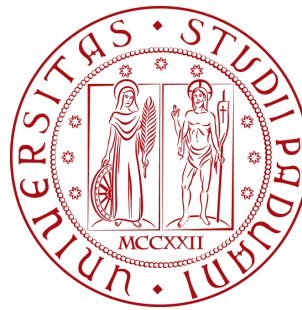


# Are we getting interactions wrong?

## The role of link functions in psychological research



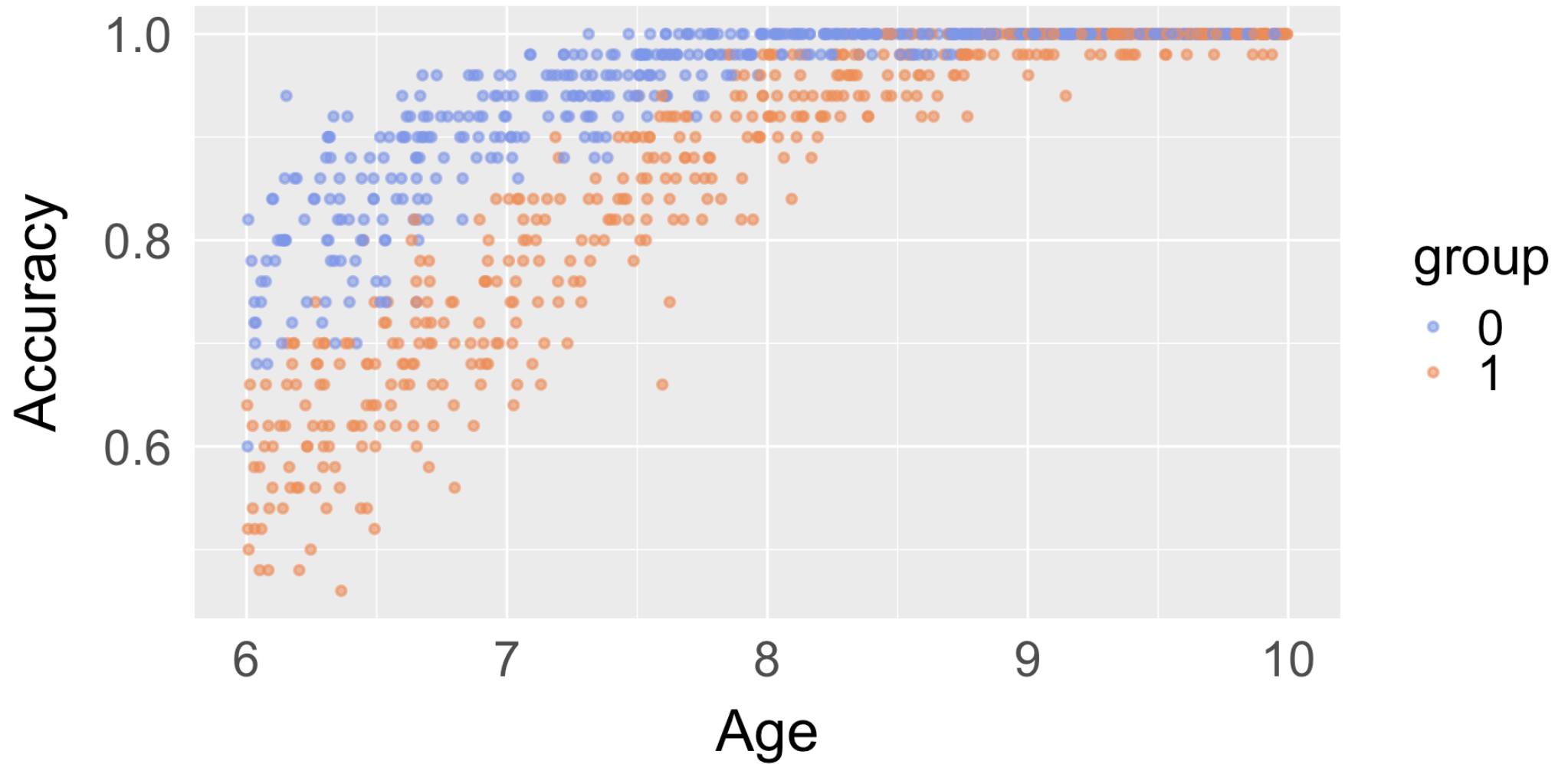
UNIVERSITÀ  
DEGLI STUDI  
DI PADOVA

Laura Sità, Margherita Calderan, Tommaso Feraco,  
Filippo Gambarota, Enrico Toffalini

# Simulated dataset

- 1,000 subjects
  - 500 typically developing children (`group = 0`)
  - 500 children with dyslexia (`group = 1`)
- 50 trials per participant
- Independent variable 1: **age** (in years)
- Independent variable 2: **group**
- Dependent variable: **accuracy** in a TRUE/FALSE task

# Simulated dataset



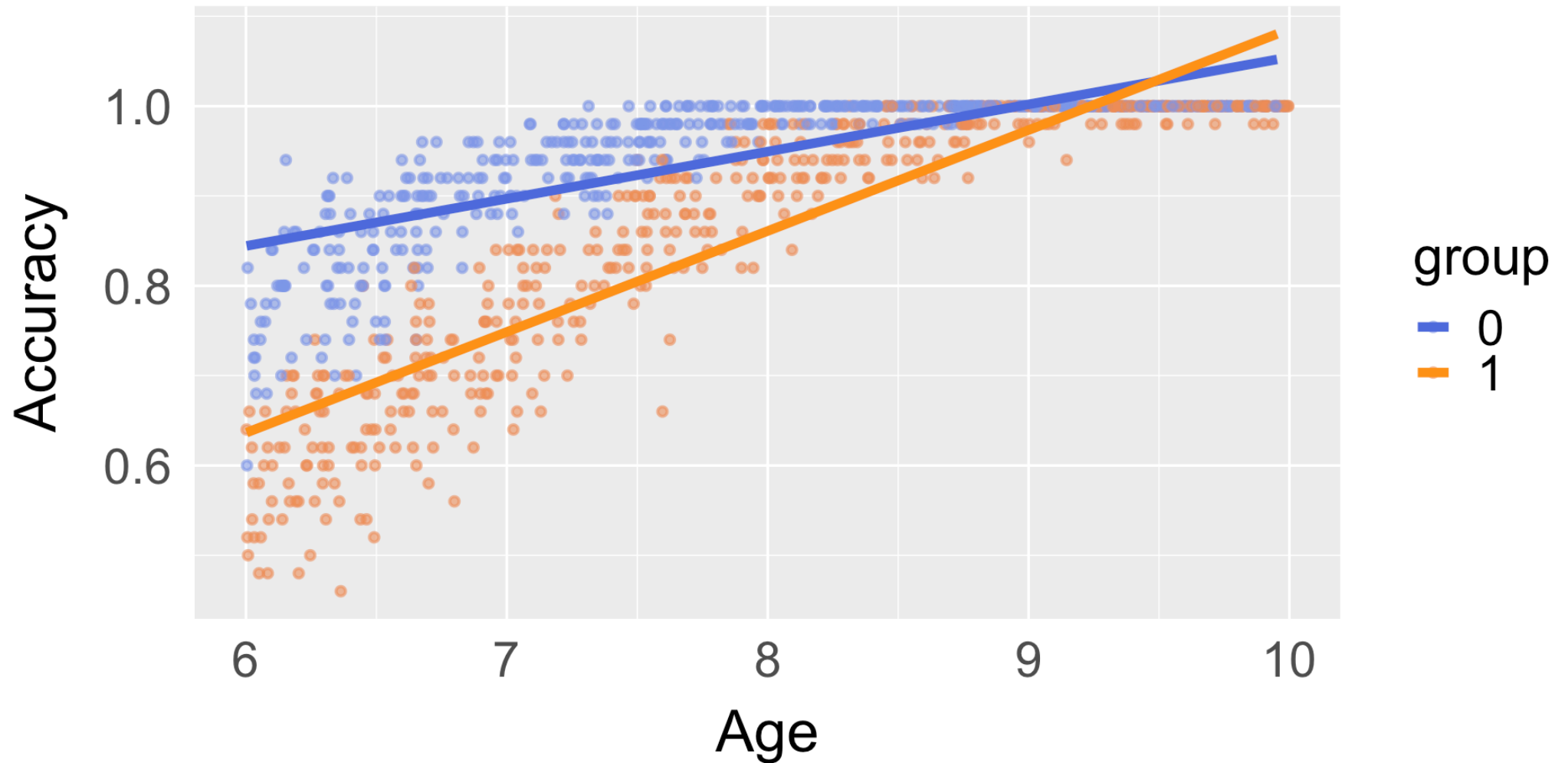
# Building the model

Key choices:

- **family**  
specifies the response distribution and its valid range  
(e.g., unbounded,  $[0, 1]$ , counts)
- **link function**  
maps the linear predictor  $\beta_0 + \beta_1 \cdot \text{age} + \beta_2 \cdot \text{group}$   
onto the scale of the response variable  $Y$

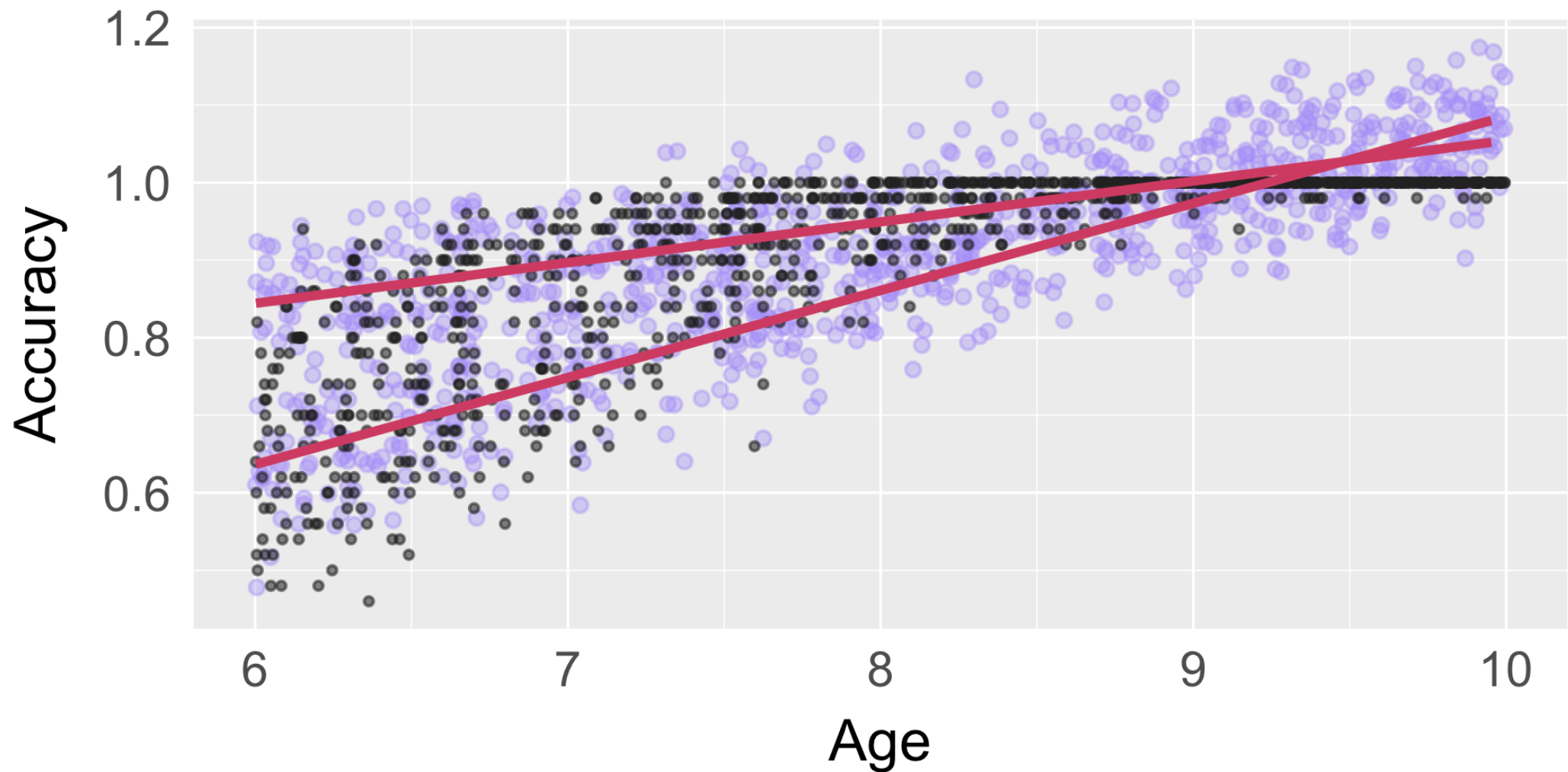
# Linear model

`family=gaussian(link="identity")`



# Predictive check

New predicted values fall outside the valid range for accuracy [0,1]



# family=gaussian(link="identity")

A **positive** interaction emerges

```
1 fit = glm(accuracy ~ age*group, family=gaussian(link="identity"), dat
2 summary(fit)
```

Call:

```
glm(formula = accuracy ~ age * group, family = gaussian(link =
"identity"),
     data = d)
```

Coefficients:

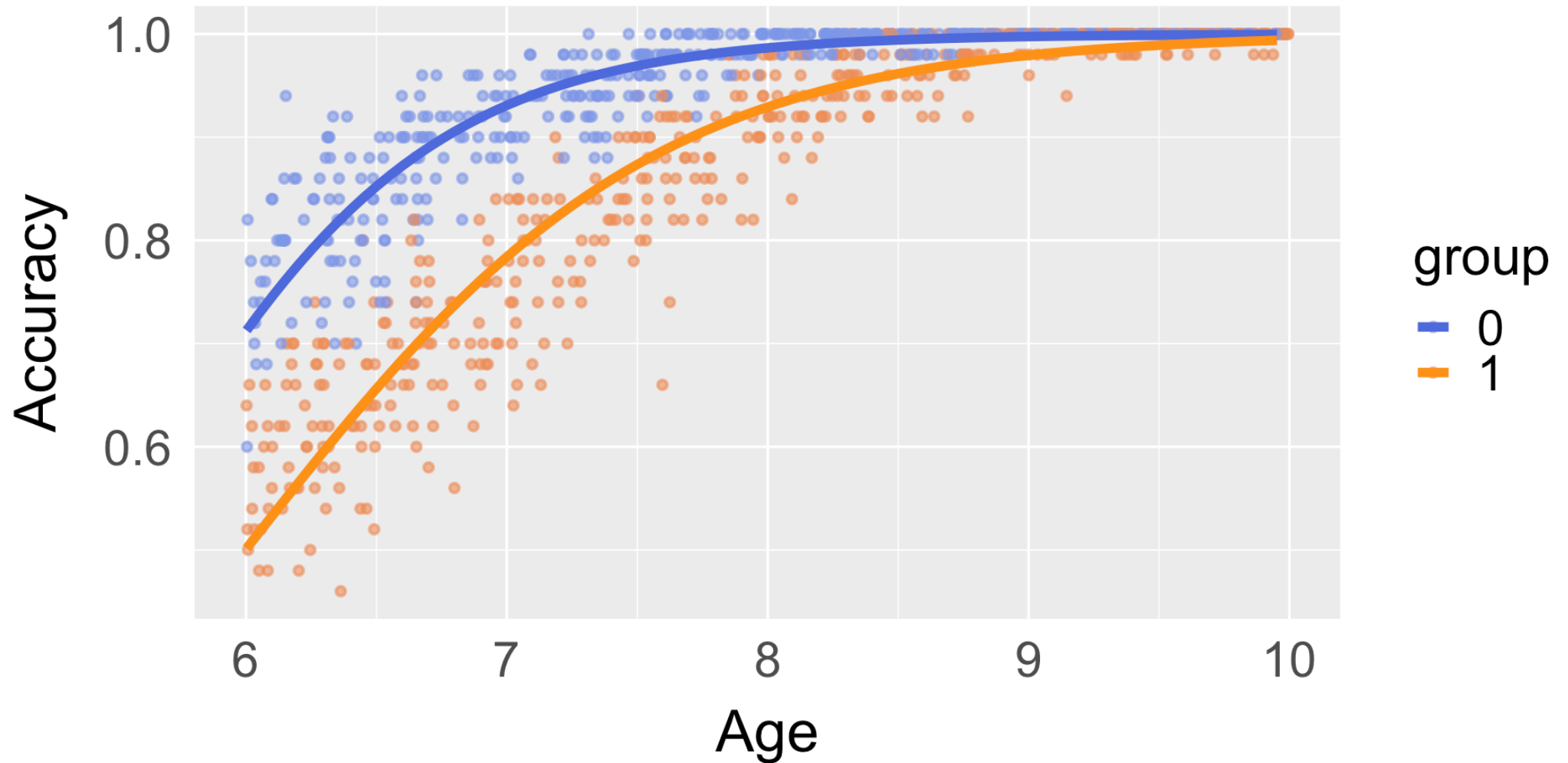
	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	0.529062	0.016916	31.28	<2e-16	***
age	0.052541	0.002103	24.99	<2e-16	***
group1	-0.566758	0.023871	-23.74	<2e-16	***
age:group1	0.059790	0.002967	20.15	<2e-16	***

----



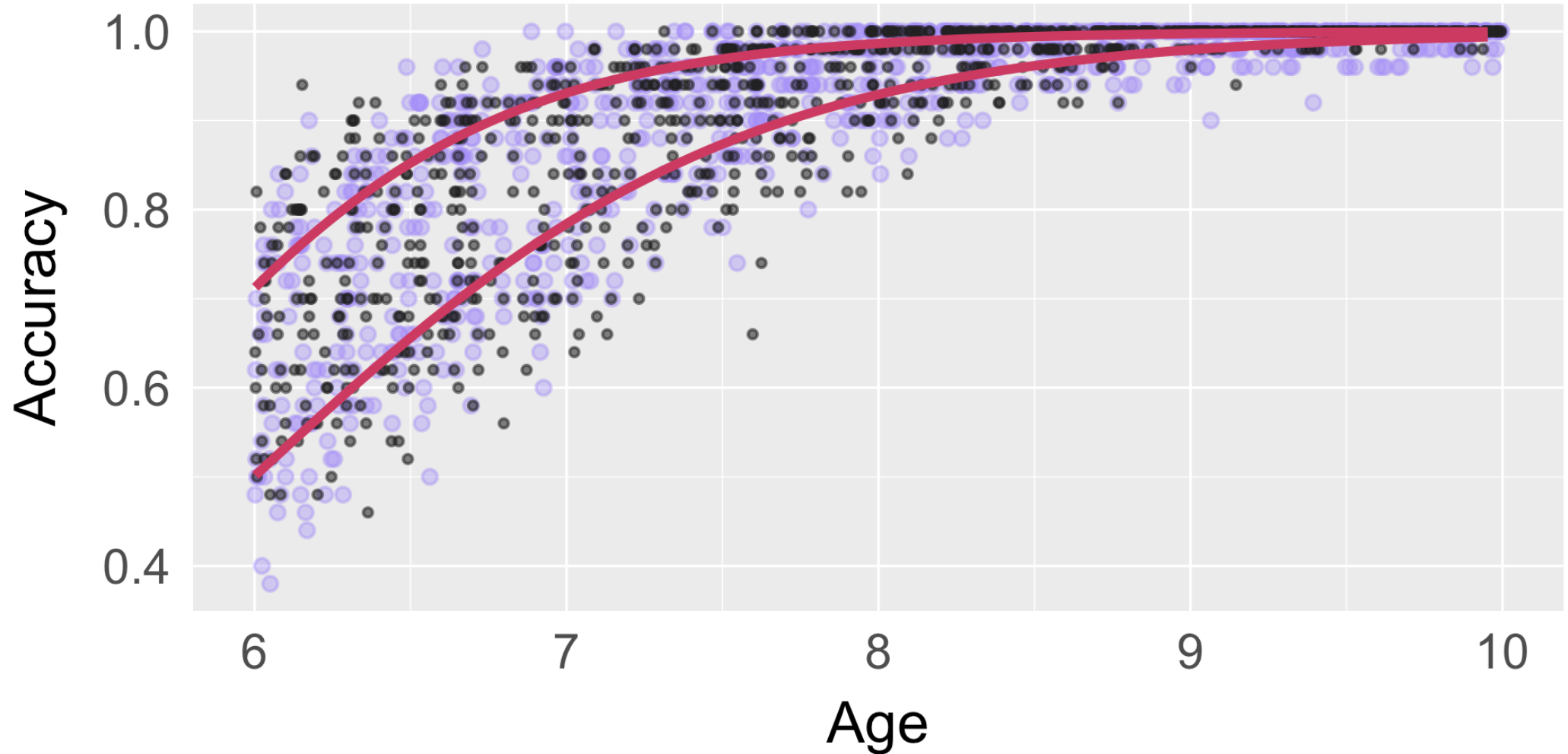
# Logistic regression model

`family=binomial(link="logit")`



# Predictive check

New predicted values fall within the valid range for accuracy [0,1]



# family=binomial(link="logit")

A **negative** interaction emerges

```
1 fit = glm(accuracy ~ age*group, data=d, family=binomial(link="logit"))
2 summary(fit)
```

Call:

```
glm(formula = accuracy ~ age * group, family = binomial(link = "logit"),
     data = d, weights = rep(k, nrow(d)))
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-9.26482	0.32430	-28.568	< 2e-16	***
age	1.69491	0.04842	35.006	< 2e-16	***
group1	1.55052	0.36909	4.201	2.66e-05	***
age:group1	-0.40870	0.05457	-7.490	6.90e-14	***

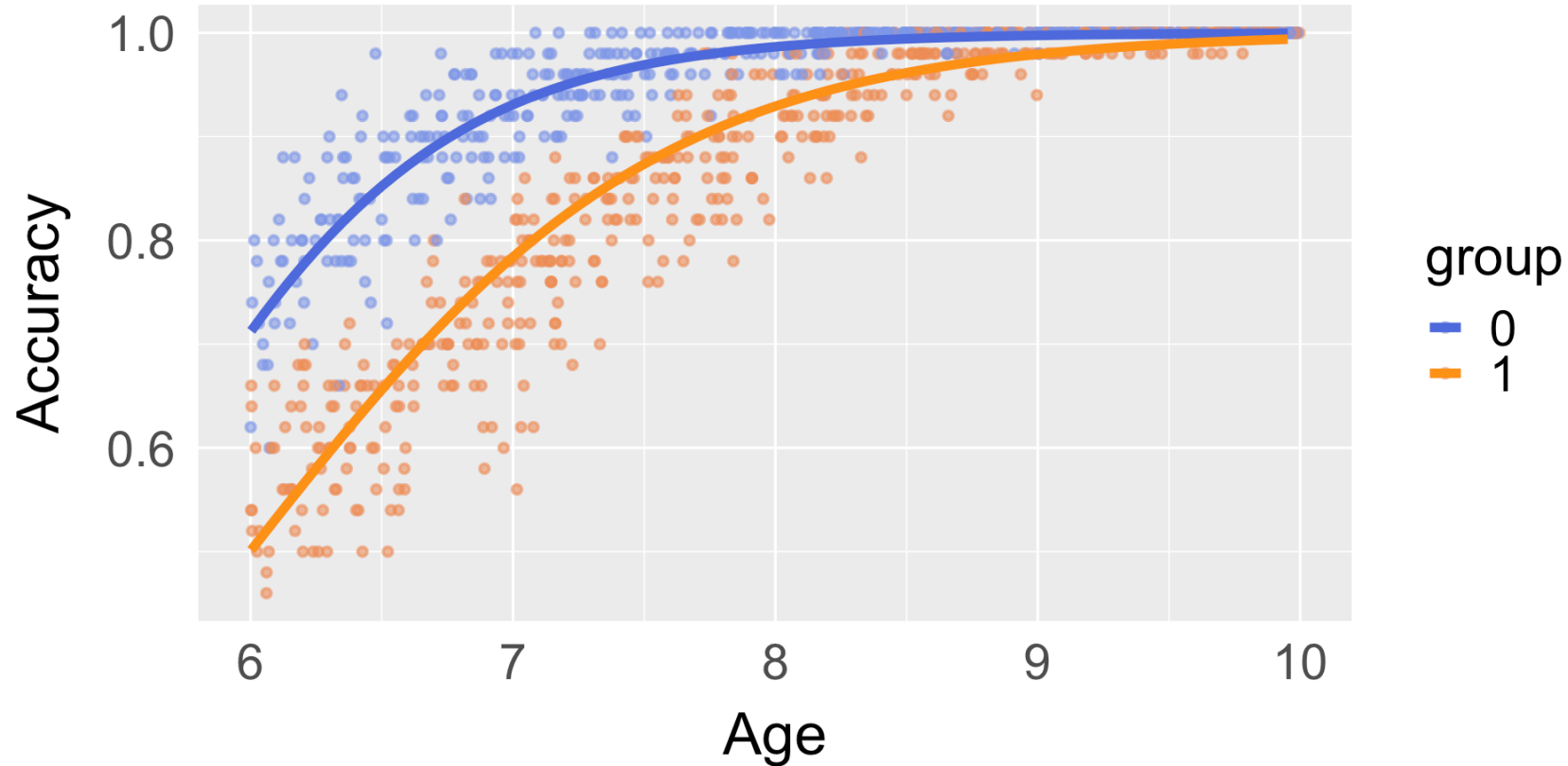
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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# The appropriate model

# What was actually simulated

► Code



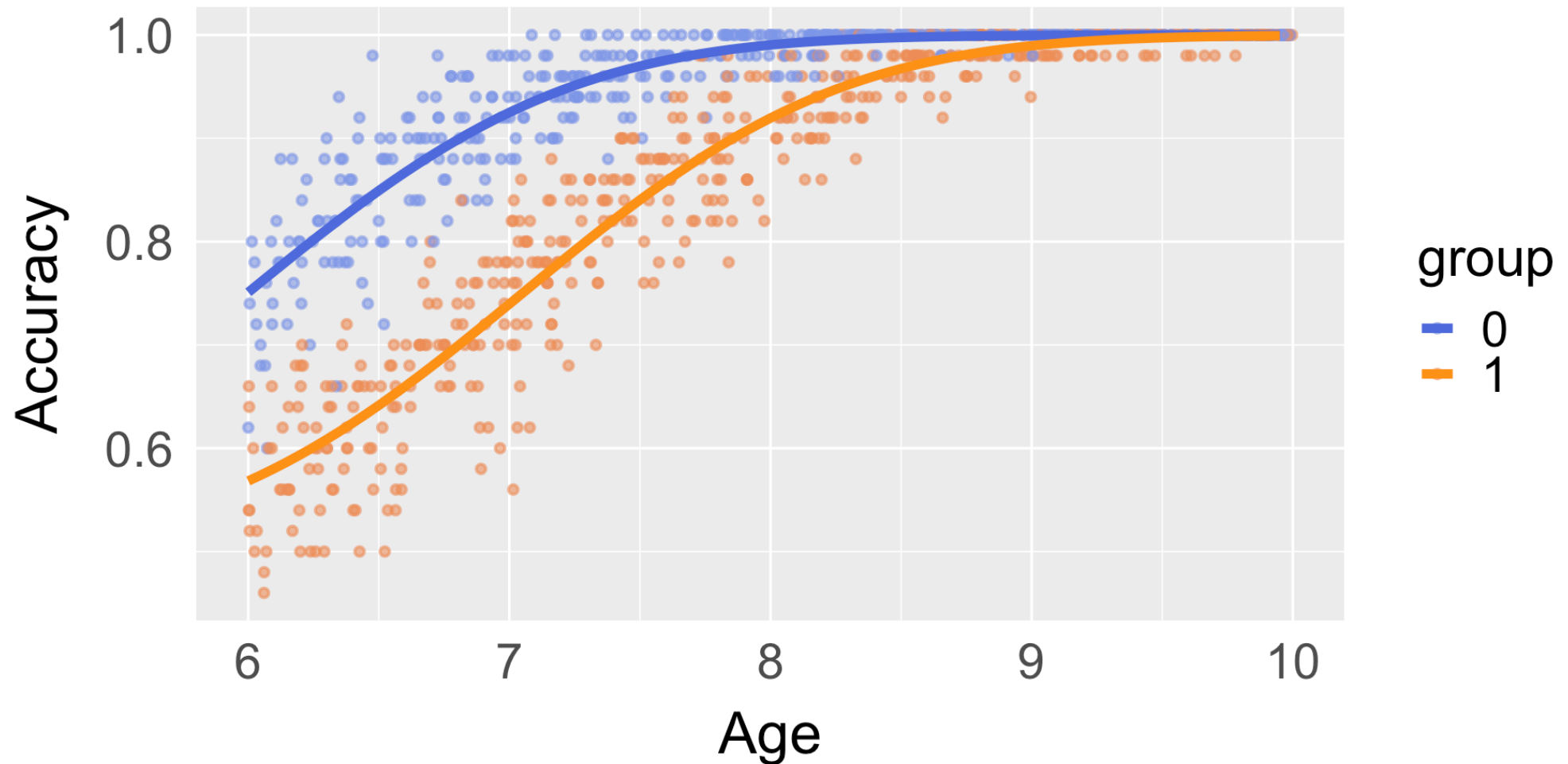
No interaction was simulated

Both models are detecting **an interaction that does not exist**

```
family=binomial(link=mafc.probit(.m=2))
```

To account for the 50% chance level in a TRUE / FALSE task:

**2 alternatives forced-choice probit link**



# family=binomial(link=mafc.probit(.m=2))

No interaction emerges, in line with how the data were generated

```
1 fit = glm(accuracy ~ age*group, data=d, family=binomial(link=mafc.probit(.m=2)))
2 summary(fit)
```

Call:

```
glm(formula = accuracy ~ age * group, family = binomial(link =
mafc.probit(.m = 2)),
    data = d, weights = rep(k, nrow(d)))
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-6.18888	0.23090	-26.803	< 2e-16	***
age	1.03219	0.03323	31.064	< 2e-16	***
group1	-1.16738	0.28399	-4.111	3.95e-05	***
age:group1	0.01123	0.03971	0.283	0.777	

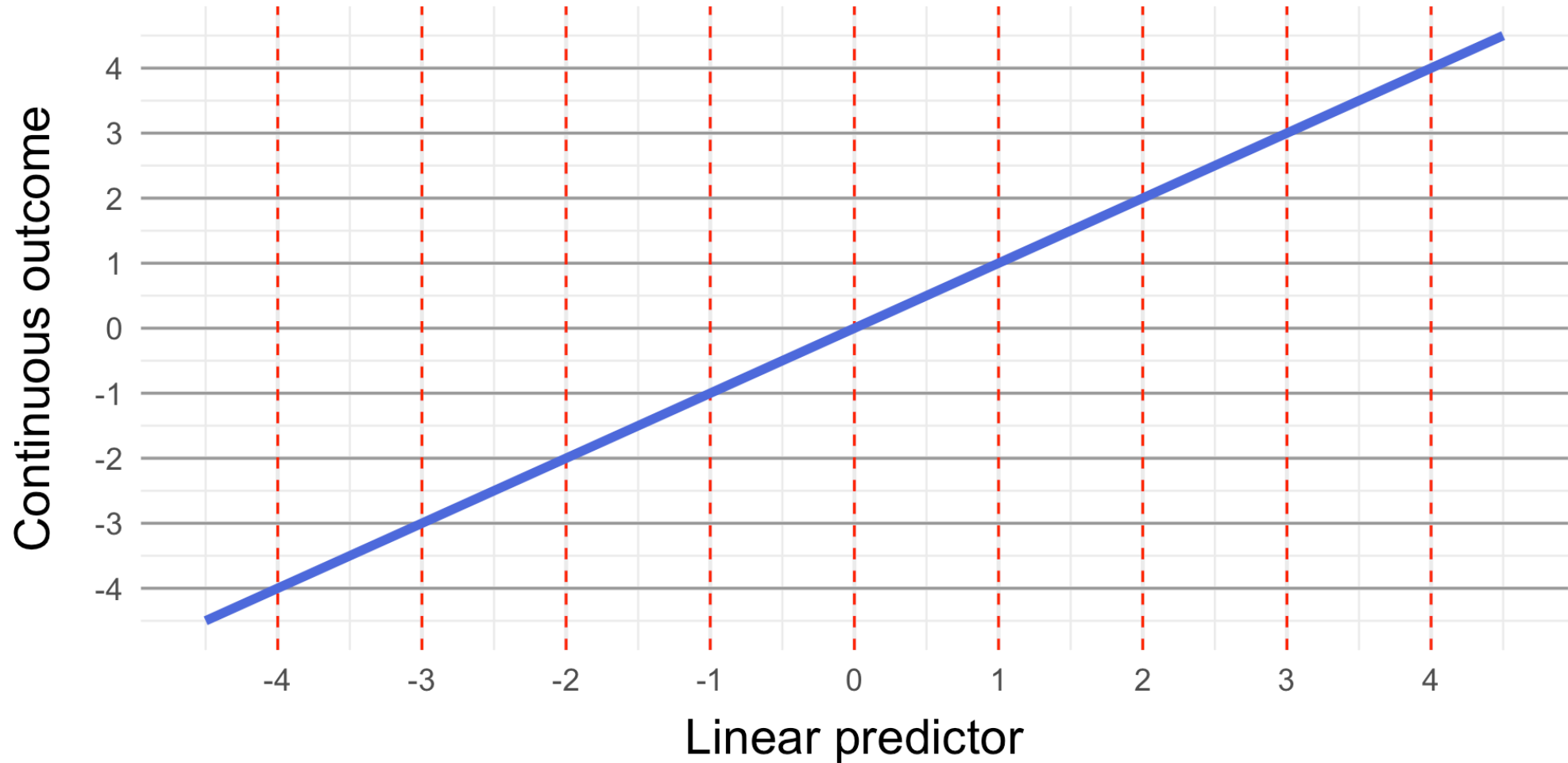
---



# Why interactions

`link="identity"`

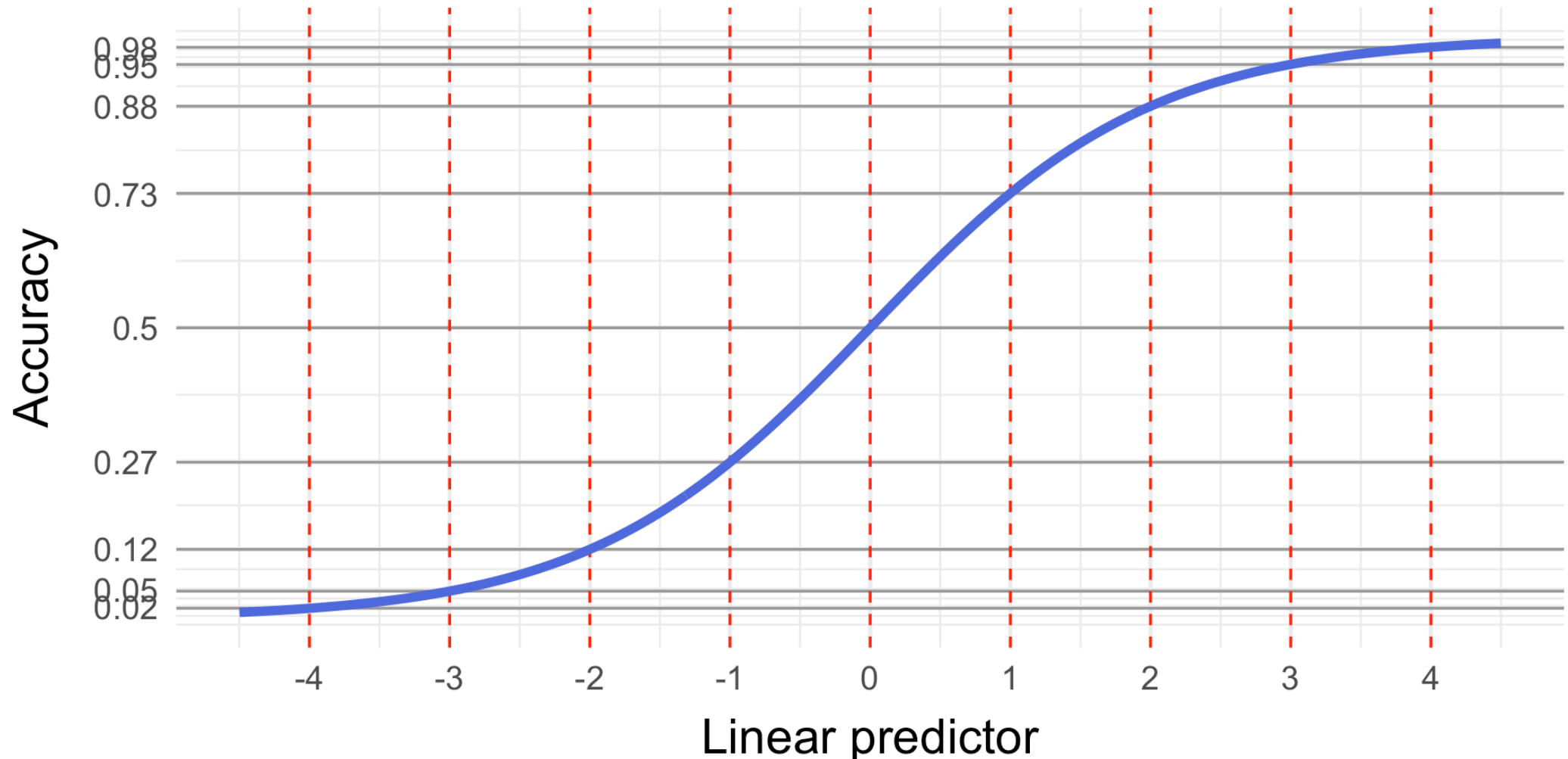
Equal intervals on X correspond to equal intervals on Y



In our example the linear predictor is  $\beta_0 + \beta_1 \cdot \text{age} + \beta_2 \cdot \text{group}$

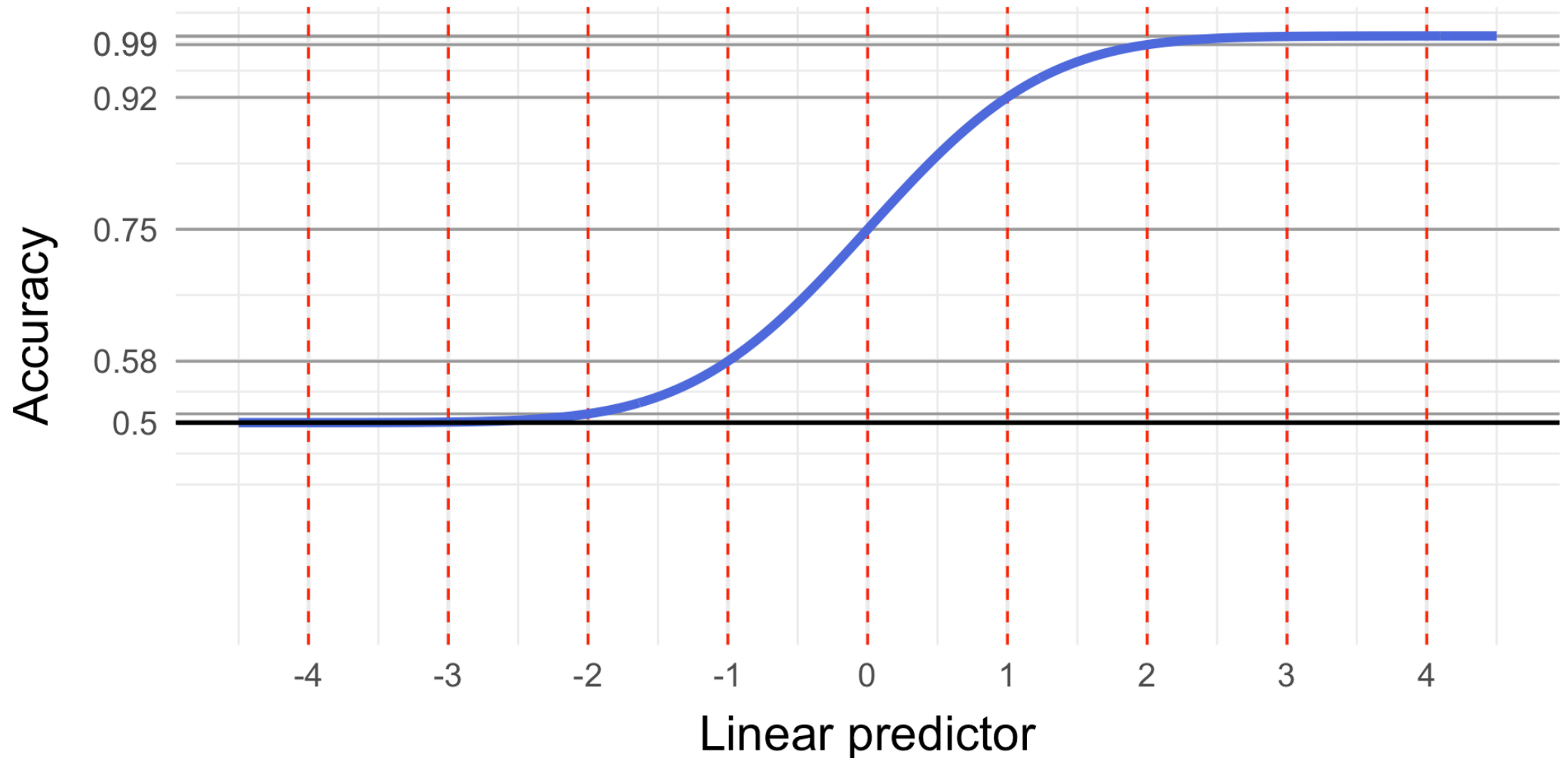
# link="logit"

Equal intervals on X correspond to equal ratios (NOT equal intervals) on Y



# `link=mafc.probit(2)`

Equal intervals on X do NOT correspond to equal intervals on Y



# Conclusions

Building a model means approximating the data-generating process  
(never observed directly in real data)

Key choices:



Tip

**Appropriate distribution (family):**

predicted values remain within the outcome's valid range



Tip

**Appropriate link function:**

the wrong link can create spurious interactions

# Our **systematic review** of psychological research

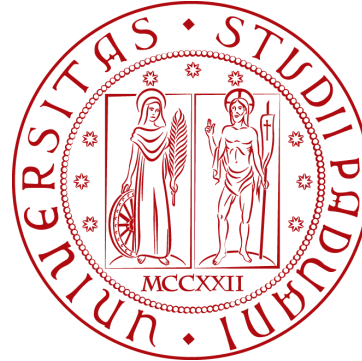
How often

- inappropriate link functions are used when testing interactions?
- do they lead to significant results?

# Materials & Contact

Data simulation, code and presentation are available on GitHub:  
[sitalaura/link-functions](#)

Questions and feedbacks: [laura.sita@studenti.unipd.it](mailto:laura.sita@studenti.unipd.it)



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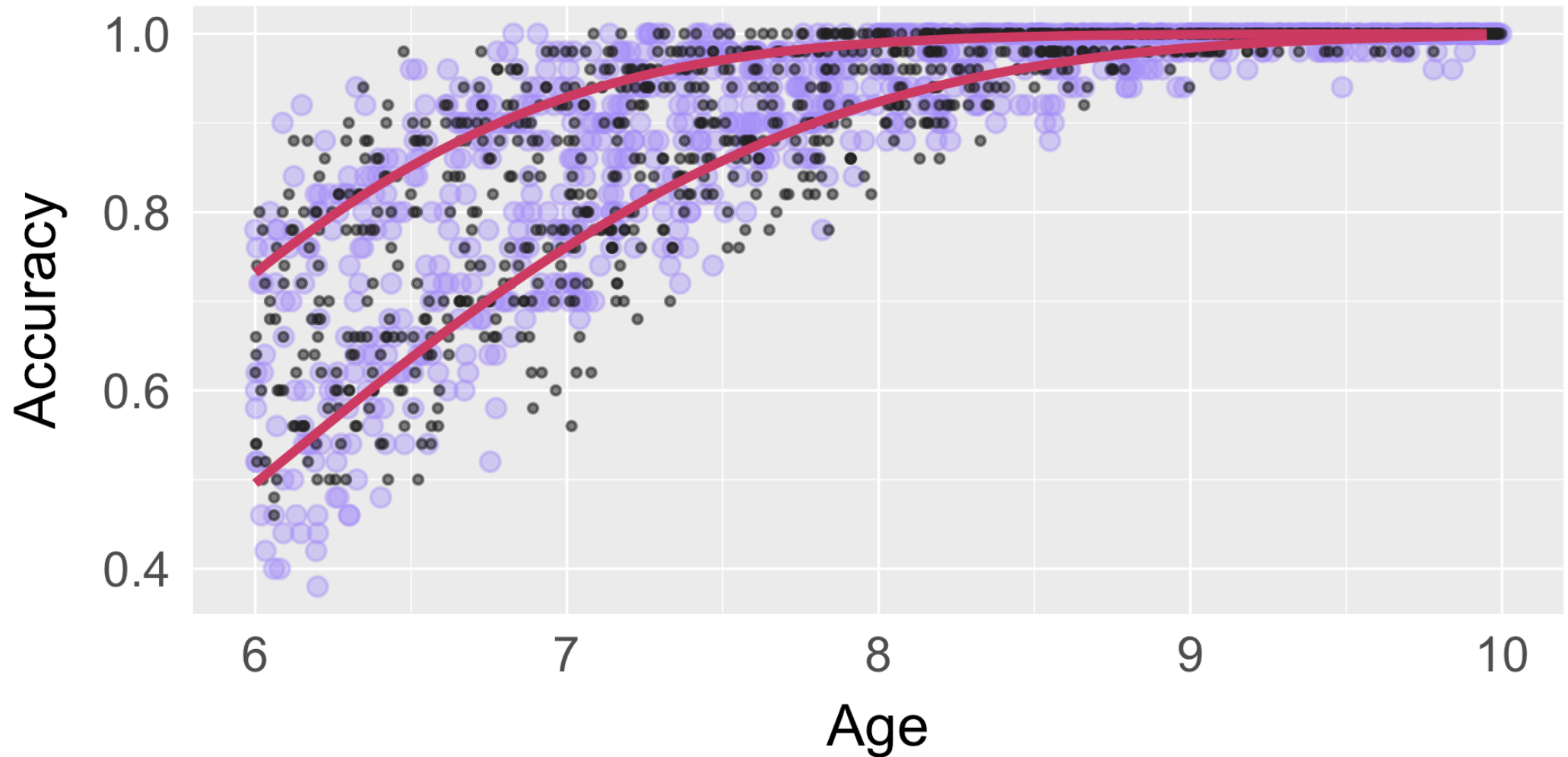


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# Supplementary materials

# Predictive check with `link="probit"`



# family=binomial(link="probit")

A **negative** interaction emerges

```
1 fit = glm(accuracy ~ age*group, data=d, family=binomial(link="probit")
2 summary(fit)
```

Call:

```
glm(formula = accuracy ~ age * group, family = binomial(link =
"probit"),
     data = d, weights = rep(k, nrow(d)))
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-4.48333	0.17709	-25.316	< 2e-16	***
age	0.85008	0.02590	32.824	< 2e-16	***
group1	0.14918	0.19965	0.747	0.455	
age:group1	-0.12958	0.02886	-4.489	7.14e-06	***

----