

No evidence that more physically attractive women have higher estradiol or progesterone

Code ▾

BC Jones et al. (ben.jones@glasgow.ac.uk (<mailto:ben.jones@glasgow.ac.uk>))

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```
# Load packages
library(tidyverse)
library(lmerTest)
library(viridis)
library(rsm)
library(knitr)
sessionInfo()
```

```
R version 3.4.1 (2017-06-30)
Platform: x86_64-apple-darwin15.6.0 (64-bit)
Running under: macOS Sierra 10.12.6

Matrix products: default
BLAS: /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framework/Versions/A/libBLAS.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/3.4/Resources/lib/libRlapack.dylib

locale:
[1] en_GB.UTF-8/en_GB.UTF-8/en_GB.UTF-8/C/en_GB.UTF-8/en_GB.UTF-8

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
[1] bindrcpp_0.2      knitr_1.15.1      rsm_2.8           viridis_0.4.0     viridisLite_0.2.0
[6] lmerTest_2.0-33  lme4_1.1-13       Matrix_1.2-10    dplyr_0.7.4       purrr_0.2.3
[11] readr_1.1.1      tidyr_0.7.1       tibble_1.3.4     ggplot2_2.2.1     tidyverse_1.1.1

loaded via a namespace (and not attached):
[1] httr_1.3.1        jsonlite_1.5       splines_3.4.1      modelr_0.1.1       Formula_1.2-1
[6] assertthat_0.2.0 latticeExtra_0.6-28 cellranger_1.1.0   backports_1.0.5    lattice_0.20-35
[11] glue_1.1.1        digest_0.6.12      RColorBrewer_1.1-2 checkmate_1.8.2    rvest_0.3.2
[16] minga_1.2.4       sandwich_2.4-0     colorspace_1.3-2  htmltools_0.3.6    plyr_1.8.4
[21] psych_1.7.3.21    pkgconfig_2.0.1    broom_0.4.2        haven_1.1.0        xtable_1.8-2
[26] mvtnorm_1.0-6     scales_0.4.1       lsmeans_2.27-2    htmlTable_1.9      TH.data_1.0-8
[31] nnet_7.3-12       lazyeval_0.2.0     mnormt_1.5-5      survival_2.41-3    magrittr_1.5
[36] readxl_1.0.0      estimability_1.2   nlme_3.1-131      MASS_7.3-47        forcats_0.2.0
[41] xml2_1.1.1        foreign_0.8-69     tools_3.4.1       data.table_1.10.4  hms_0.3
[46] multcomp_1.4-7    stringr_1.2.0      munsell_0.4.3     cluster_2.0.6      compiler_3.4.1
[51] rlang_0.1.2       grid_3.4.1         nloptr_1.0.4      htmlwidgets_0.9    base64enc_0.1-3
[56] codetools_0.2-15 gtable_0.2.0       reshape2_1.4.2    R6_2.2.0           zoo_1.8-0
[61] gridExtra_2.2.1   lubridate_1.6.0    bindr_0.1         Hmisc_4.0-2        stringi_1.1.5
[66] parallel_3.4.1   Rcpp_0.12.10      rpart_4.1-11     acepack_1.4.1      tidyselect_0.1.1
[71] coda_0.19-1
```

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```
# read in the raw data
raw <- read_csv("ratings_anon.csv")
```

Remove outlier hormone values

Remove values below bottom sensitivity thresholds for assays (progesterone < 5, estrogen < 0.1). Remove outlier values (+/- 3SD from the mean).

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```

horm_no_outliers <- raw %>%
  mutate(
    rater_sex.e = ifelse(rater_sex=="male", 0.5, -0.5),
    prog1 = ifelse(progesterone >= 5, progesterone, NA),
    estr1 = ifelse(estradiol >= 0.1, estradiol, NA),
    prog = ifelse(prog1>mean(prog1, na.rm=TRUE)+3*sd(prog1, na.rm=TRUE) |
      prog1<mean(prog1, na.rm=TRUE)-3*sd(prog1, na.rm=TRUE), NA, prog1),
    estr = ifelse(estr1>mean(estr1, na.rm=TRUE)+3*sd(estr1, na.rm=TRUE) |
      estr1<mean(estr1, na.rm=TRUE)-3*sd(estr1, na.rm=TRUE), NA, estr1)
  )
# how many included?
horm_no_outliers %>%
  group_by(face_id, session) %>%
  summarise(
    e = is.na(mean(estr)),
    p = is.na(mean(prog))
  ) %>%
  ungroup() %>%
  select(e:p) %>%
  gather('hormone', 'na', e:p) %>%
  group_by(hormone) %>%
  summarise(
    'valid' = n() - sum(na),
    'excluded' = sum(na)
  ) %>%
  arrange(hormone) %>%
  group_by() %>%
  summarise(
    total_hormone_samples_valid = sum(valid),
    total_hormone_samples_excluded = sum(excluded)
  ) %>%
  gather("stat", "value", !! 1:length(.))

```

stat	value
<chr>	<int>
total_hormone_samples_valid	2458
total_hormone_samples_excluded	32

2 rows

Mean hormone values

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```

horm_no_outliers %>%
  summarise(
    estr_mean = mean(estr, na.rm=TRUE),
    estr_sd = sd(estr, na.rm=TRUE),
    prog_mean = mean(prog, na.rm=TRUE),
    prog_sd = sd(prog, na.rm=TRUE)
  )

```

estr_mean	estr_sd	prog_mean	prog_sd
<dbl>	<dbl>	<dbl>	<dbl>
3.417601	1.327905	143.8992	93.33346

1 row

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NA

Center and scale hormones

Subject-mean-centre hormones (within), grand-mean-centre hormones (between), and divide by a constant to put all hormones on a similar scale for Imm analyses.

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```

data_hormones <- horm_no_outliers %>%
group_by(face_id) %>%
  mutate(prog.current.s=(prog-mean(prog, na.rm=TRUE))/400,
         estr.current.s=(estr-mean(estr, na.rm=TRUE))/5,
         prog.m = mean(prog, na.rm=TRUE),
         estr.m = mean(estr, na.rm=TRUE)) %>%
ungroup() %>%
as.data.frame() %>%
mutate(prog.mean.s = (prog.m - mean(prog.m, na.rm=TRUE))/400,
       estr.mean.s = (estr.m - mean(estr.m, na.rm=TRUE))/5) %>%
filter(!is.na(prog.current.s) & !is.na(estr.current.s))

```

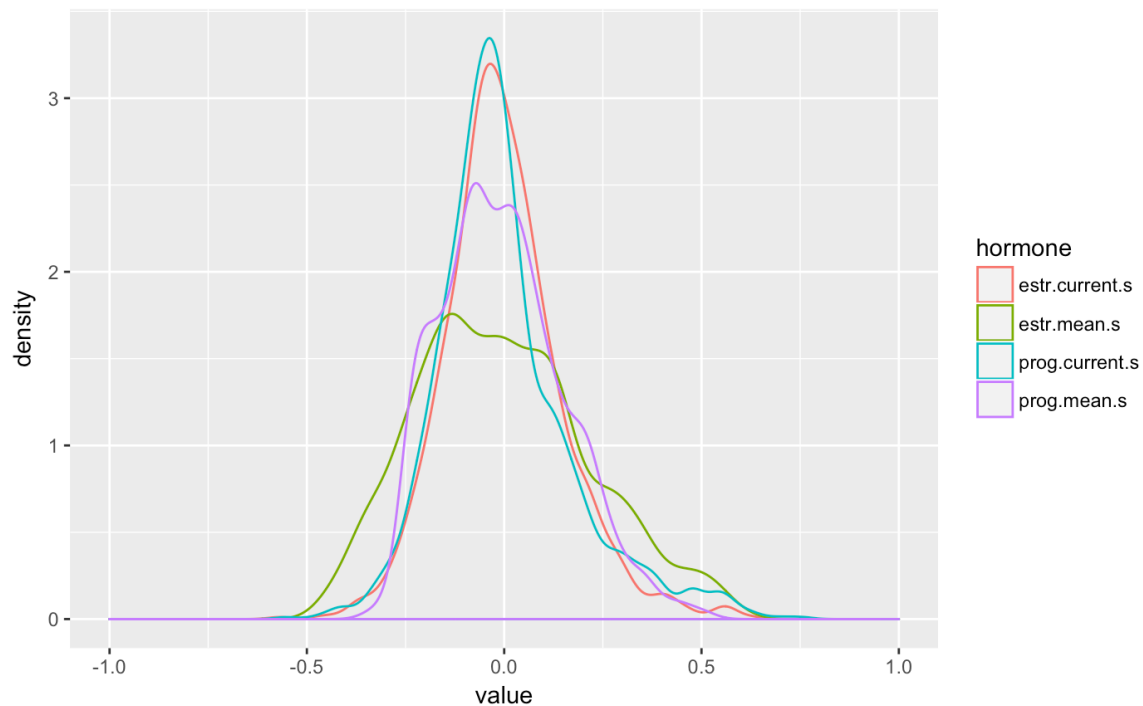
Graph hormone distributions

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```

data_hormones %>%
group_by(face_id, session, prog.current.s, estr.current.s, prog.mean.s, estr.mean.s) %>%
summarise(n = n()) %>%
ungroup() %>%
gather("hormone", "value", prog.current.s:estr.mean.s) %>%
ggplot(aes(value, colour=hormone)) +
geom_density(alpha=.5) +
scale_x_continuous(limits = c(-1,1))

```



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Model within-woman E and P & between-women E and P

- rating = attractiveness rating on 1 (much less attractive than average) to 7 (much more attractive than average) scale
- rater_sex.e = rater sex (effect-coded as -0.5 is female and +0.5 is male)
- estr.current.s = current (i.e., state) estradiol (subject-specific mean centered and divided by 5 to rescale from pg/mL)
- prog.current.s = current (i.e., state) progesterone (subject-specific mean centered and divided by 400 to rescale from pg/mL)
- estr.mean.s = mean (i.e., trait) estradiol (grand mean centered and divided by 5 to rescale from pg/mL)
- prog.mean.s = mean (i.e., trait) progesterone (grand mean centered and divided by 400 to rescale from pg/mL)

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```
fit.ep <- lmer(rating ~ estr.current.s * prog.current.s * rater_sex.e + estr.mean.s * prog.mean.s * rater_sex.e +
              (1 | face_id) +
              (0 + estr.current.s:prog.current.s:rater_sex.e || face_id) +
              (1 | rater_id) +
              (0 + estr.current.s:prog.current.s + estr.mean.s:prog.mean.s || rater_id) +
              (1 | face_id:session) +
              (0 + rater_sex.e || face_id:session),
              data = data_hormones,
              REML = FALSE)
model.ep <- summary(fit.ep)
model.ep
```

Linear mixed model fit by maximum likelihood t-tests use Satterthwaite approximations to degrees of freedom [lmerMod]

```
Formula: rating ~ estr.current.s * prog.current.s * rater_sex.e + estr.mean.s *
  prog.mean.s * rater_sex.e + (1 | face_id) + ((0 + estr.current.s:prog.current.s:rater_sex.e |
  face_id) + (1 | rater_id) + ((0 + estr.current.s:prog.current.s |
  rater_id) + (0 + estr.mean.s:prog.mean.s | rater_id)) + (1 |
  face_id:session) + ((0 + rater_sex.e | face_id:session))
Data: data_hormones
```

AIC	BIC	logLik	deviance	df.resid
97997.4	98182.9	-48976.7	97953.4	33942

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5605	-0.6402	-0.0453	0.5939	4.6089

Random effects:

Groups	Name	Variance	Std.Dev.
face_id.session	rater_sex.e	0.0004693	0.02166
face_id.session.1	(Intercept)	0.0140364	0.11848
face_id	estr.current.s:prog.current.s:rater_sex.e	3.1125215	1.76423
face_id.1	(Intercept)	0.4406590	0.66382
rater_id	estr.mean.s:prog.mean.s	0.7026012	0.83821
rater_id.1	estr.current.s:prog.current.s	0.0294292	0.17155
rater_id.2	(Intercept)	0.4546629	0.67429
Residual		1.0001873	1.00009

Number of obs: 33964, groups: face_id:session, 1213; face_id, 249; rater_id, 28

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.118e+00	1.353e-01	3.540e+01	23.041	<2e-16 ***
estr.current.s	-1.047e-02	4.518e-02	9.643e+02	-0.232	0.8168
prog.current.s	-6.518e-02	3.935e-02	9.645e+02	-1.657	0.0979 .
rater_sex.e	-6.973e-01	2.551e-01	2.800e+01	-2.733	0.0108 *
estr.mean.s	-1.525e-01	2.095e-01	2.484e+02	-0.728	0.4673
prog.mean.s	-6.029e-02	2.885e-01	2.492e+02	-0.209	0.8346
estr.current.s:prog.current.s	-5.366e-01	2.438e-01	8.370e+01	-2.201	0.0305 *
estr.current.s:rater_sex.e	1.779e-02	7.762e-02	1.198e+03	0.229	0.8188
prog.current.s:rater_sex.e	-2.424e-02	6.807e-02	1.075e+03	-0.356	0.7219
estr.mean.s:prog.mean.s	6.880e-01	1.220e+00	2.546e+02	0.564	0.5732
rater_sex.e:estr.mean.s	-7.087e-04	5.442e-02	1.210e+03	-0.013	0.9896
rater_sex.e:prog.mean.s	-8.999e-02	7.671e-02	1.212e+03	-1.173	0.2410
estr.current.s:prog.current.s:rater_sex.e	4.154e-01	4.427e-01	3.040e+01	0.938	0.3555
rater_sex.e:estr.mean.s:prog.mean.s	2.311e-01	4.487e-01	2.770e+01	0.515	0.6107

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as p = 14 > 12.

Use `print(x, correlation=TRUE)` or
`vcov(x)` if you need it

Hide

```
confint(fit.ep, method = "Wald") %>%
  as.data.frame() %>%
  rownames_to_column() %>%
  filter(!is.na(`2.5 %`)) %>%
  kable(digits = 3)
```

rowname	2.5 %	97.5 %
(Intercept)	2.853	3.383

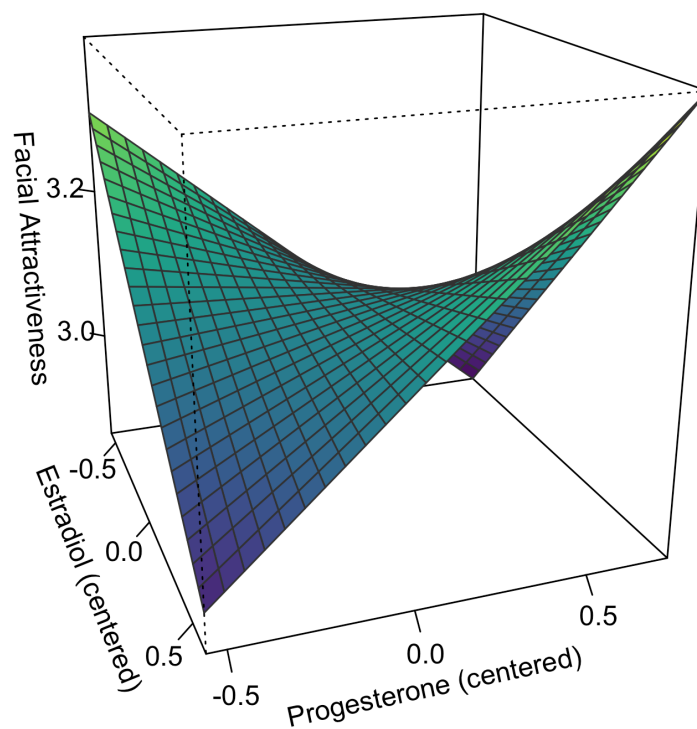
rowname	2.5 %	97.5 %
estr.current.s	-0.099	0.078
prog.current.s	-0.142	0.012
rater_sex.e	-1.197	-0.197
estr.mean.s	-0.563	0.258
prog.mean.s	-0.626	0.505
estr.current.s:prog.current.s	-1.014	-0.059
estr.current.s:rater_sex.e	-0.134	0.170
prog.current.s:rater_sex.e	-0.158	0.109
estr.mean.s:prog.mean.s	-1.703	3.079
rater_sex.e:estr.mean.s	-0.107	0.106
rater_sex.e:prog.mean.s	-0.240	0.060
estr.current.s:prog.current.s:rater_sex.e	-0.452	1.283
rater_sex.e:estr.mean.s:prog.mean.s	-0.648	1.111

Graph of current E by current P interaction following Puts et al. (2013 Hormones & Behavior)

```

coded.data_hormones <- coded.data(data_hormones,
  formula = estr.current.co ~ estr.current.s,
            prog.current.co ~ prog.current.s,
            rater_sex.co ~ rater_sex.e,
            estr.mean.co ~ estr.mean.s,
            prog.mean.co ~ prog.mean.s,
            rater_sex.co ~ rater_sex.e)
model.rsm <- rsm(rating ~ F0(prog.mean.co, estr.mean.co, rater_sex.co) + TWI(estr.current.co, prog.current.co),
  data = coded.data_hormones)
persp(model.rsm, ~ estr.current.co + prog.current.co,
  zlab = "\nFacial Attractiveness",
  xlabs = c("\nEstradiol (centered)", "Progesterone (centered)"),
  col = viridis(256),
  border = "grey20",
  nticks = 3,
  atpos = 0,
  theta = 70,
  phi = 20,
  hook = list(
    pre.plot = function(lab) { png(file = "e_by_p.png", width = 7, height = 6, units = "in", res = 300) },
    post.plot = function(lab) { dev.off() }
  )
)

```



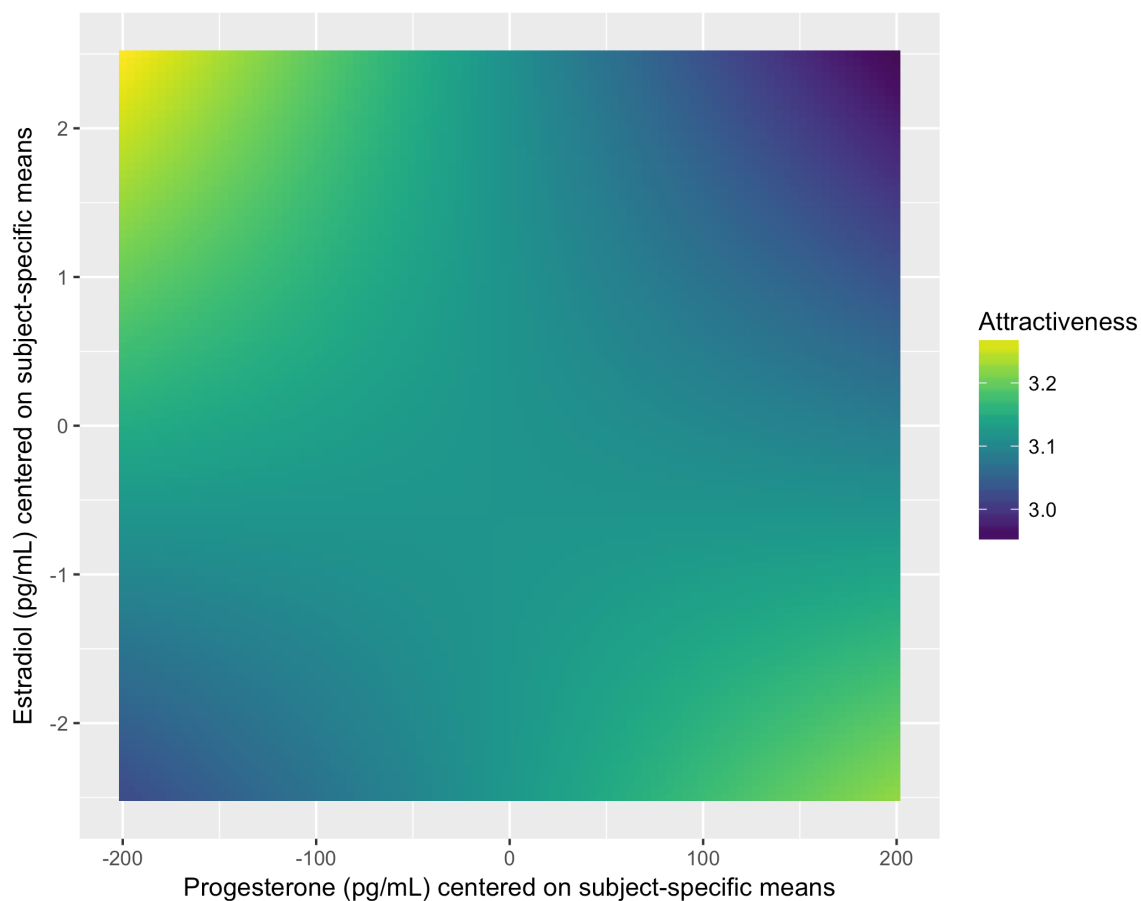
Graph of current E by current P interaction

Fit data for prog.current.s and estr.current.s in grid from -0.5 to +0.5, holding all other variables constant at 0

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```
fitdata = data.frame(
  prog.current.s = rep(seq(-.5, .5,length.out=100),each=100),
  estr.current.s = rep(seq(-.5, .5 ,length.out=100),times=100)
) %>%
mutate(
  prog.mean.s = 0,
  estr.mean.s = 0,
  rater_sex.e = 0,
  face_id = "F",
  rater_id = "R",
  session = rep(seq(1,5),length.out = 100*100)
)

pred_att = predict(fit.ep, newdata = fitdata, allow.new.levels = TRUE)
## graph estr.current.s by prog.current.s interaction
## multiply by scale constants (e = 5, p = 400) to put back on pg/mL centered
e_by_p2 <- fitdata %>%
  mutate(pred = pred_att) %>%
  ggplot(aes(prog.current.s*400, estr.current.s*5, fill=pred)) +
  scale_fill_viridis() +
  geom_tile() +
  ylab("Estradiol (pg/mL) centered on subject-specific means") +
  xlab("Progesterone (pg/mL) centered on subject-specific means") +
  labs(fill="Attractiveness")
ggsave("e_by_p_flat.png", width = 7, height = 5.5)
```



Model within-woman E and P only

[Hide](#)

```
fit.ep.w <- lmer(rating ~ estr.current.s * prog.current.s * rater_sex.e +
  (1 | face_id) +
  (0 + estr.current.s:prog.current.s:rater_sex.e || face_id) +
  (1 | rater_id) +
  (0 + estr.current.s:prog.current.s || rater_id) +
  (1 | face_id:session) +
  (0 + rater_sex.e || face_id:session),
  data = data_hormones,
  REML = FALSE)
model.ep.w <- summary(fit.ep.w)
model.ep.w
```

Linear mixed model fit by maximum likelihood t-tests use Satterthwaite approximations to degrees of freedom [lmerMod]

```
Formula: rating ~ estr.current.s * prog.current.s * rater_sex.e + (1 |
  face_id) + ((0 + estr.current.s:prog.current.s:rater_sex.e |
  face_id)) + (1 | rater_id) + ((0 + estr.current.s:prog.current.s |
  rater_id)) + (1 | face_id:session) + ((0 + rater_sex.e |
  face_id:session))
Data: data_hormones
```

AIC	BIC	logLik	deviance	df.resid
97995.2	98121.7	-48982.6	97965.2	33949

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5749	-0.6415	-0.0445	0.5961	4.6113

Random effects:

Groups	Name	Variance	Std.Dev.
face_id.session	rater_sex.e	0.0005417	0.02328
face_id.session.1	(Intercept)	0.0140041	0.11834
face_id	estr.current.s:prog.current.s:rater_sex.e	3.1021380	1.76129
face_id.1	(Intercept)	0.4426018	0.66528
rater_id	estr.current.s:prog.current.s	0.0274750	0.16576
rater_id.1	(Intercept)	0.4590850	0.67756
Residual		1.0010742	1.00054

Number of obs: 33964, groups: face_id:session, 1213; face_id, 249; rater_id, 28

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.12707	0.13498	34.40000	23.168	<2e-16 ***
estr.current.s	-0.01038	0.04518	964.40000	-0.230	0.8183
prog.current.s	-0.06517	0.03935	964.50000	-1.656	0.0980 .
rater_sex.e	-0.69360	0.25635	28.00000	-2.706	0.0115 *
estr.current.s:prog.current.s	-0.53740	0.24364	85.00000	-2.206	0.0301 *
estr.current.s:rater_sex.e	0.01935	0.07765	1199.80000	0.249	0.8033
prog.current.s:rater_sex.e	-0.02375	0.06811	1078.80000	-0.349	0.7274
estr.current.s:prog.current.s:rater_sex.e	0.39741	0.44197	30.80000	0.899	0.3755

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	estr..	prg.c.	rtr_s.	es...:	e...:	p...:
estr.crrnt.	0.001						
prg.crrnt.s	0.002	-0.312					
rater_sex.e	0.000	0.000	0.000				
estr.cr...:	-0.014	-0.029	-0.109	0.000			
estr.cr.:_.	0.000	0.000	0.000	0.001	0.000		
prg.crr.:_.	0.000	0.000	0.000	0.002	0.000	-0.298	
est...:._.	0.000	0.000	0.000	-0.011	0.000	-0.016	-0.073

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```
confint(fit.ep.w, method = "Wald") %>%
  as.data.frame() %>%
  rownames_to_column() %>%
  filter(!is.na(`2.5 %`)) %>%
  kable(digits = 3)
```

rowname	2.5 %	97.5 %
(Intercept)	2.863	3.392
estr.current.s	-0.099	0.078
prog.current.s	-0.142	0.012
rater_sex.e	-1.196	-0.191
estr.current.s:prog.current.s	-1.015	-0.060
estr.current.s:rater_sex.e	-0.133	0.172
prog.current.s:rater_sex.e	-0.157	0.110
estr.current.s:prog.current.s:rater_sex.e	-0.469	1.264

Model between-women E and P only

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```
fit.ep.h <- lmer(rating ~ estr.mean.s * prog.mean.s * rater_sex.e +
  (1 | face_id) +
  (0 + rater_sex.e || face_id) +
  (1 | rater_id) +
  (0 + estr.mean.s:prog.mean.s | rater_id) +
  (1 | face_id:session) +
  (0 + rater_sex.e || face_id:session),
  data = data_hormones,
  REML = FALSE)
model.ep.h <- summary(fit.ep.h)
model.ep.h
```

Linear mixed model fit by maximum likelihood t-tests use Satterthwaite approximations to degrees of freedom [lmerMod]

```
Formula: rating ~ estr.mean.s * prog.mean.s * rater_sex.e + (1 | face_id) +
  ((0 + rater_sex.e | face_id) + (1 | rater_id) + (0 + estr.mean.s:prog.mean.s |
  rater_id) + (1 | face_id:session) + ((0 + rater_sex.e | face_id:session))
Data: data_hormones
```

AIC	BIC	logLik	deviance	df.resid
97934.9	98061.4	-48952.4	97904.9	33949

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.4427	-0.6369	-0.0424	0.5954	4.4887

Random effects:

Groups	Name	Variance	Std.Dev.
face_id.session	rater_sex.e	0.00000	0.0000
face_id.session.1	(Intercept)	0.01476	0.1215
face_id	rater_sex.e	0.02640	0.1625
face_id.1	(Intercept)	0.43952	0.6630
rater_id	estr.mean.s:prog.mean.s	0.72132	0.8493
rater_id.1	(Intercept)	0.45463	0.6743
Residual		0.99433	0.9972

Number of obs: 33964, groups: face_id:session, 1213; face_id, 249; rater_id, 28

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.113916	0.135284	35.360000	23.018	<2e-16 ***
estr.mean.s	-0.154100	0.209277	248.450000	-0.736	0.4622
prog.mean.s	-0.062047	0.288171	249.290000	-0.215	0.8297
rater_sex.e	-0.693967	0.255350	28.100000	-2.718	0.0111 *
estr.mean.s:prog.mean.s	0.673933	1.218583	254.850000	0.553	0.5807
estr.mean.s:rater_sex.e	0.007665	0.073972	248.680000	0.104	0.9176
prog.mean.s:rater_sex.e	-0.109288	0.103294	260.550000	-1.058	0.2910
estr.mean.s:prog.mean.s:rater_sex.e	0.216369	0.536036	50.680000	0.404	0.6882

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	estr..	prg.m.	rtr_s.	es....	e.:_.	p.:_.
estr.mean.s	0.005						
prog.mean.s	0.003	-0.378					
rater_sex.e	0.000	0.000	0.000				
estr.mn..._	-0.118	-0.042	-0.019	0.000			
estr.mn.:_.	0.000	0.000	0.000	0.001	0.000		
prg.mn.s:._	0.000	0.000	0.000	0.002	0.000	-0.386	
est....._.	0.000	0.000	0.000	-0.018	0.000	-0.020	-0.023

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```
confint(fit.ep.h, method = "Wald") %>%
  as.data.frame() %>%
  rownames_to_column() %>%
  filter(!is.na(`2.5 %`)) %>%
  kable(digits = 3)
```

rowname	2.5 %	97.5 %
(Intercept)	2.849	3.379
estr.mean.s	-0.564	0.256
prog.mean.s	-0.627	0.503

rowname	2.5 %	97.5 %
rater_sex.e	-1.194	-0.193
estr.mean.s:prog.mean.s	-1.714	3.062
estr.mean.s:rater_sex.e	-0.137	0.153
prog.mean.s:rater_sex.e	-0.312	0.093
estr.mean.s:prog.mean.s:rater_sex.e	-0.834	1.267

Waist-to-hip ratio and mean hormone levels

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```
data_whr <- data_hormones %>%
  group_by(face_id, prog.mean.s, estr.mean.s, whr) %>%
  summarise()
WHRm <- mean(data_whr$whr, na.rm=TRUE)
WHRsd <- sd(data_whr$whr, na.rm=TRUE)
paste0("WHR mean = ", round(WHRm, 3) , ", SD = ", round(WHRsd, 3) )
```

```
[1] "WHR mean = 0.751, SD = 0.054"
```

WHR-Estradiol correlation

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```
cor.test(data_whr$whr, data_whr$estr.mean.s)
```

```
Pearson's product-moment correlation

data: data_whr$whr and data_whr$estr.mean.s
t = 3.6758, df = 246, p-value = 0.0002911
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.1066422 0.3429962
sample estimates:
      cor
-0.2281782
```

WHR-Progesterone correlation

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```
cor.test(data_whr$whr, data_whr$prog.mean.s)
```

```
Pearson's product-moment correlation

data: data_whr$whr and data_whr$prog.mean.s
t = -1.1686, df = 246, p-value = 0.2437
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
-0.19704476 0.05073535
sample estimates:
      cor
-0.07430137
```