionidae(Tenebrio_molitor, Tribolium_confusum, Zophobas_atratus),
(Chrysomelinae(Melasoma_populi, Andrector_ruficornis),
Cucujidae(Cucujus_cinnaberinus)))),((Lepdioptera(Pyralidae(Ephestia_kuehniella),
(Geometridae(Epilobophora_sabinata_teriolensis), (Lasiocampidae(Lasiocampa_pini),

```
(Saturniidae(Saturnia_pyri),
Sphingidae(Hyles_livornica))))),(Diptera(Caliphoridae(Lucilia_sericata)))))))));"


vert.tree<-ape::read.tree(text=text.string)

plotTree(vert.tree,offset=2)


################################################

# Generate Grafen's Branch Lengths

################################################

# turning into phylogenetic correlation matrix using Grafen's method

tree <- compute.brlen(vert.tree) # Generate branch lengths; method = "Grafen" --> default


cor_tree <- vcv(tree,corr = T) # Generate phylogenetic variance-covariance matrix


############################################################

# Add observational level data

############################################################

ALL_GR_summarySE$obs <- factor(1:dim(ALL_GR_summarySE)[1])


################################################

# Heteroscedasticity test

################################################

library(car)

lmMod <- lm(ALL_GR_summarySE$Perc ~ ALL_GR_summarySE$Hemi_Holo)

par(mfrow=c(2,2))

plot(lmMod)

car::ncvTest(lmMod)
```

```
##############################################

# Linear Regression

##############################################

# Phylogenetic meta-analysis via Multivariate/Multilevel Linear (Mixed-Effects) Models


# Effect of phylogeny:

model0 <-  rma.mv(yi = RGR, V = RGR_se^2, mod = ~ 1,

            random = list(~1|Species,

                        ~1|obs),

            R = list(Species_Tree = cor_tree),

            data = ALL_GR_summarySE,

            test = "t"

)

i2_ml(model0)


# fit the meta-regression model without the intercept for the orchard plot and for the means of 2 groups [summary(model)]

model1 <-  rma.mv(yi = Perc, V = Perc_se^2, mod = ~ Hemi_Holo - 1,

              random = list(~1|Species,

                          ~1|obs),

              R = list(Species_Tree = cor_tree),

              data = ALL_GR_summarySE,

              test = "t"

)


# looking at contrast between 2 groups

model1b <-  rma.mv(yi = RGR, V = RGR_se^2, mod = ~ 1+ Hemi_Holo,

              random = list(~1|Species,

                          ~1|obs),
```

```
                R = list(Species_Tree = cor_tree),
                data = ALL_GR_summarySE,
                test = "t"
)
r2_ml(model1b)
orchard_plot(model1, mod = "Hemi_Holo", xlab = "Percentage Growth")

# modeling heteroscadasticty
model2b  <-  rma.mv(yi = log(RGR), V = RGR_se^2, mod = ~ Hemi_Holo -1,
                random = list(~ Hemi_Holo|Species,
                        ~1|obs),
                rho = 0,
                struct = "HCS",
                R = list(Species_Tree = cor_tree),
                data = ALL_GR_summarySE,
                test = "t"
)

# calculate the 'total' I^2 along with I^2 for each level
# describes the percentage of variation across studies/samples that is due to heterogeneity
# heterogeneity of the distribution of the residuals
i2_ml(model0)

# calculate marginal and conditional R^2 for mixed models
# measures the proportion of variation in the response that can be attributed to the predictor
r2_ml(model1b)

###################
```

Orchard_Plot

##################

```
Orchard_RGR <- orchard_plot_2(model2b, mod = "Hemi_Holo", xlab = "Relative Growth Rate \n [Log scale]", angle=45) + theme( axis.text.y=element_text(size=25, colour="black"), axis.text.x=element_text(size=20, colour="grey20"),axis.title.x = element_text(size = 22, margin = margin(t = 20, r = 0, b = 30, l = 0)), legend.text = element_text(size = 10), legend.title = element_text(size = 12, colour="grey20")) + theme(legend.position="bottom")+
```

```
scale_fill_manual(values = c("#D55E00","#0072B2"))+ scale_color_manual(values =
c("#D55E00","#0072B2"))+ theme(plot.title = element_text(size=25))#+xlim(0.75,2.5)



png("../Orchard_RGR.png", width = 1.25*480, height = 1*480)

Orchard_RGR

dev.off()
```

Evolutionary model

```
##########################################################################################
##################################

## Code to model a Hemi/Holometabolous life-cycle, with resource allocation between growth and
differentiation ##

##########################################################################################
##################################



## von Bertalannffy growth model

growth <- function(Lt,k,t,v,r1) {

        Lt*(1-exp(-(k+r1)*(t-v)))

        }
```

```
## von Bertalannffy differentiation model, for differentiation occurring during growth (maps to Figure 2)

change1 <- function(d,t,v,r1,r2,r3) {

	(1-exp(-(d+r2)*(t-v)))

	}


## differentiation model, simplified way of capturing differentiation occurring after growth

change2 <- function(d,t,v,r1,r2,r3) {

	r3*(1-change1(d=d,t=t,v=v,r1=r1,r2=r2,r3=r3))

	}


## define R0 for a holometab life cycle

R0 <- function(Lt,k,d,t,v,r1,r2,r3, mu1) {

	exp(-mu1*(t-v))*growth(Lt=Lt,k=k,t=t,v=v,r1=r1)^(1+change1(d=d,t=t,v=v,r1=r1,r2=r2,r3=r3)+change2(d=d,t=t,v=v,r1=r1,r2=r2,r3=r3))

	###exp(-mu1*(t-v))*growth(Lt=Lt,k=k,t=t,v=v,r1=r1)*(1+change1(d=d,t=t,v=v,r1=r1,r2=r2,r3=r3)+change2(d=d,t=t,v=v,r1=r1,r2=r2,r3=r3))



}




## define R0 for a hemimetab life cycle(i.e., r3 necessarily 0)

R0hemi <- function(Lt,k,d,t,v,r1,r2,r3, mu1) {

	exp(-mu1*(t-v))*growth(Lt=Lt,k=k,t=t,v=v,r1=r1)^(1+change1(d=d,t=t,v=v,r1=r1,r2=r2,r3=r3))

	###exp(-mu1*(t-v))*growth(Lt=Lt,k=k,t=t,v=v,r1=r1)*(1+change1(d=d,t=t,v=v,r1=r1,r2=r2,r3=r3))



}
```

```
##### 1. Illustrate broad patterns ##############################################


## Choose some parameters

Lt.=10

k.=2

d.=2

t.=10

v.=1

r1.=0.2;r2.=0.2;r3.=0.6;

mu1.=0.2



## Loop across different durations of the growth phase, calculate and then plot out the fitness landscape

test.t <- seq(1,5,length=100)

R0test.hemi <- R0test <- rep(NA,length(test.t))

for (j in 1:length(test.t)) {

        R0test[j] <- R0(Lt=Lt.,k=k.,d=d.,t=test.t[j],v=v.,r1=r1.,r2=r2.,r3=r3., mu1=mu1.)

        R0test.hemi[j] <- R0hemi(Lt=Lt.,k=k.,d=d.,t=test.t[j],v=v.,r1=r1.,r2=r2.,r3=r3., mu1=mu1.)

}

plot(test.t,R0test, type="l", xlab="end of growth", ylab=expression(R[0]))

points(test.t,R0test.hemi,type="l",col=2,lty=3)

abline(v=c(test.t[R0test==max(R0test)],test.t[R0test.hemi==max(R0test.hemi)]), col=c(1,2), lty=c(1,3))
```

```
## Start at optimal life history for t from the above, and explore R0 for r1 and r2; with assumption r1 + r2 + r3 = R = 1

t. <- test.t[R0test==max(R0test)]

R. <- 1 #total resource pool

r1test <- seq(0,R.,length=100)

r2test <- seq(0,R.,length=100)

R0.store <- matrix(NA,length(r1test),length(r2test))

for (j in 1:length(r1test)) {

for (k in 1:length(r2test)) {


        if ((r1test[j]+r2test[k])>R.) next()

        R0.store[j,k] <- R0(Lt=Lt.,k=k.,d=d.,t=t.,v=v.,

                        r1=r1test[j],r2=min(r2test[k],R.-r1test[j]),r3=R.-r1test[j]-r2test[k],
mu1=mu1.)

}}

image(r1test,r2test,exp(R0.store), xlab=expression("Resources to growth, "*r[1]),
ylab=expression("Resources to differentiation, "*r[2]))

contour(r1test,r2test,R0.store,add=TRUE)

opt <- which(R0.store==max(R0.store,na.rm=T), arr.ind=T)

r1 <- r1test[opt[1,1]]

r2 <- r2test[opt[1,2]]

r3 <- R.-r1-r2


points(r1,r2,pch=19)

print(c(r1,r2,r3))
```

```
##### 2. Function to identify optima ################################################

## Function to optimize t, r1, r2 assuming that r1+r2+r3=R
findOpt <- function(par,index=1:3,params=c(5,1,0),Lt=5,k=2,d=1,mu1=0.1,R=1,v=1) {

        params[index] <- par

        t <- params[1]
        r1 <- params[2];
        r2 <- params[3];

        rc <- (R0(Lt=Lt,k=k,d=d,t=t,v=v,r1=r1,r2=min(r2,R-r1),r3=R-r1-r2, mu1=mu1))

        return(-rc)

}

## Function to optimize t, r1, r2 assuming that r3=0
findOptHemi <- function(par,index=1:2,params=c(5,1,0),Lt=5,k=2,d=1,mu1=0.1,R=1,v=1) {

        params[index] <- par

        t <- params[1]
```

```
        r1 <- params[2];
        r2 <- R-r1

        rc <- (R0hemi(Lt=Lt,k=k,d=d,t=t,v=v,r1=r1,r2=min(r2,R-r1),r3=0, mu1=mu1))

        return(-rc)

}

## Function to optimize t, r1, r2 assuming that r1+r2+r3=R but using a loop rather than the optim function
findOptBigLoop <- function(par,Lt=5,k=2,d=1,mu1=0.1,R=1,v=1,nest=30, do.plot=FALSE) {

        t <- par[1]
        r1 <- par[2];
        r2 <- par[3];

        test.t <- seq(max(t-2,1.001),t+2,length=nest)
        test.r <- seq(0,1,length=nest)

        rc <- array(dim=c(nest,nest,nest))

        #print(k)

        for (i in 1:nest) {
        for (z in 1:nest) {
        for (l in 1:nest) {

                if ((test.r[z]+test.r[l])>1) next()
```

```
                rc[i,z,l] <- (R0(Lt=Lt,k=k,d=d,t=test.t[i],v=v,r1=test.r[z],r2=test.r[l],r3=R-test.r[z]-
test.r[l], mu1=mu1))



        }}}


        opt <- which(rc==max(rc,na.rm=TRUE), arr.ind=TRUE)


        #create format that looks like what optim returns

        tmp <- list()

        tmp$par <- c(test.t[opt[1,1]],test.r[opt[1,2]],test.r[opt[1,3]])

        tmp$value <- -max(rc,na.rm=TRUE)


        if (do.plot) {

                image(test.r,test.r,rc[opt[1,1],,], xlab="resources to growth", ylab="resources to
differentiate")

                contour(test.r,test.r,rc[opt[1,1],,],add=TRUE)

                points(tmp$par[2],tmp$par[3],pch=19)

        }


        return(tmp)


}




## Sanity check that not missing something by order that optimise the different allocation
parameters

findOptBigLoopReverse <- function(par,Lt=5,k=2,d=1,mu1=0.1,R=1,v=1,nest=30,
do.plot=FALSE) {
```

```
t <- par[1]

r1 <- par[2];

r3 <- par[3];


test.t <- seq(max(t-2,1.001),t+2,length=nest)

test.r <- seq(0,1,length=nest)


rc <- array(dim=c(nest,nest,nest))


#print(k)


for (i in 1:nest) {

for (z in 1:nest) {

for (l in 1:nest) {


        if ((test.r[z]+test.r[l])>1) next()

        rc[i,z,l] <- (R0(Lt=Lt,k=k,d=d,t=test.t[i],v=v,r1=test.r[z],r2=R-test.r[z]-
test.r[l],r3=test.r[l], mu1=mu1))


}}}


opt <- which(rc==max(rc,na.rm=TRUE), arr.ind=TRUE)


#create format that looks like what optim returns

tmp <- list()

tmp$par <- c(test.t[opt[1,1]],test.r[opt[1,2]],R-test.r[opt[1,2]]-test.r[opt[1,3]])

tmp$value <- -max(rc,na.rm=TRUE)


if (do.plot) {
```

```
        image(test.r,test.r,rc[opt[1,1],,], xlab="resources to growth", ylab="resources to
differentiate")

        contour(test.r,test.r,rc[opt[1,1],,],add=TRUE)

        points(tmp$par[2],tmp$par[3],pch=19)

    }


    return(tmp)


}
```

```
## sanity check

#tmp <- optim(par=c(5,1,0), findOpt,Lt=5,k=0.001,d=0,mu1=0.1,v=1,R=1, method="L-BFGS-
B",lower=c(1.001,0,0),upper=c(30,1,1))

#tmp1 <- findOptBigLoop(par=c(5,1,0), Lt=5,k=0.001,d=0,mu1=0.1,v=1,R=1,nest=30,
do.plot=TRUE)

#tmp2 <- findOptBigLoopReverse(par=c(5,1,0), Lt=5,k=0.001,d=0,mu1=0.1,v=1,R=1,nest=30,
do.plot=TRUE)




## check optimize just one parameter...

#R0(Lt=5,k=0.001,d=0,t=tmp1$par[1],v=1,r1=tmp1$par[2],r2=tmp1$par[3],r3=1-tmp1$par[2]-
tmp1$par[3],mu1=0.1)

#tmp <- optim(par=4.1,index=1,params=tmp1$par, findOpt,Lt=5,k=0.001,d=0,mu1=0.1,v=1,R=1,
method="L-BFGS-B",lower=c(1.001,0,0),upper=c(30,1,1))
```

```
##### 3. Function to identify when to switch to holometabolous
################################################



## Function to find the optimal switch point

findKswitch <- function(d=0.1,mu1=0.1,R=1,Lt=5, ntest=40,nest=50,do.plot=FALSE,
ktest=c(seq(0.01,1.2,length=ntest-1),1.5)) {


  #storage; index 1 indicates hemimetab; and is stored first in the R0 matrix...

  storePar1 <- storePar <- matrix(NA,ntest,3)

  storeR0 <- matrix(NA,ntest,2)


  #loop

  for (j in 1:ntest) {




          ##HEMIMETABOLOUS - start and use as starting parameters

          tmp1 <- optim(par=c(4,1), index=1:2,params=c(4,1,0),

                  findOptHemi,Lt=Lt,k=ktest[j],d=d,mu1=mu1,R=R,v=1, method="L-BFGS-B",

                  lower=c(1.001,0,0),upper=c(30,1,1))

          tmp1x <- tmp1


          #jiggle to ensure that have optimal

          for (xx in 1:10) {

            tmp1x <-
optim(par=pmin(pmax(rnorm(2,tmp1$par,pmax(tmp1$par/5,0.1)),c(1.001,0)),c(30,1)),

                  index=1:2,params=tmp1$par,
```

```
            findOptHemi,Lt=Lt,k=ktest[j],d=d,mu1=mu1,R=R,v=1, method="L-BFGS-B",
            lower=c(1.001,0),upper=c(30,1))
 if (tmp1x$value<tmp1$value) tmp1 <- tmp1x
}
storePar1[j,] <- c(tmp1$par,0)
storePar1[j,3] <- 1-storePar1[j,2]



##HOLMETABOLOUS
tmp <- findOptBigLoop(par=storePar1[j,1:3],
                      Lt=Lt,k=ktest[j],d=d,mu1=mu1,R=R,v=1,nest=nest,do.plot=do.plot)
tmpx <- optim(par=tmp$par,findOpt,
                      index=1:3,params=tmp$par,
                      Lt=Lt,k=ktest[j],d=d,mu1=mu1,R=R,v=1, method="L-BFGS-B",
                      lower=c(1.001,0,0),upper=c(30,1,1))
if (tmpx$value<tmp$value) tmp <- tmpx

#jiggle to ensure
for (xx in 1:10) {
  tmpx <-
optim(par=pmin(pmax(rnorm(3,tmp$par,pmax(tmp$par/5,0.1)),c(1.001,0,0)),c(30,1,1)),
            findOpt,Lt=Lt,k=ktest[j],d=d,mu1=mu1,R=R,v=1, method="L-BFGS-B",
            lower=c(1.001,0,0),upper=c(30,1,1))
 if (tmpx$value<tmp$value) {tmp <- tmpx; print("improve")}
}



## Put into storage matrix
```

```
storePar[j,] <- tmp$par
storePar[j,3] <- min(storePar[j,3],1-storePar[j,2])

## Store R0
storeR0[j,] <- c(tmp1$value,tmp$value)



}

#find switch point and gradient
if (sum(storePar[,3]<1e-4)>0) {
        switch.point <- range(which(storePar[,3]<1e-4,arr.ind=TRUE))
        if (min(switch.point)==1) {
                switch.index <- max(switch.point)
                switch.point <- ktest[max(switch.point)]
                kgradient <- storePar[min(switch.index+1,ntest),2]/(ktest[2]-ktest[1])
        } else {
                switch.index <- (switch.point[1])
                switch.point <- ktest[switch.point[1]]
                kgradient <- storePar[max(switch.index-1,1),2]/(ktest[2]-ktest[1])
        }

} else {
        switch.point <- 0; kgradient <- NA
}

return(list(switch.point=switch.point,switch.index=switch.index,
kgradient=kgradient,storePar=storePar,storePar1=storePar1,storeR0=storeR0,ktest=ktest))
```

```
}


## function to plot this out, showing different parameter optima, and the switch point across a gradient of k.

makePlot.k.impact<-function(k.impact){


	#[more visually applealing to put the vertical line right before the switch point]

	loc.vert.line <- max(k.impact$switch.index-1,1)

	vert.line <- k.impact$ktest[max(k.impact$switch.index-1,1)]


	par(mfrow=c(1,4))

	plot(k.impact$ktest,k.impact$storePar[,1],

		xlab=expression("Growth rate, "*italic(k)), ylab=expression("Optimal duration of the growth phase, "*italic(t)),

		type="l", ylim=range(c(k.impact$storePar[,1],k.impact$storePar1[,1])),lwd=2)

	points(k.impact$ktest,k.impact$storePar1[,1], type="l",lty=3, col="darkgrey",lwd=2)

	if (k.impact$switch.point>0) abline(v=vert.line, col=4,lty=1)

	points(k.impact$ktest[loc.vert.line],k.impact$storePar[loc.vert.line,1],pch=19)


	plot(k.impact$ktest,k.impact$storePar[,2],

		xlab=expression("Growth rate, "*italic(k)), ylab=expression("Optimal growth allocation, "*r[1]), type="l", ylim=c(0,1),lwd=2)

	points(k.impact$ktest,k.impact$storePar1[,2],type="l", lty=3, col="darkgrey",lwd=2)

	if (k.impact$switch.point>0) abline(v=vert.line, col=4,lty=1)

	points(k.impact$ktest[loc.vert.line],k.impact$storePar[loc.vert.line,2],pch=19)


	plot(k.impact$ktest,k.impact$storePar[,3],
```

```
        xlab=expression("Growth rate, "*italic(k)), ylab=expression("Optimal growth phase allocation to diff. "*r[2]), type="l", ylim=c(0,1),lwd=2)

    points(k.impact$ktest,k.impact$storePar1[,3],type="l", lty=3, col="darkgrey",lwd=2)

    if (k.impact$switch.point>0) abline(v=vert.line, col=4,lty=1)

    points(k.impact$ktest[loc.vert.line],k.impact$storePar[loc.vert.line,3],pch=19)



    plot(k.impact$ktest,pmax(1-k.impact$storePar[,2]-k.impact$storePar[loc.vert.line,3],0),

        xlab=expression("Growth rate, "*italic(k)), ylab=expression("Optimal allocation to differentiate post-growth, "*r[3]), type="l", ylim=c(0,1),lwd=2)

    if (k.impact$switch.point>0) abline(v=vert.line, col=4,lty=1)

    points(k.impact$ktest[loc.vert.line],pmax(1-k.impact$storePar[loc.vert.line,2]-k.impact$storePar[loc.vert.line,3],0),pch=19)



}




## explore the different optima under low mortality

aa <- findKswitch(d=0,mu1=0.01,R=1,Lt=5, ntest=30,nest=30)

makePlot.k.impact(aa)



## explore the different optima under high mortality - note r3 should be 1 but is so high makes no difference

aa1 <- findKswitch(d=0,mu1=0.5,R=1,Lt=5, ntest=30,nest=30)

makePlot.k.impact(aa1)




################################################################################
################################################################################
```

```
#choose a k and then look at fitness across a focal parameter with other parameters set at their optimal, to unpack patterns and compare low and high effects




## For parameter t ##########################


### 1. for low mortality

chs.k <- 20

tst.t <- seq(1,9,length=100)

store.R0s <- matrix(NA,length(tst.t),2)

for (jx in 1:length(tst.t)) {

	store.R0s[jx,1] <- R0(Lt=5,k=aa$ktest[chs.k],d=0,t=tst.t[jx],v=1,r1=aa$storePar[chs.k,2],r2=aa$storePar[chs.k,3],r3=1-sum(aa$storePar[chs.k,2:3]), mu1=0.01)

	store.R0s[jx,2] <- R0hemi(Lt=5,k=aa$ktest[chs.k],d=0,t=tst.t[jx],v=1,r1=aa$storePar1[chs.k,2],r2=aa$storePar1[chs.k,3],r3=0, mu1=0.01)

}


### 2. for high mortality

store.R0s1 <- matrix(NA,length(tst.t),2)

for (jx in 1:length(tst.t)) {

	store.R0s1[jx,1] <- R0(Lt=5,k=aa1$ktest[chs.k],d=0,t=tst.t[jx],v=1,r1=aa1$storePar[chs.k,2],r2=aa1$storePar[chs.k,3],r3=1-sum(aa1$storePar[chs.k,2:3]), mu1=0.5)

	store.R0s1[jx,2] <- R0hemi(Lt=5,k=aa1$ktest[chs.k],d=0,t=tst.t[jx],v=1,r1=aa1$storePar1[chs.k,2],r2=aa1$storePar1[chs.k,3],r3=0, mu1=0.5)

}




par(mfrow=c(1,1),bty="l")
```

```
plot(tst.t, store.R0s[,1], type="l", xlab="t", ylab=expression(R[0]),
ylim=range(store.R0s,c(store.R0s1),na.rm=TRUE),lwd=1.5)

points(tst.t,store.R0s[,2], type="l", col="grey",lty=3,lwd=1.5)

#abline(v=tst.t[store.R0s[,1]==max(store.R0s[,1])])

points(tst.t[store.R0s[,1]==max(store.R0s[,1])],max(store.R0s[,1]),pch=19,cex=1.2,col="black")

#abline(v=tst.t[store.R0s[,2]==max(store.R0s[,2])])

points(tst.t[store.R0s[,2]==max(store.R0s[,2])],max(store.R0s[,2]),pch=19,cex=1.2,col="grey")


#plot(tst.t, store.R0s1[,1], type="l", xlab="t", ylab=expression(R[0]),
ylim=range(store.R0s1,na.rm=TRUE),lwd=1.5)

points(tst.t,store.R0s1[,1], type="l", col="black",lty=1,lwd=1.5)

points(tst.t,store.R0s1[,2], type="l", col="grey",lty=3,lwd=1.5)

#abline(v=tst.t[store.R0s1[,1]==max(store.R0s1[,1])])

points(tst.t[store.R0s1[,1]==max(store.R0s1[,1])],max(store.R0s1[,1]),pch=19,cex=1.2,col="black")

#abline(v=tst.t[store.R0s1[,2]==max(store.R0s1[,2])])

points(tst.t[store.R0s1[,2]==max(store.R0s1[,2])],max(store.R0s1[,2]),pch=19,cex=1.2,col="grey")




## For parameter r1 ############################


### 1. for low mortality

chs.k <- 30

tst.r <- seq(0,0.4,length=100)

store.R0s <- matrix(NA,length(tst.r),2)

for (jx in 1:length(tst.t)) {
```

```
        store.R0s[jx,1] <- R0(Lt=5,k=aa$ktest[chs.k],d=0,t=aa$storePar[chs.k,1],v=1,r1=tst.r[jx],

                              r2=min(aa$storePar[chs.k,3],1-tst.r[jx]),r3=max(1-
sum(aa$storePar[chs.k,3]+tst.r[jx]),0), mu1=0.01)

        store.R0s[jx,2] <-
R0hemi(Lt=5,k=aa$ktest[chs.k],d=0,t=aa$storePar1[chs.k,1],v=1,r1=tst.r[jx],r2=1-tst.r[jx],r3=0,
mu1=0.01)

}



### 2. for high mortality

store.R0s1 <- matrix(NA,length(tst.r),2)

for (jx in 1:length(tst.t)) {

        store.R0s1[jx,1] <-
R0(Lt=5,k=aa1$ktest[chs.k],d=0,t=aa1$storePar[chs.k,1],v=1,r1=tst.r[jx],

                              r2=min(aa1$storePar[chs.k,3],1-tst.r[jx]),r3=max(1-
sum(aa1$storePar[chs.k,3]+tst.r[jx]),0), mu1=0.5)

        store.R0s1[jx,2] <-
R0hemi(Lt=5,k=aa1$ktest[chs.k],d=0,t=aa1$storePar1[chs.k,1],v=1,r1=tst.r[jx],r2=1-tst.r[jx],r3=0,
mu1=0.5)

}




par(mfrow=c(1,1),bty="l")



plot(tst.r, store.R0s[,1], type="l", xlab=expression(r[1]), ylab=expression(R[0]),
ylim=range(store.R0s,c(store.R0s1),na.rm=TRUE),lwd=1.5)

points(tst.r,store.R0s[,2], type="l", col="grey",lty=3,lwd=1.5)

#abline(v=tst.r[store.R0s[,1]==max(store.R0s[,1])])

points(tst.r[store.R0s[,1]==max(store.R0s[,1])],max(store.R0s[,1]),pch=19,cex=1.2,col="black")

#abline(v=tst.r[store.R0s[,2]==max(store.R0s[,2])])

points(tst.r[store.R0s[,2]==max(store.R0s[,2])],max(store.R0s[,2]),pch=19,cex=1.2,col="grey")
```

```
#plot(tst.r, store.R0s1[,1], type="l", xlab="t", ylab=expression(R[0]),
ylim=range(store.R0s1,na.rm=TRUE),lwd=1.5)

points(tst.r,store.R0s1[,1], type="l", col="black",lty=1,lwd=1.5)

points(tst.r,store.R0s1[,2], type="l", col="grey",lty=3,lwd=1.5)

#abline(v=tst.r[store.R0s1[,1]==max(store.R0s1[,1])])

points(tst.r[store.R0s1[,1]==max(store.R0s1[,1])],max(store.R0s1[,1]),pch=19,cex=1.2,col="black"
)

#abline(v=tst.r[store.R0s1[,2]==max(store.R0s1[,2])])

points(tst.r[store.R0s1[,2]==max(store.R0s1[,2])],max(store.R0s1[,2]),pch=19,cex=1.2,col="grey")




## For r2 ############################


### 1. for low mortality

chs.k <- 30

tst.r <- seq(0,0.9,length=100)

store.R0s <- matrix(NA,length(tst.r),2)

for (jx in 1:length(tst.t)) {

        store.R0s[jx,1] <- R0(Lt=5,k=aa$ktest[chs.k],d=0,t=aa$storePar[chs.k,1],v=1,r2=tst.r[jx],

                        r1=min(aa$storePar[chs.k,2],1-tst.r[jx]),r3=max(1-
sum(aa$storePar[chs.k,2]+tst.r[jx]),0), mu1=0.01)

        store.R0s[jx,2] <-
R0hemi(Lt=5,k=aa$ktest[chs.k],d=0,t=aa$storePar1[chs.k,1],v=1,r2=tst.r[jx],r1=1-tst.r[jx],r3=0,
mu1=0.01)

}


### 2. for high mortality

store.R0s1 <- matrix(NA,length(tst.r),2)

for (jx in 1:length(tst.t)) {
```

```
        store.R0s1[jx,1] <-
R0(Lt=5,k=aa1$ktest[chs.k],d=0,t=aa1$storePar[chs.k,1],v=1,r2=tst.r[jx],

                           r1=min(aa1$storePar[chs.k,2],1-tst.r[jx]),r3=max(1-
sum(aa1$storePar[chs.k,2]+tst.r[jx]),0), mu1=0.5)

        store.R0s1[jx,2] <-
R0hemi(Lt=5,k=aa1$ktest[chs.k],d=0,t=aa1$storePar1[chs.k,1],v=1,r2=tst.r[jx],r1=1-tst.r[jx],r3=0,
mu1=0.5)

}




par(mfrow=c(1,1),bty="l")



plot(tst.r, store.R0s[,1], type="l", xlab=expression(r[1]), ylab=expression(R[0]),
ylim=range(store.R0s,c(store.R0s1),na.rm=TRUE),lwd=1.5)

points(tst.r,store.R0s[,2], type="l", col="grey",lty=3,lwd=1.5)

#abline(v=tst.r[store.R0s[,1]==max(store.R0s[,1])])

points(tst.r[store.R0s[,1]==max(store.R0s[,1])],max(store.R0s[,1]),pch=19,cex=1.2,col="black")

#abline(v=tst.r[store.R0s[,2]==max(store.R0s[,2])])

points(tst.r[store.R0s[,2]==max(store.R0s[,2])],max(store.R0s[,2]),pch=19,cex=1.2,col="grey")



#plot(tst.r, store.R0s1[,1], type="l", xlab="t", ylab=expression(R[0]),
ylim=range(store.R0s1,na.rm=TRUE),lwd=1.5)

points(tst.r,store.R0s1[,1], type="l", col="black",lty=1,lwd=1.5)

points(tst.r,store.R0s1[,2], type="l", col="grey",lty=3,lwd=1.5)

#abline(v=tst.r[store.R0s1[,1]==max(store.R0s1[,1])])

points(tst.r[store.R0s1[,1]==max(store.R0s1[,1])],max(store.R0s1[,1]),pch=19,cex=1.2,col="black"
)

#abline(v=tst.r[store.R0s1[,2]==max(store.R0s1[,2])])

points(tst.r[store.R0s1[,2]==max(store.R0s1[,2])],max(store.R0s1[,2]),pch=19,cex=1.2,col="grey")
```

```
##########################################################################################
##########################################################################################
###############
```

```
### Loop over d and mu1 to identify the switch point (Lt has not effect) ####

ntest <- 200

d.test <- seq(0,0.1,length=2)

mu1.test <- seq(0.01,0.5,length=100)


store.rc <- array(dim=c(length(d.test),length(mu1.test)))

store.gradient <- array(dim=c(length(d.test),length(mu1.test)))

par.homo <- array(dim=c(length(d.test),length(mu1.test),ntest,3))

par.hemi <- array(dim=c(length(d.test),length(mu1.test),ntest,3))

holo.hemi.distance <- array(dim=c(length(d.test),length(mu1.test)))

holo.hemi.params.dist.lowgrow <- holo.hemi.params.dist.highgrow <-  holo.hemi.params.dist <-
array(dim=c(length(d.test),length(mu1.test),3))

switch.index <- array(dim=c(length(d.test),length(mu1.test)))


#for (j in 1:length(d.test)) {

j<-1

for (k in 1:length(mu1.test)) {

        tpp <- findKswitch(d=d.test[j],mu1=mu1.test[k],R=1,Lt=5, ntest=ntest,nest=40)

        store.rc[j,k] <- tpp$switch.point

        store.gradient[j,k] <- tpp$kgradient

        par.homo[j,k,,] <- tpp$storePar

        par.hemi[j,k,,] <- tpp$storePar1
```

```
        switch.index[j,k] <- tpp$switch.index


        before.switch <- max(switch.index[j,k]-1,1) #switch.index[j,k]#

        if (length(before.switch)>0) {

        holo.hemi.distance[j,k] <- sum((par.homo[j,k,before.switch,c(1,2,3)]-
par.hemi[j,k,before.switch,c(1,2,3)])^2)

        holo.hemi.params.dist[j,k,] <- par.hemi[j,k,before.switch,c(1,2,3)]-
par.homo[j,k,before.switch,c(1,2,3)]

        holo.hemi.params.dist.lowgrow[j,k,] <- par.hemi[j,k,1,c(1,2,3)]-par.homo[j,k,1,c(1,2,3)]

        holo.hemi.params.dist.highgrow[j,k,] <- par.hemi[j,k,ntest,c(1,2,3)]-
par.homo[j,k,ntest,c(1,2,3)]

        }

}#}




cols <- colorRampPalette(c("blue", "red"))(ntest)




## just look at death for d=0 (d=1 is consistent pattern)

par(mfrow=c(1,1), bty="l")

plot(mu1.test, store.rc[1,], type="l",

                xlab=expression("Mortality during growth phase,  "*mu[G]),

                ylab=expression("Threshold "*italic(k)*" for holometab."),lwd=1.3)


## plot with full range

par(mfrow=c(1,1), bty="l")

plot(mu1.test, store.rc[1,], type="l",

                xlab=expression("Mortality during growth phase,  "*mu[G]),

                ylab=expression("Threshold "*italic(k)*" for holometab."),lwd=1.3, ylim=c(0,1))
```

```
## just look at death for d=0 - at a particular k (not the switch one)
par(mfrow=c(3,4), bty="l", mar=c(5,4,1,1))

for (kchs in c(1,10,20)) {
plot(mu1.test, par.homo[1,,kchs,1], type="l",
                xlab=expression("Mortality during growth phase, "*expression(mu[G])),
                ylab=expression(italic(t)),lwd=1.3)
points(mu1.test, par.hemi[1,,kchs,1], type="l",lty=3,col="grey")

plot(mu1.test, par.homo[1,,kchs,2], type="l",ylim=c(0,1),
                xlab=expression("Mortality during growth phase, "*expression(mu[G])),
                ylab=expression(italic(r[1])),lwd=1.3)
points(mu1.test, par.hemi[1,,kchs,2], type="l",lty=3,col="grey")

plot(mu1.test, par.homo[1,,kchs,3], type="l",ylim=c(0,1),
                xlab=expression("Mortality during growth phase, "*expression(mu[G])),
                ylab=expression(italic(r[2])),lwd=1.3)
points(mu1.test, par.hemi[1,,kchs,3], type="l",lty=3,col="grey")



plot(mu1.test, 1-par.homo[1,,kchs,2]-par.homo[1,,kchs,3], type="l",ylim=c(0,1),
                xlab=expression("Mortality during growth phase, "*expression(mu[G])),
                ylab=expression(italic(r[3])),lwd=1.3)
}
```