Preliminary analyses GCCR001 April 19th 4 PM

Database creation

1. Confirm there are no email duplicates.

Descriptives

```
## Non-numerical variable(s) ignored: Country_of_Residence, Gender, Group
```

0.46 ## ## 0.50 0.00 ## \mathtt{Min} 19.00 0.00 ## Q1 32.00 0.00 0.00 ## Median 40.00 0.00 0.00 ## QЗ 50.00 1.00 1.00 ## Max 120.00 1.00 1.00 ## 0.00 0.00 MAD 13.34 ## IQR 18.00 1.00 1.00 ## CV0.30 1.09 1.24 0.44 0.17 Skewness 0.42 SE.Skewness 0.04 ## 0.04 0.04 ## Kurtosis -0.17-1.82-1.97## N.Valid 3858.00 3858.00 3858.00

100.00

100.00

Table: Table continues below

Pct.Valid

##

100.00

##

##		Changes_in_basic_tastes_savory/umami	Changes_in_basic_tastes_sour
##			
##	Mean	0.27	0.38
##	Std.Dev	0.44	0.48
##	Min	0.00	0.00
##	Q1	0.00	0.00
##	Median	0.00	0.00
##	Q3	1.00	1.00
##	Max	1.00	1.00

##	MAD	0.00	0.00
##	IQR	1.00	1.00
##	CV	1.65	1.29
##	Skewness	1.04	0.51
##	SE.Skewness	0.04	0.04
##	Kurtosis	-0.91	-1.74
##	N.Valid	3858.00	3858.00
##	Pct.Valid	100.00	100.00
##			

Table: Table continues below

##

##		Changes_in_basic_tastes_sweet	Chemesthesis_change	
## -				
##	Mean	0.45	-37.30	
##	Std.Dev	0.50	36.04	
##	Min	0.00	-100.00	
##	Q1	0.00	-69.50	
##	Median	0.00	-33.10	
##	Q3	1.00	-0.80	
##	Max	1.00	100.00	
##	MAD	0.00	48.63	
##	IQR	1.00	68.65	
##	CV	1.12	-0.97	
##	Skewness	0.22	-0.14	
##	SE.Skewness	0.04	0.04	
##	Kurtosis	-1.95	-0.96	
##	N.Valid	3858.00	3858.00	
##	Pct.Valid	100.00	100.00	
##				

Table: Table continues below

##

##		Combustible_cigarette_use_no	COVID_diagnosis	E-cigarette_use_no
##				
##	Mean	0.55	1.35	0.75
##	Std.Dev	0.50	0.51	0.43
##	Min	0.00	1.00	0.00
##	Q1	0.00	1.00	1.00
##	Median	1.00	1.00	1.00
##	Q3	1.00	2.00	1.00
##	Max	1.00	3.00	1.00
##	MAD	0.00	0.00	0.00
##	IQR	1.00	1.00	0.00
##	CV	0.91	0.37	0.57
##	Skewness	-0.19	0.91	-1.16
##	SE.Skewness	0.04	0.04	0.04
##	Kurtosis	-1.96	-0.48	-0.64
##	N.Valid	3858.00	3858.00	3858.00
##	Pct.Valid	100.00	100.00	100.00
##				

Table: Table continues below

##						
##						
##		Nasal_patency_change	parosmia	phantosmia	Sanity_check	Smell_change
## -						
##	Mean	22.34	0.08	0.08	0.00	-79.43
##	Std.Dev	32.40	0.27	0.28	0.00	28.91
##	Min	-100.00	0.00	0.00	0.00	-100.00
##	Q1	0.00	0.00	0.00	0.00	-99.10
##	Median	10.20	0.00	0.00	0.00	-91.40
##	Q3	44.40	0.00	0.00	0.00	-74.60
##	Max	100.00	1.00	1.00	0.00	77.50
##	MAD	16.01	0.00	0.00	0.00	12.75
##	IQR	44.40	0.00	0.00	0.00	24.50
##	CV	1.45	3.47	3.30	NaN	-0.36
##	Skewness	0.48	3.18	3.00	NaN	1.83
##	SE.Skewness	0.04	0.04	0.04	0.04	0.04
##	Kurtosis	0.52	8.11	6.99	NaN	2.44
##	N.Valid	3858.00	3858.00	3858.00	3858.00	3858.00
##	Pct.Valid	100.00	100.00	100.00	100.00	100.00

Table: Table continues below

##	
##	

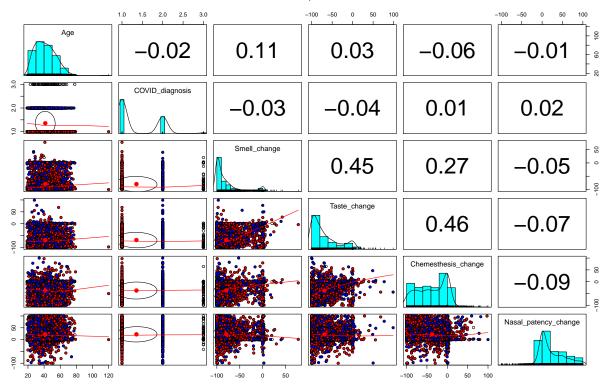
##

##

##

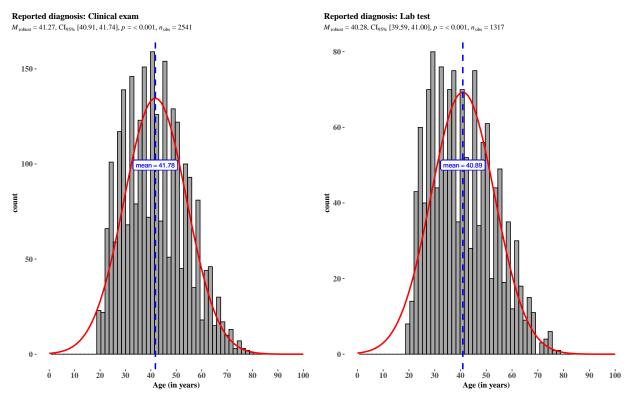
##		${\tt smell_fluctuations}$	${\tt smell_loss}$	Taste_change
##				
##	Mean	0.14	0.86	-68.88
##	Std.Dev	0.34	0.35	32.62
##	Min	0.00	0.00	-100.00
##	Q1	0.00	1.00	-95.70
##	Median	0.00	1.00	-80.60
##	Q3	0.00	1.00	-51.40
##	Max	1.00	1.00	99.00
##	MAD	0.00	0.00	26.39
##	IQR	0.00	0.00	44.28
##	CV	2.53	0.41	-0.47
##	Skewness	2.13	-2.05	1.09
##	SE.Skewness	0.04	0.04	0.04
##	Kurtosis	2.53	2.22	0.23
##	N.Valid	3858.00	3858.00	3858.00
##	Pct.Valid	100.00	100.00	100.00

Red = COVID-19 clinical exam; Blue = COVID-19 lab tested



Age by Group

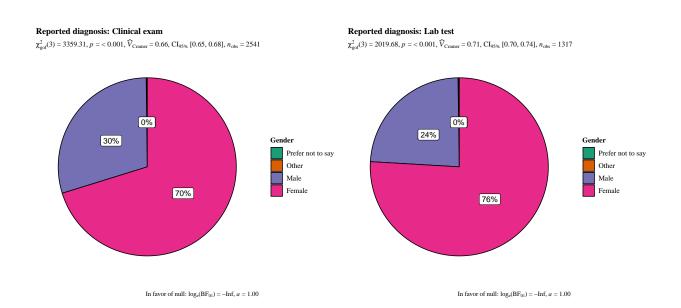
Age in COVID-19 lab tested vs. clinically examined respondents



Gender by Group

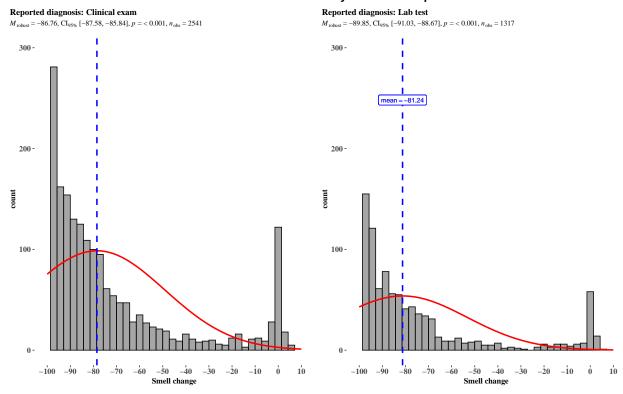
!!!! Order of labels and color of the scale need adjustment Stats on comparison between groups missing

Gender in COVID-19 lab tested vs. clinically examined respondents

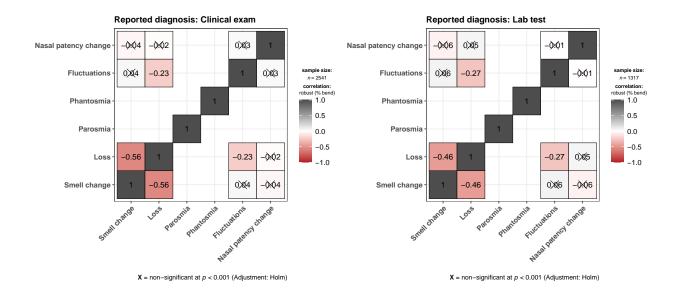


Smell Change by Group

Smell change during – before disease in COVID-19 lab tested vs. clinically examined respondents

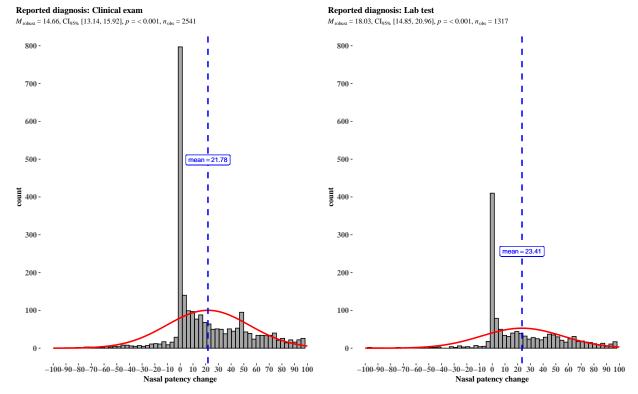


Characterization - Smell change



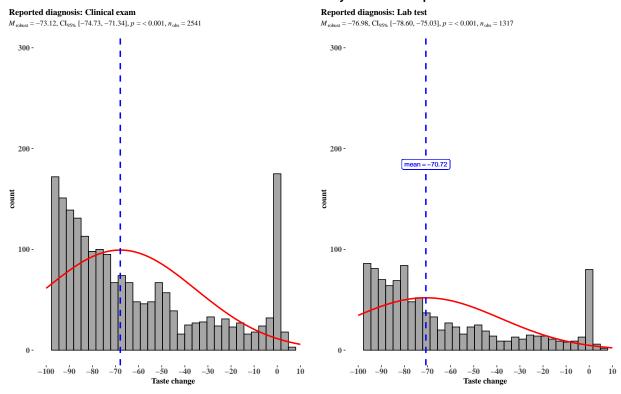
Nasal Patency Change by Group

Nasal patency change during – before disease in COVID-19 lab tested vs. clinically examined respondents

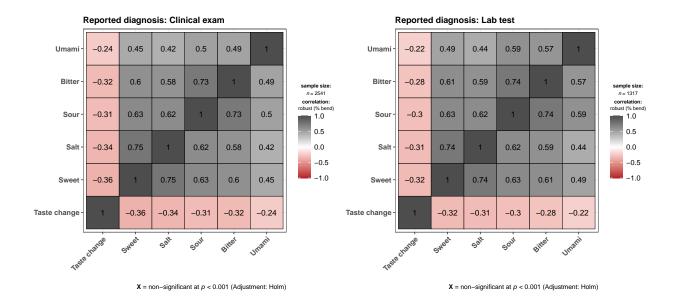


Taste Change by Group

Taste change during – before disease in COVID-19 lab tested vs. clinically examined respondents

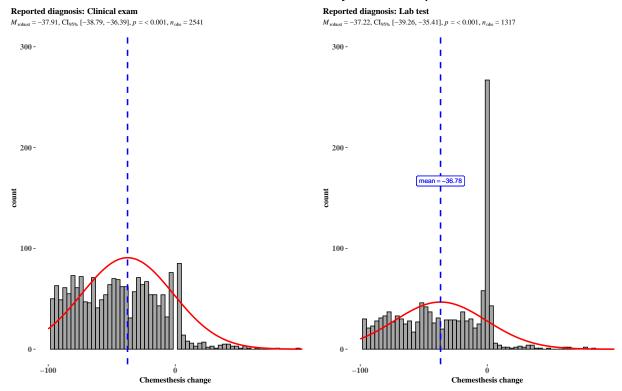


Characterization - Taste change



Chemestesis Change by Group

Chemesthesis change during – before disease in COVID-19 lab tested vs. clinically examined respondents



Bayesian analyses

Age

```
data_GCCR001$Group<-as.numeric(data_GCCR001$Group)</pre>
(bfttest_Age <- ttestBF(formula = Age ~ Group, data = data_GCCR001))[1]</pre>
## Bayes factor analysis
## [1] Alt., r=0.707 : 0.3555399 \pm 0\%
## Against denominator:
##
    Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS
#bfttest_smell[1] # Evidence for difference bigger than 0 vs null (no difference)
#bfttest_smell[1] / bfttest_smell[2] # Evidence for difference bigger than 0 vs smaller than zero
#On top of a Theory testing approach, we will quantify the uncertainty about the parameters by sampling
\#(bfttest\_smell2 \leftarrow ttestBF(formula = Smell\_change \sim Group, \ data = data\_GCCR001))
#chains_smell = posterior(bfttest_smell2, iterations = 1e4)
\#summary(chains\_smell[,'beta (1 - 2)'][chains[, 'beta (1 - 2)'] < 0])
#plot(chains_smell[,2])
```

Smell change

```
(bfttest_smell <- ttestBF(formula = Smell_change ~ Group, data = data_GCCR001))[1]
## Bayes factor analysis
## [1] Alt., r=0.707 : 1.917936 ±0%
##
## Against denominator:
    Null, mu1-mu2 = 0
##
## ---
## Bayes factor type: BFindepSample, JZS
#bfttest_smell[1] # Evidence for difference bigger than 0 vs null (no difference)
#bfttest_smell[1] / bfttest_smell[2] # Evidence for difference bigger than 0 vs smaller than zero
#On top of a Theory testing approach, we will quantify the uncertainty about the parameters by sampling
\#(bfttest\_smell2 \leftarrow ttestBF(formula = Smell\_change \sim Group, data = data\_GCCR001))
#chains_smell = posterior(bfttest_smell2, iterations = 1e4)
\#summary(chains\_smell[,'beta (1 - 2)'][chains[, 'beta (1 - 2)'] < 0])
#plot(chains_smell[,2])
```

Nasal patency

```
#(bfttest_nasalpatency <- ttestBF(formula = Nasal_Patency_change ~ Group, data = data_GCCR001))[1]
#bfttest_nasalpatency[1] # Evidence for difference bigger than 0 vs null (no difference)
#bfttest_nasalpatency[1] / bfttest_nasalpatency[2] # Evidence for difference bigger than 0 vs smaller t

#On top of a Theory testing approach, we will quantify the uncertainty about the parameters by sampling
#(bfttest_nasalpatency2 <- ttestBF(formula = Nasal_Patency_change ~ Group, data = data_GCCR001))
#chains_nasalpatency = posterior(bfttest_nasalpatency2, iterations = 1e4)
#summary(chains_nasalpatency[,'beta (1 - 2)'][chains[, 'beta (1 - 2)'] < 0])
#plot(chains_nasalpatency[,2])</pre>
```

Taste change

```
(bfttest_taste <- ttestBF(formula = Taste_change ~ Group, data = data_GCCR001))[1]

## Bayes factor analysis
## -------
## [1] Alt., r=0.707 : 0.8917328 ±0%

##
## Against denominator:
## Null, mu1-mu2 = 0
## ---
## Bayes factor type: BFindepSample, JZS</pre>
```

```
#bfttest_taste[1] # Evidence for difference bigger than 0 vs null (no difference)
#bfttest_taste[1] / bfttest_taste[2] # Evidence for difference bigger than 0 vs smaller than zero

#On top of a Theory testing approach, we will quantify the uncertainty about the parameters by sampling
#(bfttest_taste2 <- ttestBF(formula = Taste_change ~ Group, data = data_GCCR001))
#chains_taste = posterior(bfttest_taste2, iterations = 1e4)
#summary(chains_taste[,'beta (1 - 2)'][chains[, 'beta (1 - 2)'] < 0])
#plot(chains_taste[,2])</pre>
```

Chemesthesis change

```
(bfttest_chemesthesis <- ttestBF(formula = Chemesthesis_change ~ Group, data = data_GCCR001))[1]

## Bayes factor analysis
## -------
## [1] Alt., r=0.707 : 0.04687988 ±0%

##

## Against denominator:
## Null, mu1-mu2 = 0

## ---
## Bayes factor type: BFindepSample, JZS

#bfttest_chemesthesis[1] # Evidence for difference bigger than 0 vs null (no difference)
#bfttest_chemesthesis[1] / bfttest_chemesthesis[2] # Evidence for difference bigger than 0 vs smaller t

#On top of a Theory testing approach, we will quantify the uncertainty about the parameters by sampling
#(bfttest_chemesthesis2 <- ttestBF(formula = Chemesthesis_change ~ Group, data = data_GCCR001))
#chains_chemesthesis = posterior(bfttest_chemesthesis2, iterations = 1e4)
#summary(chains_chemesthesis[, 2])</pre>
```

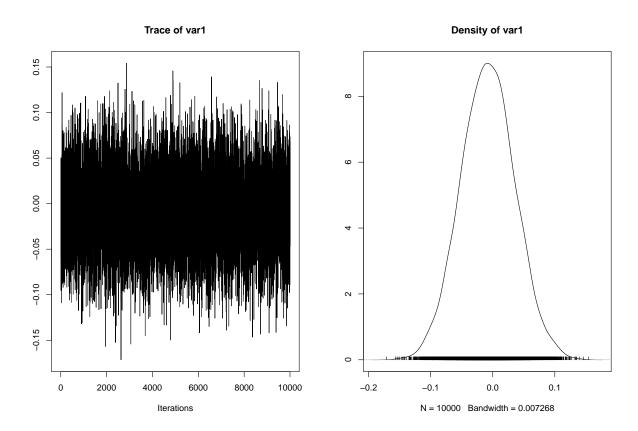
Smell nasal patency effect

!!! Computationally intense with random factor

```
## Bayes factor analysis
## ------
## [1] Nasal_patency_change + Group + Nasal_patency_change:Group : 0.1038786 ±0.01%
##
## Against denominator:
## Smell_change ~ Nasal_patency_change + Group
## ---
## Bayes factor type: BFlinearModel, JZS

## Bayes factor analysis
## -------
## [1] Nasal_patency_change + Group + Nasal_patency_change:Group : 0.1038786 ±0.01%
##
## Against denominator:
```

```
## Smell_change ~ Nasal_patency_change + Group
## ---
## Bayes factor type: BFlinearModel, JZS
```



`geom_smooth()` using formula 'y ~ x'

