

CONFORMITY

1 What is conformity?

1.1 With two types

The general framework is that of an infinite population, represented as a continuum $[0; 1]$. There are two types θ_1 and θ_2 , distributed in proportions $q_1 = q \in [0; 1]$ and $q_2 = 1 - q$ respectively. We give two general examples of what mechanisms we have in mind we speaking about conformity.

Conformity can arise in several contexts. One is *transmission processes*, for which type is inherited. Assuming new individuals appear in the population, they are assigned type θ_1 with probability $p_1 = p \in [0; 1]$, or type θ_2 with probability $p_2 = 1 - p$. The probability p may depend on several factors, but the one in which we are interested here is the frequency of types in the population, $p : q \mapsto p(q)$. In this case, conformity bias can be understood as a disproportionate likelihood to inherit the majority type in the population: formally, it can be roughly understood as saying that $p(q) > q$ if $q > \frac{1}{2}$.

Another is *learning processes*. Imagine now that type corresponds to a behavioral trait which can be modified by the individual. At a given time, an individual of type θ_1 may choose to remain θ_1 or to become a type θ_2 (idem for type θ_2). The former happens with probability $p_1 = p \in [0; 1]$ while the latter happens with probability $p_2 = 1 - p$. Once again, we are interested in the case where p is a function of frequency, i.e. $p : q \mapsto p(q)$.

In these contexts, the function p satisfies the equality $p(1 - q) = 1 - p(q)$ for all $q \in [0; 1]$. We will furthermore suppose the following.

Assumption 1: p is a continuous, increasing function of q .

We then define conformity as is done in a large part of the literature.

Definition 1: We say that a transmission process has a *conformity bias* (also called *positive frequency-dependent bias*) if

$$\forall q \geq \frac{1}{2}, p(q) \geq q.$$

Conversely, we say it has an *anti-conformity bias* if this inequality is reversed.

From this definition and the assumption that p is continuous, simple properties follow.

Consequence 1: A function p which satisfies conformity bias verifies $p(0) = 0$, $p(1) = 1$, $p(\frac{1}{2}) = \frac{1}{2}$, and $\forall q \leq \frac{1}{2}, p(q) \leq q$.

Proof. First note that the definition of conformity bias implies $p(1) = 1$. Then we use that $\forall q \in [0; 1]$, $p(1 - q) = 1 - p(q)$, from which we get $p(0) = 0$ (taking $q = 1$), and $\forall q \leq \frac{1}{2}$, $p(q) = 1 - \underbrace{p(1 - q)}_{\geq 1 - q \text{ since } 1 - q \geq \frac{1}{2}} \leq 1 - (1 - q) = q$. By continuity of p , it must therefore be the case that $p(\frac{1}{2}) = \frac{1}{2}$. \square

One specific case of conformity bias is therefore when the function p is *s-shaped*. An inverted *s* instead corresponds to anti-conformity. Finally, the function defined by $p(q) = q$ displays both conformity as well as anti-conformity bias: we will refer to this baseline function as *unbiased*. These three cases are depicted in figure 1.

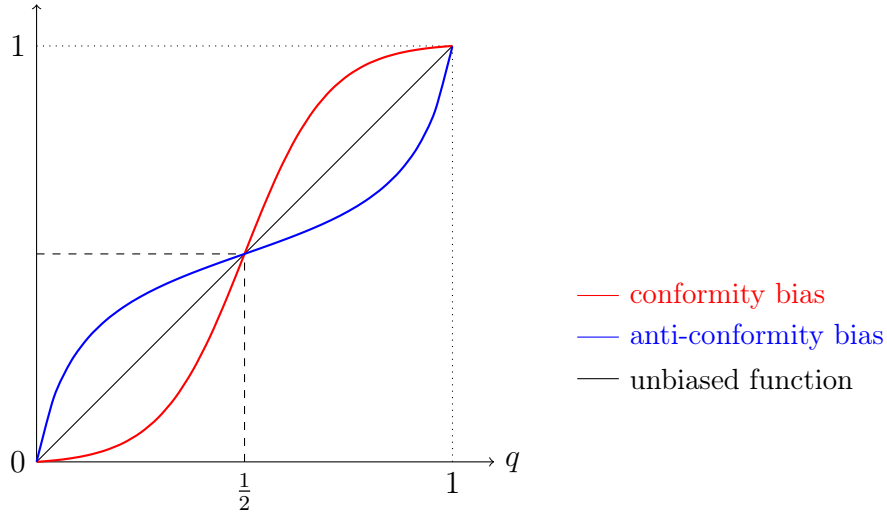


Figure 1 – Probability of adopting a trait given type frequency: conformity, anti-conformity, and unbiased function.

More about the unbiased case. In the transmission process context, it can for example correspond to the case in which each new individual copies his parents or his mother; or to the case each copies a random individual in the population.

We can also note that the step function $p : q \mapsto \begin{cases} 0 & \text{if } q < \frac{1}{2} \\ \frac{1}{2} & \text{if } q = \frac{1}{2} \\ 1 & \text{if } q > \frac{1}{2} \end{cases}$ can be indefinitely approached using continuous, conformity-biased functions, and is thereby a limit case of conformity bias.¹

1.2 With n types

There are now n types $\theta_1, \dots, \theta_n$ distributed in the population with fractions q_1, \dots, q_n such that $\sum_{i=1}^n q_i = 1$.

Suppose that the probability of adopting a trait is again a function of the frequency of this trait; furthermore, we assume it is the same for everyone.² p is the same for all types, i.e. for all i , $p_i = p(q_i)$.

Definition 2: We say that the population has a conformity bias if the probability p_i of adopting trait θ_i is greater than q_i when θ_i is overrepresented in the population compared to the uniform distribution, i.e. $p(q) \geq q$ when $q \geq \frac{1}{n}$.

¹For example, consider the sequence $(p_n)_{n \in \mathbb{N}}$ defined by $p_n(q) = \frac{\tanh[n(q - \frac{1}{2})] - \tanh[-\frac{n}{2}]}{\tanh[\frac{n}{2}] - \tanh[-\frac{n}{2}]}$.

²Actually, as in the two-types case, we only need to assume p is the same for $n - 1$ types, and it follows that it is also the same for the n -th type by the equality $p_n(q_n) = 1 - \sum_{i=1}^{n-1} p_i(q_i)$.

\rightarrow FALSE

Consequence 2: A function p which satisfies conformity bias verifies the following:

- (a) $p(0) = 0$, $p(1) = 1$, and $p(\frac{1}{n}) = \frac{1}{n}$,
- (b) $\forall q \leq \frac{1}{n}$, $p(q) \leq q$,
- (c) p is convex on $[0; \frac{1}{n}]$ and concave on $[\frac{1}{n}; 1]$.