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Inheritance Models of Evolutionary Theory

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ABSTRACT

In this paper, we study transmission of traits through generations in multifactorial inheritance models with sex- and time-dependent heritability. We further analyze the implications of these models under heavy-tailedness of traits' distributions. Among other results, we show that in the case of a trait (for instance, a medical or behavioral disorder or a phenotype with significant heritability affecting human capital in an economy) with not very thick-tailed initial density, the trait distribution becomes increasingly more peaked, that is, increasingly more concentrated and unequally spread, with time. But these patterns are reversed for traits with sufficiently heavy-tailed initial distributions (e.g., a medical or behavioral disorder for which there is no strongly expressed risk group or a relatively equally distributed ability with significant genetic influence). Such traits' distributions become less peaked over time and increasingly more spread in the population.

In addition, we study the intergenerational transmission of the sex ratio in models of threshold (e.g., polygenic or temperature-dependent) sex determination with long-tailed sex-determining traits. Among other results, we show that if the distribution of the sex determining trait is not very thick-tailed, then several properties of these models are the same as in the case of log-concave densities analyzed by Karlin (1984, 1992). In particular, the excess of males (females) among parents leads to the same pattern for the population of the offspring. Thus, the excess of one sex over the other one accumulates with time and the sex ratio in the total alive population cannot stabilize at the balanced sex ratio value of $1/2$. We further show that the above properties are reversed for sufficiently heavy-tailed distributions of sex determining traits. In such settings, the sex ratio of the offspring oscillates around the balanced sex ratio value and an excess of males (females) in the initial period leads to an excess of females (males) offspring next period. Therefore, the sex ratio in the total living population can, in fact, stabilize at $1/2$. Interestingly, these results are related, in particular, to the analysis of correlation between human sex ratios and socioeconomic status of parents as well as to the study of the variation of the sex ratio due to parental hormonal levels.

The proof of the results in the paper is based on the general results on majorization properties of heavy-tailed distributions obtained recently in Ibragimov (2004) and several their extensions derived in this work.

Keywords and phrases: Multifactorial inheritance models; Phenotypic traits; Heritability; Sex ratio; Human capital.

JEL Classification: C10, C32, I10, Q50, Q57

1 Introduction and discussion of the results

1.1 Motivation and review of the literature

In recent years, there has been a growing interest in inheritance models and related problems in economics. This strand of research is motivated, in part, by significant influence of an individual's genetic endowment on achievable economic outcomes and strong dependence of the distribution of human capital on the distribution of abilities and rates of illness in population and on the transmission of genes through generations (see, among others, Becker, 1993, Ch. 4, 5, Currie, 2000, Frank and McGuire, 2000, Haveman and Wolfe, 2000, and Zak, 2002, and references therein). It was demonstrated in a number of studies that heritability is significant and often exceeds environmental effects for many human psychological, psychiatric and neurological phenotypes affecting human capital in an economy (e.g., Ehrman and Parsons, 1977, the contributions in Fuller and Simmel, 1983, Plomin, deFries and McClearn, 1990, Plomin, Owen and McGuffin, 1994, Rowe, 1994, and Gilger, 2000). Significant heritability has been found for such traits as intelligence (IQ), scholastic achievement, risk-taking behavior, learning and learning disabilities, socioeconomic status, memory, nonverbal thinking skills, aggressive behavior, delinquent or criminal behavior, for many behavioral and mental disorders including, e.g., autism, schizophrenia, depression, Alzheimer's disease and reading disability as well as for smoking behavior and drug and alcohol abuse and dependence. Additionally, significant genetic influence was found for a number of medical disorders, for example, for hypertension, ischemic heart disease, tuberculosis, arterial hypertension, bronchial asthma, rheumatoid arthritis, peptic ulcer and epilepsy and predisposition to at least several types of cancer (see Ehrman and Parsons, 1977, Plomin et. al., 1994, Lichtenstein, Holm, Verkasalo, et. al., 2000, and Risch, 2001). Motivated by the analysis of economic effects of behavioral traits and their evolution and intergenerational transmission, many authors have focused on the study of models in economics with altruism, inequity aversion and standards of fairness as well as of evolution of risk attitudes underlying strategic behavior (see Becker, 1974, 1976, Kahneman, Knetsch and Thaler, 1986, Bernheim and Ray, 1987, Simon, 1990, 1993, Samuelson (1993), Bergstrom, 1995, 2002, Robson, 1995, 2002, and references therein). Moreover, a series of studies in economics analyzed closely related models of intergenerational mobility in various contexts (see, among others, Goldberger, 1989, Peters, 1992, Zimmerman, 1992, Becker, 1993, Ch. 10, and Mulligan, 1999).

Formally, Galtonian-type multifactorial (polygenic) inheritance models (e.g., Karlin, 1984, 1992, and Karlin and Lessard, 1986) with sex- and time-dependent heritability have the form

$$X_{t+1}(\lambda, \kappa) = \lambda_t X_t^p + \kappa_t X_t^m + (1 - \lambda_t - \kappa_t)\epsilon_t, \tag{1}$$

$t = 0, 1, ...,$ where X_{t+1} is the trait value of the offspring; and X_t^p and X_t^m, $t = 0, 1, 2, ...,$ are, respectively, paternal and maternal contributions, ϵ_t, $t = 0, 1, 2, ...,$ is an independent residual (environmental) contribution of mean 0 and $\lambda = \{\lambda_t\}_{t=0}^{\infty}$ and $\kappa = \{\kappa_t\}_{t=0}^{\infty}$ are sequences of nonnegative numbers such that $0 \leq \lambda_t + \kappa_t \leq 1$, $t = 0, 1, ...$ (several patterns of the models considered in this paper are more general than those in Karlin, 1984, 1992, and Karlin and Lessard, 1986, and our notations differ from those in the above works). The parameters λ_t and κ_t are sex-dependent heritability coefficients; we assume that heritability can change with time t. Note that in the standard case when X_t^p and X_t^m do not depend on the future values of λ_s and κ_s, $s = t + 1, t + 2, ...,$ the

trait values X_{t+1} depend on the "histories" $\lambda^{(t)} = (\lambda_0, \lambda_1, ..., \lambda_t)$ and $\kappa^{(t)} = (\kappa_0, \kappa_1, ..., \kappa_t)$ of the coefficients of λ and κ up to time t. In the case of symmetric and time-independent heritability, $\lambda_t = \kappa_t = h^2/2$, $t = 0, 1, 2, ...$, where h^2 is the heritability coefficient of Galton (1886) given by the coefficient at the regression of an offspring on the midparent value at an equilibrium (see Roughgarden, 1979, Ch. 9, Bulmer, 1980, Ch. 6, and Becker, 1993, Ch. 10). Models (1) with $\lambda_t \neq \kappa_t$ represent asymmetric transmission from parents. The case $\lambda_t + \kappa_t = 1$ describes the model of purely parental transmission

$$X_{t+1}(\lambda) = \lambda_t X_t^p + (1 - \lambda_t) X_t^m \tag{2}$$

In what follows, we denote $\overline{\lambda} = (1/2, 1/2, ...)$. Process (2) with $\lambda_t = 1/2$, $t = 0, 1, 2, ...$ (that is, with $\lambda = \overline{\lambda}$), corresponds to the Galtonian blending model

$$X_{t+1}(\overline{\lambda}) = (X_t^p + X_t^m)/2. \tag{3}$$

Let, for $t = 0, 1, 2, ...$, X_t' and X_t'' denote independent copies of the random variable (r.v.) $X_t = X_t(\lambda)$ and let the trait X_0 have a sex-independent distribution in the population at time $t = 0$. In the case when

$$(X_t^p, X_t^m) = (X_t', X_t'') \quad a.s., \tag{4}$$

$t = 0, 1, 2, ...$, time series (2) model transmission through generations of the trait X_0 with time-dependent and asymmetric heritability.

Models (1) with[2] $\lambda_t = 0$, $t = 0, 1, 2, ...$ (or with $X_t^p = X_t^m = X_t$ a.s., $t = 0, 1, 2, ...$) have exactly the same form as the models of intergenerational mobility $X_{t+1} = h^2 X_t + \epsilon_t$, $t = 0, 1, 2, ...$, where X_t is the measure of economic status such as earnings or income and ϵ_t is an independent error term[3].

A problem of interest in inheritance models (1) and, in particular, in models (2), (4) is how the distributional characteristics of the trait X transmit through generations. In particular, the question as to whether the trait X becomes increasingly more peaked (concentrated) about some value $\mu \in \mathbf{R}$ over time is important - for instance, whether there appears to be a risk group for a trait representing a behavioral or medical disorder or whether genetic diversity or inequality in the distribution of a phenotype affecting human capital in an economy increases with time.

Bulmer and Bull (1982), Karlin (1984) and Karlin and Lessard (1986) used models (3) with the parental contributions X_t^p and X_t^m given by independent r.v.'s with the cdf's

$$P(X_t^p \leq x) = P(X_t \leq x | X_t > K), \quad P(X_t^m \leq x) = P(X_t \leq x | X_t \leq K), \tag{5}$$

$K \in \mathbf{R}$, $t = 0, 1, ...$, to model polygenic (multifactorial) and environmental sex determination. Under polygenic sex determination, a large number of factors (loci) contribute to sex expression; such mechanism of sex determination is exhibited by, e.g., several fish species (see Bacci, 1965, and Karlin and Lessard, 1986). Environmental mechanisms of sex determination are defined as those instances where an offspring sex is determined

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[2]In mathematical evolutionary theory, such models represent intergenerational transmission of a phenotype maternally affecting itself, see Roff (1997, pp. 250-254).

[3]Note that the case of shocks ϵ_t with $E\epsilon_t = \mu \in \mathbf{R}$, contains the mobility models with the usually included intercept term μ that represents the growth in income or earnings across generations.

by environmental conditions after conception (e.g., Bulmer and Bull, 1982, Karlin, 1984, Karlin and Lessard, 1986, and Janzen and Paukstis, 1991). For example, in several reptile species sex determination mechanism is temperature dependent: the sex of an embryo is determined by incubation temperature (see Bull, 1981, Cherfas and Gribbin, 1985, Ch. 5, Bull and Charnov, 1989, and Janzen and Paukstis, 1991). In many turtles embryos hatch as males in cool and as females in warm conditions, with a sharp transition from all-male to all-female broods. Alligators, crocodiles and some lizards exhibit the opposite pattern in sex determination: males develop at warm and females at cool temperatures. Some theories have suggested that environmental sex-determination could have been the cause of dinosaur extinction. If sex determination mechanism in dinosaurs was temperature-dependent, like in modern reptiles, then they might have gone extinct because one sex was no longer produced due a major temperature change on Earth (Cherfas and Gribbin, 1985, Ch. 5). One should note here that, since the length of the temperature interval at which both sexes are produced might be as small as 8 degrees C, as in the case of turtles, a relatively small change in environmental conditions might be sufficient for extinction of some species. This is particularly important for conservation of threatened species living today (see Cherfas and Gribbin, 1985).

The cases considered by Bulmer and Bull (1982), Karlin (1984) and Karlin and Lessard (1986) model a situation where a sex response trait is determined by a continuous phenotype or environmental variable X (such as size, fitness, exposure to sunlight, food resources, temperature, humidity, etc.). An individual with $X = \tilde{x}$ becomes a male if the value of $\tilde{x}$ is greater than the threshold level K, and a female otherwise.

Many studies have found evidence that mammalian and, in particular, human, sex ratios at birth are partially controlled by parental hormone levels at the time of conception, high levels of androgens and oestrogens and low levels of gonadotrophin and progesterone being associated with male offspring (see James, 1995, 1997, Grant, 1996, and the reviews in James, 1994, 1996). These studies have suggested that hormone levels are responsible for the association between the sex ratios of the offspring in humans and parental dominance, occupation of parents, psychological stress, several illnesses, including Non-Hodgkin's lymphoma, prostatic cancer and multiple sclerosis, and, partly, parental socioeconomic status found in numerous works. In addition, dependence of the sex ratio of the offspring on the hormone levels of parents was suggested to account for the rise in the human sex ratios during and just after the war in belligerent countries, in part because of the stress associated with a shortage of partners (see James, 1995, 1996, and Edlund, 1999). With respect to the trait of social ranking, we also note that a large number of studies have found positive correlation between socioeconomic status and maleness of offspring (see Trivers and Willard, 1973, James, 1994, and Edlund, 1999), however, prenatal sex determination and sex selective abortion and postnatal discrimination appear to have a larger order of magnitude in affecting the observed variations in the sex ratio in humans than the parental hormone levels (see Edlund, 1999, and references therein). One should further indicate here that human sex ratios, parental sex preferences and gender control were emphasized by several authors as being of significant importance in economic models (see Samuelson, 1985, Pollak, 1990, Davies and Zhang, 1997, and Edlund, 1999). For example, as Edlund (1999) has shown, if parents prefer children who reproduce and sons to daughters, prenatal sex determination and offspring sex choice can consistently result in the birth of daughters into low-status families and sons into high-status families, thus resulting in the propagation of a female underclass and, possibly, a caste structure.

Furthermore, according to Edlund (1999), under these assumptions, the pattern of complete segregation with sons born to the upper class and daughters to the underclass is possible to appear.

Models (2) with the parental contributions given by (5) can be used as first approximations in the analysis of the part of the variation of sex ratio in humans controlled by parental hormonal levels as well as in the study of the properties of extreme cases of dependence of sex determination on such traits as, e.g., socioeconomic status or parental income, with complete segregation in the choice of sex of the offspring (in the above cases, the threshold values K represent cut-off points of the parental hormonal levels, wealth or income).

Similar to general time series (1), a crucial issue in models of threshold sex determination (3), (5) is how the sex ratio r_t given by the tail probability $r_t = P(X_t(\overline{\lambda}) > K)$ changes with time. Karlin (1984, 1992) studied the following questions for the above models: under what conditions $r_0 < 1/2$ (the excess of females over males among parents at time $t = 0$) implies $r_1 < 1/2$ (the excess of females over males among the offspring at time $t = 1$) or $r_1 > 1/2$ (the excess of males over females among the offspring). Based on the results of Proschan (1965) on peakedness of linear combinations of log-concavely distributed r.v.'s (that is, r.v.'s with log-concave densities) given by Proposition 2 in Appendix A1 in this paper, Karlin (1984) obtained the following result.

Proposition 1 *(Karlin, 1984, Proposition 8.1). Consider model (3) with the cdf's of the parental contributions given by (5). Let X_0 be a symmetric r.v. with a density $f(x)$ such that the function $\log f(x)$ is concave in $x \in \mathbf{R}$. If $r_0 < 1/2$ (equivalently, $K > 0$), then $r_1 < 1/2$. If $r_0 > 1/2$ (equivalently, $K < 0$), then $r_1 > 1/2$.*

Proposition 1 implies that if the initial distribution of the phenotype trait X_0 that determines the sex of the offspring has a log-concave density and thus is extremely light-tailed (see Corollary 1 in An, 1998, and Section 2 in this paper), then the excess of males (females) among parents leads to the same pattern for the population of the offspring. In particular, one arrives at the conclusion that if the life of parents is greater than one period then the excess of one sex over the other one accumulates with time and thus the sex ratio in the total alive population cannot stabilize at the balanced sex-ratio value of $r = 1/2$.

In recent years, a number of studies in human genetics and psychology found departures from normality assumptions in many phenotypic data, including (moderate) thick-tailedness of distribution of many human traits, in particular, of different achievement and psychometric measures (see Micceri, 1989, and the discussion in Allison et. al., 1999, and Allison et. al., 2000) as well as sex differences in the distribution of extreme outliers for several traits related to, e.g., intellectual abilities (see Hedges and Nowell, 1995). These findings prompted many authors to focus on developing statistical procedures for biometric data robust to non-Gaussianity and heavy-tailedness assumptions, including robust techniques for detection of genes influencing complex quantitative traits (see Allison et. al., 1999, and Allison et. al., 2000, and references therein).

In the studies based on models incorporating fat-tailed r.v.'s, it is usually assumed that the distributions of the r.v.'s belong to the class of stable laws. Although there are several alternatives to the stable modelling of heavy-tailed data (e.g., the use of Pareto distributions), focusing on stable distribution models is justified in many cases and has a number of advantages, as discussed in, e.g., Adler, Feldman and Gallagher, 1998. In particular, the statistical methods for stable laws work as well for the data in the domain of attraction of

stable distributions. Furthermore, stable laws and the long-tailed distributions in the domain of their attraction behave similarly at the tails of the distributions which is usually the region of interest for heavy-tailed techniques. Finally, there are few reliable approaches available in the case of heavy-tailed r.v.'s not in a stable domain of attraction (Adler, Feldman and Gallagher, 1998).

We emphasize here that distributions with log-concave densities *cannot* be used to model heavy-tailed phenomena since any such density has at most an exponential tail and thus *all* its moments are finite (see An, 1998, and Section 2 in the present paper).

1.2 Discussion of the results

In this paper, we study transmission of the distributional properties of traits through generations in polygenic inheritance models and analyze implications of these models under heavy-tailedness of traits. We obtain results concerning the transmission of peakedness (concentration) properties of fat-tailed traits in general inheritance model (2) with sex- and time-dependent heritability. For instance, from our results it follows that the following conclusions hold (see Theorem 1 and Remark 2 following Theorem 2).

Consider model (2) with the parental contributions given by (4). Let the distribution of $X_0 - \mu$ be a convolution of symmetric log-concave distributions and symmetric stable distributions[4] with characteristic exponents in the interval $[1, 2)$. Then for all $t = 0, 1, 2, ...$, the r.v. $X_{t+1}(\lambda)$ is more peaked about μ than is $X_t(\lambda)$, but is less peaked than is $X_{t+1}(\overline{\lambda})$. That is, $P(|X_{t+1}(\overline{\lambda}) - \mu| > x) \leq P(|X_{t+1}(\lambda) - \mu| > x) \leq P(|X_t(\lambda) - \mu| > x)$ for all $x \geq 0$ and all $t = 0, 1, 2, ...$ Suppose now that the distribution of $X_0 - \mu$ is a convolution of symmetric stable distributions with characteristic exponents in the interval $(0, 1]$. Then for all $t = 0, 1, 2, ...$, the r.v. $X_{t+1}(\lambda)$ is less peaked about μ than is $X_t(\lambda)$, but is more peaked than is $X_{t+1}(\overline{\lambda})$. That is, $P(|X_t(\lambda) - \mu| > x) \leq P(|X_{t+1}(\lambda) - \mu| > x) \leq P(|X_{t+1}(\overline{\lambda}) - \mu| > x)$ for all $x \geq 0$ and all $t = 0, 1, 2, ...$

According to the above results, if the initial distribution of the trait X (say, a behavioral or medical disorder or an ability for which heritability is significant) in the population is not extremely heavy tailed, then the trait distribution becomes increasingly more peaked over time. Roughly speaking, concentration of the distribution of the disorder about some risk group in the population and inequality in the distribution of the ability becomes increasingly more pronounced. Furthermore, at any given time, peakedness of the trait is maximal (the spread of the trait in the population is minimal) in the case of symmetric heritability. In the case of a trait with an extremely heavy-tailed initial distribution (say, a medical or behavioral disorder for which there is no strongly expressed risk group or a relatively equally distributed ability with significant genetic influence), the situation is reversed: the trait distribution becomes less peaked with time and increasingly more spread in the population. Moreover, peakedness of the trait is minimal (the spread of the trait in the population is maximal) in the case of symmetric heritability.

In addition, we show *inter alia* that Karlin's (1984) results on the transmission of sex ratio through generations under threshold (e.g., polygenic or temperature-dependent) sex determination (3), (5) given by Proposition

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[4]So that X_0 is symmetric about μ.

1 remain valid for not very heavy-tailed distributions, as modelled by convolutions of stable distributions with (different) characteristic exponents in the interval $(1, 2)$ and log-concave distributions (Theorem 3).

We also show that the results by Karlin (1984) concerning the evolution of the sex ratio r in models of threshold sex determination (3), (5) are reversed under sufficiently fat-tailed distributions of the initial trait X_0. More specifically, we show that the following result holds (see Theorem 4):

Let in model (3) with the parental contributions given by (5), X_0 be a r.v. with a distribution which is a convolution of symmetric stable distributions with indices of stability in the interval $(0, 1)$. If $r_0 < 1/2$, then $r_1 > 1/2$. If $r_0 > 1/2$, then $r_1 < 1/2$.

It is interesting to point out that (see Remark 1 following Theorem 4) if the distribution of the initial trait X_0 is Cauchy, then the value of the sex ratio in the population of the offspring (period $t = 1$) stabilizes at the balanced sex ratio level $r_1 = 1/2$ *regardless* of the value of the sex ratio r_0 among parents (period $t = 0$).

According to the above results, in contrast to threshold sex determination model (3), (5) with log-concavely distributed phenotypic value X_0, in the case of very heavy-tailed initial distributions of the trait X, the sex ratio of the offspring oscillates[5] around the balanced sex ratio value $r = 1/2$. That is, an excess of males (females) in the initial period leads to an excess of female (male) offsprings next period. This means that the sex ratio in the total living population can, in fact, stabilize at the balanced sex ratio value $r = 1/2$ for some models (3), (5) if parents live longer than one period. For example, we show that if the initial trait X_0 has a sufficiently fat-tailed distribution, namely, a symmetric stable distribution with the index of stability less than $1/2$, then the value of the sex-ratio in the total population at period $t = 1$ stabilizes at the balanced sex-ratio value $1/2$ for some values of the sex-ratio among parents r_0 (conclusion (18) in Theorem 5). We also obtain results on the magnitude of intergenerational changes in the distances from the sex-ratios r_t to the balanced sex-ratio value in the case of arbitrary symmetric stable distributions of the initial trait X_0. Our results demonstrate, in particular, that for all the above distributions of X_0, the sex-ratio among offspring (and, therefore, the sex-ratio in the total alive population) at $t = 1$ becomes closer to the value $r = 1/2$, if the sex-ratio among parents ($t = 0$) is sufficiently far from it (relation (15) in Theorem 5). The same holds if the distribution of X_0 is symmetric and stable with the index of stability greater than $1/2$ and the sex ratio in period 0 is close to $1/2$ (relation (16)). However, if the distribution of the initial trait is symmetric and stable with the characteristic exponent less than $1/2$, and the sex-ratio value among parents r_0 is sufficiently close to $r = 1/2$, then the oscillations in the sex-ratio r_t about the balanced sex-ratio value are increasing in the magnitude (conclusion (17) of Theorem 5).

Similarly, we obtain analogues of our results on multifactorial inheritance models in a more general setting with traits' distributions given by convolutions of a wide class of transforms of stable r.v.'s.

The proof of the main results is based on the results on majorization properties of linear combinations of heavy-tailed r.v.'s recently obtained in Ibragimov (2004) and several their generalizations derived in this paper. To our knowledge, the results in Ibragimov (2004) are the first ones available in the literature that show that general majorization properties of convex combinations of symmetric log-concavely distributed r.v.'s derived by

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[5]Interestingly, similar patterns of oscillations are also found for firm sizes in firm growth models with extremely heavy-tailed signals, see Ibragimov (2004).

Proschan (1965) are reversed for certain classes of distributions, see the discussion in Ibragimov (2004). These results provide the key to reversals of implications of several inheritance models built upon the log-concavity assumption, similar to a number of economic models in Ibragimov (2004).

In this work, we focus on the analysis of multifactorial inheritance models (2) with purely parental transmission of phenotypes through generations. However, the approach developed in the paper can also be applied in the study of models (1) involving both parental and environmental contributions as well as of models of intergenerational mobility. Generalizations of the results in the case of those models are left for further research.

The paper is organized as follows: Section 2 contains notations and definitions of classes of distributions used throughout the paper and reviews their basic properties. In Section 3, we present the main results on the properties of polygenic inheritance models under heavy-tailedness of traits' distributions. Appendix A1 reviews peakedness properties of log-concavely distributed r.v.'s derived by Proschan (1965) and their analogues for thick-tailed distributions obtained in Ibragimov (2004). Finally, Appendix A2 contains proofs of the main results obtained in the paper.

2   Notations and classes of distributions

In this section, we introduce certain classes of distributions we will be dealing with throughout the paper. The notations for these classes are similar to those in Ibragimov (2004).

We say that a r.v. X with density $f : \mathbf{R} \to \mathbf{R}$ and the convex distribution support $\Omega = \{x \in \mathbf{R} : f(x) > 0\}$ is log-concavely distributed if $log\, f(x)$ is concave in $x \in \Omega$, that is, if for all $x_1, x_2 \in \Omega$, and any $\lambda \in [0, 1]$,

$$f(\lambda x_1 + (1 - \lambda) x_2) \geq (f(x_1))^{\lambda} (f(x_2))^{1-\lambda}. \tag{6}$$

(see An, 1998). A distribution is said to be log-concave if its density f satisfies (6).

Examples of log-concave distributions include (see, for instance, Marshall and Olkin, 1979, p. 493) the normal distribution $\mathcal{N}(\mu, \sigma^2)$, the uniform density $\mathcal{U}(\theta_1, \theta_2)$, the exponential density, the logistic distribution, the Gamma distribution $\Gamma(\alpha, \beta)$ with the shape parameter $\alpha \geq 1$, the Beta distribution $\mathcal{B}(a, b)$ with $a \geq 1$ and $b \geq 1$; the Weibull distribution $\mathcal{W}(\gamma, \alpha)$ with the shape parameter $\alpha \geq 1$.

If a r.v. X is log-concavely distributed, then its density has at most an exponential tail, that is, $f(x) = o(exp(-\lambda x))$ for some $\lambda > 0$, as $x \to \infty$ and all the power moments $E|X|^{\gamma}, \gamma > 0$, of the r.v. exist (see Corollary 1 in An, 1998).

For $0 < \alpha \leq 2$, $\sigma > 0$, $\beta \in [-1, 1]$ and $\mu \in \mathbf{R}$, we denote by $S_{\alpha}(\sigma, \beta, \mu)$ the stable distribution with the characteristic exponent (index of stability) α, the scale parameter σ, the symmetry index (skewness parameter) β and the location parameter μ. That is, $S_{\alpha}(\sigma, \beta, \mu)$ is the distribution of a r.v. X with the characteristic function

$$E(e^{ixX}) = \begin{cases} exp\left\{i\mu x - \sigma^{\alpha} |x|^{\alpha} (1 - i\beta sign(x) tan(\pi\alpha/2))\right\}, & \alpha \neq 1, \\ exp\left\{i\mu x - \sigma |x| (1 + (2/\pi) i\beta sign(x) ln|x|)\right\}, & \alpha = 1, \end{cases} \tag{7}$$

$x \in \mathbf{R}$, where $i^2 = -1$ and $sign(x)$ is the sign of x defined by $sign(x) = 1$ if $x > 0$, $sign(0) = 0$ and $sign(x) = -1$ otherwise. For a detailed review of properties of stable distributions the reader is referred to, e.g., the monograph by Zolotarev (1986).

In what follows, we write $X \sim S_\alpha(\sigma, \beta, \mu)$, if the r.v. X has the stable distribution $S_\alpha(\sigma, \beta, \mu)$.

A closed form expression for the density $f(x)$ of the distribution $S_\alpha(\sigma, \beta, \mu)$ is available in the following cases (and only in those cases): $\alpha = 2$ (Gaussian distributions); $\alpha = 1$ and $\beta = 0$ (Cauchy distributions); $\alpha = 1/2$ and $\beta \pm 1$ (Lévy distributions). Degenerate distributions correspond to the limiting case $\alpha = 0$.

The index of stability α characterizes the heaviness (the rate of decay) of the tails of stable distributions. In particular, if $X \sim S_\alpha(\sigma, \beta, \mu)$, then there exists a constant $C > 0$ such that

$$\lim_{x \to +\infty} x^\alpha P(|X| > x) = C. \tag{8}$$

This implies that the p-th absolute moments $E|X|^p$ of a r.v. $X \sim S_\alpha(\sigma, \beta, \mu)$, $\alpha \in (0, 2)$ are finite if $p < \alpha$ and are infinite otherwise. The symmetry index β characterizes the skewness of the distribution. The stable distributions with $\beta = 0$ are symmetric about the location parameter μ. In the case $\alpha > 1$ the location parameter μ is the mean of the distribution $S_\alpha(\sigma, \beta, \mu)$. The scale parameter σ is a generalization of the concept of standard deviation; it coincides with the standard deviation in the special case of Gaussian distributions ($\alpha = 2$).

As in Ibragimov (2004), we denote by $\mathcal{LC}$ the class of symmetric log-concave distributions[6].

Further, we consider the class $\overline{\mathcal{CS}}$ of distributions which are convolutions of symmetric stable distributions $S_\alpha(\sigma, 0, 0)$ with characteristic exponents[7] $\alpha \in [1, 2]$ and $\sigma > 0$. That is, $\overline{\mathcal{CS}}$ consists of distributions of r.v.'s X such that, for some $k \geq 1$, $X = Y_1 + ... + Y_k$, where Y_i, $i = 1, ..., k$, are independent r.v.'s such that $Y_i \sim S_{\alpha_i}(\sigma_i, 0, 0)$, $\alpha_i \in (1, 2]$, $\sigma_i > 0$, $i = 1, ..., k$.

By $\overline{\mathcal{CSLC}}$, we denote the class of convolutions of distributions from the classes $\mathcal{LC}$ and $\overline{\mathcal{CS}}$. That is, $\overline{\mathcal{CSLC}}$ is the class of convolutions of symmetric distributions which are either log-concave or stable with characteristic exponents greater than one[8]. In other words, $\overline{\mathcal{CSLC}}$ consists of distributions of r.v.'s X such that $X = Y_1 + Y_2$, where Y_1 and Y_2 are independent r.v.'s with distributions belonging to $\mathcal{LC}$ or $\overline{\mathcal{CS}}$.

$\underline{\mathcal{CS}}$ stands for the class of distributions which are convolutions of symmetric stable distributions $S_\alpha(\sigma, 0, 0)$ with indices of stability[9] $\alpha \in (0, 1)$ and $\sigma > 0$. That is, $\underline{\mathcal{CS}}$ consists of distributions of r.v.'s X such that, for some $k \geq 1$, $X = Y_1 + ... + Y_k$, where Y_i, $i = 1, ..., k$, are independent r.v.'s such that $Y_i \sim S_{\alpha_i}(\sigma_i, 0, 0)$, $\alpha_i \in (0, 1)$, $\sigma_i > 0$, $i = 1, ..., k$.

Let $\mathbf{R}_+ = [0, \infty)$. Throughout the paper, $\overline{M}$ denotes the class of differentiable odd functions $f : \mathbf{R} \to \mathbf{R}$ such that f is concave and increasing on $\mathbf{R}_+$ and $\underline{M}$ denotes the class of odd functions $f : \mathbf{R} \to \mathbf{R}$ such that f is convex and increasing on $\mathbf{R}_+$.

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[6] $\mathcal{LC}$ stands for "log-concave".

[7] Here and below, $\mathcal{CS}$ stands for "convolutions of stable"; the overline indicates relation to stable distributions with indices of stability *greater* than the threshold value 1.

[8] $\mathcal{CSLC}$ stands for "convolutions of stable and log-concave".

[9] The underline indicates relation to stable distributions with indices of stability *less* than the threshold value 1.

By[10] $\overline{\mathcal{CTSLC}}$, we denote the class of convolutions of log-concave distributions and distributions of transforms $f(Y)$, $f \in \overline{M}$, of symmetric stable r.v.'s $Y \sim S_\alpha(\sigma, 0, 0)$ with characteristic exponents $\alpha \in (1, 2]$ and $\sigma > 0$. That is, $\overline{\mathcal{CTSLC}}$ consists of distributions of r.v.'s X such that, for some $k \geq 1$,

$$X = \gamma Y_0 + f_1(Y_1) + ... + f_k(Y_k), \tag{9}$$

where $\gamma \in \{0, 1\}$, $f_i \in \overline{M}$, $i = 1, ..., k$, and Y_i, $i = 0, 1, ..., k$, are independent r.v.'s such that $Y_0 \sim \mathcal{LC}$ and $Y_i \sim S_{\alpha_i}(\sigma_i, 0, 0)$, $\alpha_i \in (1, 2]$, $\sigma_i > 0$, $i = 1, ..., k$.

We note that (see Ibragimov, 2004) the class $\overline{\mathcal{CS}}$ of *convolutions* of symmetric stable distributions with *different* indices of stability $\alpha \in (1, 2]$ is wider than the class of *all* symmetric stable distributions $S_\alpha(\sigma, 0, 0)$ with $\alpha \in (1, 2]$ and $\sigma > 0$. Similarly, the class $\underline{\mathcal{CS}}$ is wider than the class of *all* symmetric stable distributions $S_\alpha(\sigma, 0, 0)$ with $\alpha \in (0, 1)$ and $\sigma > 0$.

Clearly, one has $\mathcal{LC} \subset \overline{\mathcal{CSLC}}$, $\overline{\mathcal{CS}} \subset \overline{\mathcal{CSLC}}$ and $\overline{\mathcal{CSLC}} \subset \overline{\mathcal{CTSLC}}$. Note also that the class $\overline{\mathcal{CSLC}}$ is wider than the class of (two-fold) convolutions of log-concave distributions with stable distributions $S_\alpha(\sigma, 0, 0)$ with $\alpha \in (1, 2]$ and $\sigma > 0$.

In some sense, symmetric (about 0) Cauchy distributions $S_1(\sigma, 0, 0)$ are at the dividing boundary between the classes $\underline{\mathcal{CS}}$ and $\overline{\mathcal{CSLC}}$.

In what follows, we write $X \sim \mathcal{LC}$ (resp., $X \sim \overline{\mathcal{CSLC}}$, $X \sim \underline{\mathcal{CS}}$ or $X \sim \overline{\mathcal{CTSLC}}$) if the distribution of the r.v. X belongs to the class $\mathcal{LC}$ (resp., $\overline{\mathcal{CSLC}}$, $\underline{\mathcal{CS}}$ or $\overline{\mathcal{CTSLC}}$).

3   Main results

The following concept of peakedness of r.v.'s was introduced by Birnbaum (1948).

Definition 1 *(Birnbaum, 1948, see also Proschan, 1965, and Marshall and Olkin, 1979, p. 372). A r.v. X is more peaked about $\mu \in \mathbf{R}$ than is Y if $P(|X - \mu| > x) \leq P(|Y - \mu| > x)$ for all $x \geq 0$. If these inequalities are strict whenever the two probabilities are not both 0 or both 1, then the r.v. X is strictly more peaked about μ than is Y. A r.v. X is said to be (strictly) less peaked about μ than is Y if Y is (strictly) more peaked about μ than is X.*

In the case $\mu = 0$, we simply say that the r.v. X is (strictly) more or less peaked than Y.

Roughly speaking, a r.v. X is more peaked about $\mu \in \mathbf{R}$ than is Y, if the distribution of X is more concentrated about μ than is that of Y.

Theorem 1 below provides results on the peakedness properties of the distribution of the trait X in general model (2) with the parental contributions determined by (4) and sex- and time-dependent heritability. Let, as

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[10]$\mathcal{CTSLC}$ stands for "convolutions of transforms of stable and log-concave".

in the introduction, for $t = 0, 1, 2, ...$, $\lambda^{(t)} = (\lambda_0, \lambda_1, ..., \lambda_t)$ be the vectors of "histories" of the coefficients in model (2) up to time t. Further, for $t = 0, 1, 2, ...$, denote $\overline{\lambda}^{(t)} = (1/2, 1/2, ..., 1/2) \in \mathbf{R}^{t+1}$.

Theorem 1 *Consider model (2) with the parental contributions determined by (4). Let $\mu \in \mathbf{R}$, $t \in \{0, 1, 2, ...\}$ and let $\lambda_t \notin \{0, 1\}$ and $\lambda^{(t)} \neq \overline{\lambda}^{(t)}$. If $X_0 \sim S_\alpha(\sigma, \beta, \mu)$ for some $\sigma > 0$, $\beta \in [-1, 1]$ and $\alpha \in (1, 2]$, or $X_0 = \mu + Y$, where $Y \sim \overline{\mathcal{CSLC}}$, then the r.v. $X_{t+1}(\lambda)$ is strictly more peaked about μ than is $X_t(\lambda)$, but is strictly less peaked than is $X_{t+1}(\overline{\lambda})$. That is,*

$$P(|X_{t+1}(\overline{\lambda}) - \mu| > x) < P(|X_{t+1}(\lambda) - \mu| > x) < P(|X_t(\lambda) - \mu| > x) \tag{10}$$

for all $x > 0$. If $X_0 \sim S_\alpha(\sigma, \beta, \mu)$ for some $\sigma > 0$, $\beta \in [-1, 1]$ and $\alpha \in (0, 1)$, or $X_0 = \mu + Y$, where $Y \sim \underline{\mathcal{CS}}$, then the r.v. $X_{t+1}(\lambda)$ is strictly less peaked about μ than is $X_t(\lambda)$, but is strictly more peaked than is $X_{t+1}(\overline{\lambda})$. That is,

$$P(|X_t(\lambda) - \mu| > x) < P(|X_{t+1}(\lambda) - \mu| > x) < P(|X_{t+1}(\overline{\lambda}) - \mu| > x) \tag{11}$$

for all $x > 0$.

According to the following theorem, in the case of Galtonian blending model (3) with symmetric heritability, peakedness comparisons in (10) continue to hold in the case of the more general class $\overline{\mathcal{CTSLC}}$ of thick-tailed initial distributions of the phenotype X than the class $\overline{\mathcal{CSLC}}$ in Theorem 1.

Theorem 2 *Consider model (3) with the parental contributions determined by (4). Let $\mu \in \mathbf{R}$ and $t \in \{0, 1, 2, ...\}$. If $X_0 = \mu + Y$, where $Y \sim \overline{\mathcal{CTSLC}}$, then the r.v. $X_{t+1}(\overline{\lambda})$ is strictly more peaked about μ than is $X_t(\overline{\lambda})$. That is,*

$$P(|X_{t+1}(\overline{\lambda}) - \mu| > x) < P(|X_t(\overline{\lambda}) - \mu| > x) \tag{12}$$

for all $x > 0$.

The following Theorems 3 and 4 give analogues and generalizations of Proposition 1 in the case of heavy-tailed initial distributions of the phenotype X. Theorem 3 is a generalization of the proposition to the case of not too thick-tailed distributions of X_0.

Theorem 3 *Consider model (3) with the cdf's of the parental contributions given by (5). Let $X_0 \sim \overline{\mathcal{CTSLC}}$ or $X_0 = f(Y_0)$, where $f \in \overline{M}$ and $Y_0 \sim S_\alpha(\sigma, 0, 0)$, $\alpha \in (1, 2]$, $\sigma > 0$. If $r_0 < 1/2$ (equivalently, $K > 0$), then*

$$r_1 < 1/2. \tag{13}$$

If $r_0 > 1/2$ (equivalently, $K < 0$), then

$$r_1 > 1/2. \tag{14}$$

From the discussion at the end of Section 2 we get that Theorem 3 holds, in particular, for traits X with the initial distribution from the class $\overline{\mathcal{CSLC}}$.

According to Proposition 1 and Theorem 3, in the case of symmetric log-concave or not very heavy-tailed symmetric initial distributions of the phenotype X in model (3), (5), an excess of females over males or males over females in the population of parents in period $t = 0$ leads to the same phenomena for the population of the offspring in period $t = 1$. As the following Theorem 4 shows, the results given by Proposition 1 and Theorem 3 are reversed in the case of sufficiently heavy-tailed symmetric initial distributions of the phenotype X. In that case, according to the theorem, the sex ratio r exhibits a pattern of oscillation around the balanced sex ratio case $r = 1/2$, namely, an excess of females over males among parents leads to an excess of males over females among the offspring and vice versa.

Theorem 4 *Consider model (3) with the cdf's of the parental contributions given by (5). Let $X_0 \sim \mathcal{CS}$ or $X_0 = f(Y_0)$, where $f \in \underline{M}$ and $Y_0 \sim S_\alpha(\sigma, 0, 0)$, $\alpha \in (0, 1)$, $\sigma > 0$. If $r_0 < 1/2$ (equivalently, $K > 0$), then (14) holds. If $r_0 > 1/2$ (equivalently, $K < 0$), then (13) holds.*

Remark 1. The proof of Theorems 3 and 4 shows that analogues of the theorems hold for transforms of *skewed* stable distributions $S_\alpha(\sigma, \beta, 0)$ of the initial trait X_0 as well. Namely, if $X_0 = f(Y_0)$ and $Y_0 \sim S_\alpha(\sigma, \beta, 0)$ for some $\sigma > 0$, $\beta \in [-1, 1]$ and $\alpha \in (0, 2]$, then (13) holds in the case when $K > 0$, $f \in \overline{M}$ and $\alpha \in (1, 2]$ and when $K < 0$, $f \in \underline{M}$ and $\alpha \in (0, 1)$. Similarly, (14) holds if $K < 0$, $f \in \overline{M}$ and $\alpha \in (1, 2]$ or if $K > 0$, $f \in \underline{M}$ and $\alpha \in (0, 1)$. In the case of the symmetry index $\beta \neq 0$, however, the above conditions $K < 0$ and $K > 0$ are *not* equivalent to the conditions $r_0 < 1/2$ and $r_0 > 1/2$. It should also be noted that from the proof of Theorems 3 and 4 it follows that in the case of the *Cauchy-type* $S_1(\sigma, \beta, 0)$ initial distribution of the phenotype X, the sex-ratio r_1 next period stabilizes at the balanced sex-ratio value $r_1 = 1/2$, *regardless* of the values of the threshold K and the sex-ratio r_0 at the initial period.

Let us denote by $d_t = |r_t - 1/2|$, $t = 0, 1, ...$, the distances of the values of the sex-ratio among parents ($t = 0$) and among the offspring ($t = 1$) from the balanced sex-ratio value $r = 1/2$ in model (3), (5). Further, assuming that parents live longer than one period, we denote by $R = (r_0 + r_1)/2$ the sex-ratio in the total population alive at time $t = 1$. The following theorem gives results on the magnitude of intergenerational changes in the distances d_t in the case of symmetric stable distributions of the initial trait X_0. In particular, according to the theorem, for all above distributions of X_0, the sex-ratio among offspring (and, therefore, the sex-ratio in the total alive population) at $t = 1$ becomes closer to the value $r = 1/2$, if the sex-ratio among parents ($t = 0$) is sufficiently far from it. This, however, is not the case if the distribution of the initial trait is extremely heavy-tailed, as modelled by symmetric stable distributions with indices of stability less than $1/2$, and the sex-ratio value among parents r_0 is sufficiently close to $r = 1/2$. If such patterns are present, then the oscillations in the sex-ratio r_t about the balanced sex-ratio value are increasing in the magnitude. Furthermore, if the initial trait X_0 has a symmetric stable distribution with characteristic exponent less than $1/2$, then the value R of the sex-ratio in the total population at period $t = 1$ stabilizes at the balanced sex-ratio $R = 1/2$ for some values of the distance d_0 from r_0 to $r = 1/2$.

Theorem 5 *Consider model (3) with the cdf's of the parental contributions given by (5) and the initial trait $X_0 \sim S_\alpha(\sigma, 0, 0)$, $\sigma > 0$, $\alpha \in (0, 2]$, $\alpha \neq 1$. There exists $d_0^{(1)} \in (0, 1/2)$ such that*

$$d_1 < d_0 \ \ for \ \ d_0 \geq d_0^{(1)}. \tag{15}$$

Further, if $\alpha \in (1/2, 2]$, then there exists $d_0^{(2)} \in (0, 1/2)$ such that

$$d_1 < d_0, \ \ for \ \ d_0 \leq d_0^{(2)}. \tag{16}$$

If $\alpha \in (0, 1/2)$, then there exist $d_0^{(3)}, d_0^{(4)} \in (0, 1/2)$ such that

$$d_1 > d_0, \ \ for \ \ d_0 \leq d_0^{(3)}, \tag{17}$$

$$R = 1/2 \ \ (equivalently, \ d_1 = d_0) \ for \ \ d_0 = d_0^{(4)}. \tag{18}$$

Remark 2. From Remark 3 in Appendix A1 and the proof of the theorems in this section it follows that Theorems 1 and 4 continue to hold for convolutions of the distributions in the classes $\underline{\mathcal{CS}}$ and $\overline{\mathcal{CSLC}}$ with symmetric Cauchy distributions $S_1(\sigma, 0, 0)$; Theorems 2 and 3 continue to hold for (two-fold) convolutions of distributions in the class $\overline{\mathcal{CTSLC}}$ with the distributions of transforms $X_0 \sim f(Y_1)$ of symmetric Cauchy r.v.'s $Y_0 \sim S_1(\sigma, 0, 0)$, where $f \in \overline{M}$ is strictly concave on $\mathbf{R}_+$.

Appendix A1: Majorization properties of log-concave and heavy-tailed distributions

For a vector $a \in \mathbf{R}^n$, denote by $a_{[1]} \geq \ldots \geq a_{[n]}$ its components in decreasing order.

Definition 2 *(Marshall and Olkin, 1979). Let $a, b \in \mathbf{R}^n$. The vector a is said to be majorized by the vector b, written $a \prec b$, if $\sum_{i=1}^k a_{[i]} \leq \sum_{i=1}^k b_{[i]}$, $k = 1, ..., n-1$, and $\sum_{i=1}^n a_{[i]} = \sum_{i=1}^n b_{[i]}$.*

The relation $a \prec b$ implies that the components of the vector a are more diverse than those of b. In this context, it is easy to see that, for all $a \in \mathbf{R}_+^n$, the following relations hold:

$$\Big(\sum_{i=1}^n a_i/n, ..., \sum_{i=1}^n a_i/n \Big) \prec (a_1, ..., a_n) \prec \Big(\sum_{i=1}^n a_i, 0, ..., 0 \Big). \tag{19}$$

Definition 3 *(Marshall and Olkin, 1979). A function $\phi : A \to \mathbf{R}$ defined on $A \subseteq \mathbf{R}^n$ is called Schur-convex (resp., Schur-concave) on A if $(a \prec b) \implies (\phi(a) \leq \phi(b))$ (resp. $(a \prec b) \implies (\phi(a) \geq \phi(b))$) for all $a, b \in A$. If, in addition, $\phi(a) < \phi(b)$ (resp., $\phi(a) > \phi(b)$) whenever $a \prec b$ and a is not a permutation of b, then ϕ is said to be strictly Schur-convex (resp., strictly Schur-concave) on A.*

Proschan (1965) obtains the following seminal result concerning majorization properties of tail probabilities of linear combinations of log-concavely distributed r.v.'s:

Proposition 2 *(Proschan, 1965). If $X_1, ..., X_n$ are i.i.d. symmetric log-concavely distributed r.v.'s, then the function $\psi(a, x) = P\left(\sum_{i=1}^{n} a_i X_i > x\right)$ is strictly Schur-convex in $a = (a_1, ..., a_n) \in \mathbf{R}_+^n$ for $x > 0$ and is strictly Schur-concave in $a = (a_1, ..., a_n) \in \mathbf{R}_+^n$ for $x < 0$.*

Clearly, from Proposition 2 it follows that $\sum_{i=1}^{n} a_i X_i$ is strictly more peaked than $\sum_{i=1}^{n} b_i X_i$ if $a \prec b$ and a is not a permutation of b.

Proschan (1965) notes that Proposition 2 also holds for (two-fold) convolutions of log-concave distributions with symmetric Cauchy distributions and obtained results on peakedness properties of averages $(f(Y_1) + f(Y_2))/2$ of transforms of symmetric Cauchy r.v.'s Y_1 and Y_2 for $f \in \underline{M}$ and $f \in \overline{M}$ (see Lemmas 2.7 and 2.8 in Proschan, 1965).

The following Lemmas 1 and 2 concerning general majorization properties of arbitrary convex combinations of heavy-tailed r.v.'s were obtained in Ibragimov (2004) (see Theorems 4.3 and 4.4 and Remark 4.1 in that paper). According to Lemma 1, peakedness properties of linear combinations of r.v.'s with not too heavy-tailed distributions are the same as in the case of log-concave distributions in Proschan (1965).

Lemma 1 *(Ibragimov, 2004). Proposition 2 holds if $X_1, ..., X_n$ are i.i.d r.v.'s such that $X_1 \sim S_\alpha(\sigma, \beta, 0)$ for some $\sigma > 0$, $\beta \in [-1, 1]$ and $\alpha \in (1, 2]$, or $X_1 \sim \overline{\mathcal{CSLC}}$.*

According to Lemma 2, the peakedness properties given by Proposition 2 and Theorem 1 above are reversed in the case of r.v.'s with very heavy-tailed distributions, as modelled by convolutions of stable distributions with indices of stability not greater than one.

Lemma 2 *(Ibragimov, 2004). If $X_1, ..., X_n$ are i.i.d. r.v.'s such that $X_1 \sim S_\alpha(\sigma, \beta, 0)$ for some $\sigma > 0$, $\beta \in [-1, 1]$ and $\alpha \in (0, 1)$, or $X_1 \sim \underline{\mathcal{CS}}$, then the function $\psi(a, x)$ in Proposition 2 is strictly Schur-concave in $(a_1, ..., a_n) \in \mathbf{R}_+^n$ for $x > 0$ and is strictly Schur-convex in $(a_1, ..., a_n) \in \mathbf{R}_+^n$ for $x < 0$.*

The following lemmas generalize Lemmas 2.7 and 2.8 in Proschan (1965) and provide new results on peakedness properties of averages of transforms of arbitrary stable r.v.'s and their convolutions. For r.v.'s $X_1, X_2, ...,$ and $n \geq 1$, we denote by $\overline{X}_n$ the sample mean $\overline{X}_n = (1/n) \sum_{i=1}^{n} X_i$ (in particular, $\overline{X}_2$ denotes $\overline{X}_2 = (X_1 + X_2)/2$).

Lemma 3 *If X_1 and X_2 are i.i.d r.v.'s such that $X_1 = f(Y_1)$, where $f \in \overline{M}$ and $Y_1 \sim S_\alpha(\sigma, \beta, 0)$, $\alpha \in (1, 2]$, $\sigma > 0$, $\beta \in [-1, 1]$, then $P(\overline{X}_2 > x) < P(X_1 > x)$ for $x > 0$ and $P(\overline{X}_2 > x) > P(X_1 > x)$ for $x < 0$. If $n = 2^k$, $k \geq 1$, and $X_1, ..., X_n$ are i.i.d r.v.'s such that $X_1 \sim \overline{\mathcal{CTSLC}}$, then $\overline{X}_n$ is more peaked than $\overline{X}_{n/2}$, that is, $P(|\overline{X}_n| > x) < P(|\overline{X}_{n/2}| > x)$ for all $x > 0$.*

Lemma 4 *If X_1 and X_2 are i.i.d r.v.'s such that $X_1 = f(Y_1)$, where $f \in \underline{M}$ and $Y_1 \sim S_\alpha(\sigma, \beta, 0)$, $\alpha \in (0, 1)$, $\sigma > 0$, $\beta \in [-1, 1]$, then $P(X_1 > x) < P(\overline{X}_2 > x)$ for $x > 0$ and $P(X_1 > x) > P(\overline{X}_2 > x)$ for $x < 0$.*

<u>Remark 3</u>. If r.v.'s $X_1, ..., X_n$ have a symmetric Cauchy distribution $S_1(\sigma, 0, 0)$ (with $\alpha = 1$) which is, as discussed in Section 2, exactly at the dividing boundary between the class the class $\overline{\mathcal{CSLC}}$ in Theorem 1 and the class $\underline{\mathcal{CS}}$ in Theorem 2, then the function $\psi(a, x)$ in the theorems depends only on $\sum_{i=1}^n a_i$ and x and so is *both* Schur-concave and Schur-convex in $a \in \mathbf{R}_+^n$ for all $x \in \mathbf{R}$ (see Proschan, 1965, and Remark 4.1 in Ibragimov, 2004). As noted in Ibragimov (2004), this implies that Theorems 1 and 2 continue to hold for convolutions of distributions from the classes $\overline{\mathcal{CSLC}}$ and $\underline{\mathcal{CS}}$ with symmetric Cauchy distributions. As follows from Proschan (1965), Lemma 3 holds for i.i.d. r.v.'s $X_1, X_2, ...$ such that $X_1 = f(Y_1)$, where Y_1 has the Cauchy ($\alpha = 1$) distribution $Y_1 \sim S_1(\sigma, 0, 0)$ and $f \in \overline{M}$ is strictly concave on $\mathbf{R}_+$, and Lemma 4 holds for i.i.d. r.v.'s X_1, X_2 such that $X_1 = f(Y_1)$, where $Y_1 \sim S_1(\sigma, 0, 0)$ and $f \in \underline{M}$ is strictly convex on $\mathbf{R}_+$. As in Proschan (1965), this implies that Lemma 3 continues to hold for convolutions of distributions from the class $\overline{\mathcal{CTSLC}}$ with the distributions of transforms $f(Y_1)$, $f \in \underline{M}$, of symmetric Cauchy r.v.'s $Y_1 \sim S_1(\sigma, 0, 0)$, where f is strictly concave on $\mathbf{R}_+$.

Appendix A2: Proofs

<u>Proof of Theorems 1 and 2.</u> Let $X_0 \sim S_\alpha(\beta, \sigma, \mu)$ for some $\sigma > 0$, $\beta \in [-1, 1]$ and $\alpha \in (0, 1)$ or $X_0 = \mu + Y$, where $Y \sim \underline{\mathcal{CS}}$. For $t = 0, 1, ...,$ denote $N_t = 2^t$, $0^{(t)} = (0, 0, ..., 0) \in \mathbf{R}^{N_t}$ and $\overline{a}^{(t)} = (1/N_t, 1/N_t, ..., 1/N_t) \in \mathbf{R}^{N_t}$. Let us define recursively the following vectors. Set $a^{(0)} = (1) \in \mathbf{R}^1$. For $t = 1, 2, ...,$ let $b^{(t)} = (a^{(t-1)}, 0^{(t-1)}) \in \mathbf{R}^{N_t}$ and $c^{(t)} = (0^{(t-1)}, a^{(t-1)}) \in \mathbf{R}^{N_t}$ be the vectors with the components $b_i^{(t)} = a_i^{(t-1)}$, $c_i^{(t)} = 0$, $i = 1, 2, ..., N_{t-1}$; $b_i^{(t)} = 0$, $c_i^{(t)} = a_{i-N_{t-1}}^{(t-1)}$, $i = N_{t-1} + 1, ..., N_t$. Moreover, let $a^{(t)} = \lambda_t b^{(t)} + (1 - \lambda_t) c^{(t)}$ be the vector with the components $a_i^{(t)} = \lambda_t b_i^{(t)} = \lambda_t a_i^{(t-1)}$, $i = 1, 2, ..., N_{t-1}$, $a_i^{(t)} = (1 - \lambda_t) c_i^{(t)} = (1 - \lambda_t) a_{i-N_{t-1}}^{(t-1)}$, $i = N_{t-1} + 1, ..., N_t$. Let $Y_1, Y_2, ..., Y_{N_t}$ be independent copies of the r.v. X_0. Denote $Y^{(t)} = (Y_1, Y_2, ..., Y_{N_t})$. It is not difficult to see that, for $t = 0, 1, 2, ...,$

$$X_t(\overline{\lambda}) = \overline{a}^{(t)} (Y^{(t)})', \tag{20}$$

$$X_t(\lambda) = a^{(t)} (Y^{(t)})'. \tag{21}$$

Since for $t = 1, 2, ...,$ $\sum_{i=1}^{N_t} a_i^{(t)} = \lambda_t \sum_{i=1}^{N_{t-1}} a_i^{(t-1)} + (1 - \lambda_t) \sum_{i=1}^{N_{t-1}} a_i^{(t-1)} = \sum_{i=1}^{N_{t-1}} a_i^{(t-1)} = ... = a_1^{(0)} = 1$ ($a_1^{(0)} = 1$ is the only component of the vector $a^{(0)}$), from relations (19) in Appendix A1 it follows that

$$\overline{a}^{(t)} \prec a^{(t)}. \tag{22}$$

Since the components of the vector $c^{(t)}$ are permutations of those of $b^{(t)}$, one has $c^{(t)} \prec b^{(t)}$. Further, evidently, $b^{(t)} \prec b^{(t)}$. Since for any $b \in \mathbf{R}^n$, the set $\{\tilde{b} \in \mathbf{R}^n : \tilde{b} \prec b\}$ is convex (see, e.g., Proposition 4.C.1 in Marshall and Olkin (1979)), from the above majorization comparisons we get

$$a^{(t)} = \lambda_t b^{(t)} + (1 - \lambda_t) c^{(t)} \prec b^{(t)}. \tag{23}$$

Lemma 2 in Appendix A1 and relations (20) and (22) imply that, for all $t = 0, 1, 2, ...,$ and all $x > 0$,

$$P(|X_t(\lambda) - \mu| > x) = P(|a^{(t)} (Y^{(t)})' - \mu| > x) < P(|\overline{a}^{(t)} (Y^{(t)})' - \mu| > x) = P(|X_t(\overline{\lambda}) - \mu| > x), \tag{24}$$

if $\lambda^{(t)} \neq \overline{\lambda}^{(t)}$. Similarly, from Lemma 2 and relations (21) and (23) it follows that, for all $t = 0, 1, 2, ...,$ and $x > 0$,

$$P(|X_{t+1}(\lambda) - \mu| > x) = P(|a^{(t+1)}(Y^{(t+1)})' - \mu| > x) > P(|b^{(t+1)}(Y^{(t+1)})' - \mu| > x) =$$
$$P(|(a^{(t)}, 0^{(t)})(Y^{(t+1)})' - \mu| > x) = P(|a^{(t)}(Y^{(t)})' - \mu| > x) = P(|X_t(\lambda) - \mu| > x), \tag{25}$$

$\lambda_t \notin \{0, 1\}$. Relations (24) and (25) thus imply that inequalities (11) hold. Inequalities (10) might be proven in a similar way, with the use of Lemma 1 instead of Lemma 2. Thus, Theorem 1 holds. Using Lemma 3 instead of Lemma 2, we obtain Theorem 2. The proof is complete.

Proof of Theorems 3 and 4. Let $X_0 \sim \mathcal{CS}$ or $X_0 = f(Y_0)$, where $f \in \underline{M}$ and $Y_0 \sim S_\alpha(\sigma, \beta, 0)$, $\alpha \in (0, 1)$, $\sigma > 0$, $\beta \in [-1, 1]$. Let X_0^p and X_0^m be independent r.v.'s with the cdf's (5). Further, let $r_0 = P(X_0 > K)$ be the sex-ratio in period $t = 0$ and let X_0' and X_0'' be independent copies of X_0. Define the following events: $A_0 = \{(X_0' + X_0'')/2 > K\}$, $A_1 = \{X_0' > K, X_0'' \leq K\}$, $A_2 = \{X_0' \leq K, X_0'' > K\}$, $A_3 = \{X_0' \leq K, X_0'' \leq K\}$ and $A_4 = \{X_0' > K, X_0'' > K\}$. It is not difficult to see (see Karlin, 1984, p. 263) that the sex ratio $r_1 = P(X_1 > K)$ at period $t = 1$ equals to

$$r_1 = P(A_0|A_1) = P(A_0 \cap A_1)/P(A_1). \tag{26}$$

It is easy to see that $A_0 \cap A_3 = \emptyset$ and $A_4 \subseteq A_0$. Therefore,

$$2P(A_0 \cap A_1) = P(A_0 \cap A_1) + P(A_0 \cap A_2) =$$
$$\sum_{i=1}^{4} P(A_0 \cap A_i) - P(A_0 \cap A_3) - P(A_0 \cap A_4) = P(A_0) - P(A_4). \tag{27}$$

From independence of the r.v.'s X_0' and X_0'' it follows that

$$P(A_1) = P(X_0' > K)P(X_0'' \leq K) = P(X_0 > K)(1 - P(X_0 > K)) = r_0(1 - r_0), \tag{28}$$

$$P(A_4) = P(X_0' > K)P(X_0'' > K) = r_0^2. \tag{29}$$

Using relations (26)-(29) we get

$$r_1 = (P(A_0) - P(A_4))/(2P(A_1)) = (P(A_0) - r_0^2)/(2r_0(1 - r_0)). \tag{30}$$

Lemmas 2 and 4 in Appendix A1 imply that, for $K > 0$,

$$P(A_0) = P((X_0' + X_0'')/2 > K) > P(X_0 > K) = r_0. \tag{31}$$

Relations (30) and (31) imply that $r_1 > (r_0 - r_0^2)/(2r_0(1 - r_0)) = 1/2$ for $K > 0$. Similar to the above, one gets that $r_1 < 1/2$ if $K < 0$. Therefore, Theorem 4 holds. Furthermore, using Lemma 3 instead of Lemmas 2 and 4, we obtain, similar to the above, that if $X_0 \sim \overline{\mathcal{CTSLC}}$ or $X_0 = f(Y_0)$, where $f \in \overline{M}$ and $Y_0 \sim S_\alpha(\sigma, \beta, 0)$, $\alpha \in (1, 2]$, $\sigma > 0$, $\beta \in [-1, 1]$, then $r_1 < 1/2$ in the case $K > 0$ and $r_1 > 1/2$ in the case $K < 0$. This proves Theorem 3. The proof is complete.

<u>Proof of Theorem 5.</u> Let $X_0 \sim S_\alpha(\sigma, 0, 0)$, $\sigma > 0$, $\alpha \in (0, 1) \cup (1, 2]$. Further, let, as in the proof of Theorems 3 and 4, X_0' and X_0'' be independent copies of X_0 and let $A_0 = \{(X_0' + X_0'')/2 > K\}$. Since, as it is not difficult to see, $(X_0' + X_0'')/2^{1/\alpha} \sim S_\alpha(\sigma, 0, 0)$, we have $P(A_0) = P(X_0 > 2^{1-1/\alpha}K)$. This, together with property (8) in Section 2 and asymptotic expansions for stable densities (2.4.6) and (2.5.1) in Zolotarev (1986, pp. 89, 95)[11] implies that there exist constants $C_1, C_2 > 0$ such that $r_0 = P(X_0 > K) \sim C_1/K^\alpha$, $P(A_0) \sim C_1/(2^{\alpha-1}K^\alpha)$, $K \to +\infty$; $r_0 \sim 1 - C_1/|K|^\alpha$, $P(A_0) \sim 1 - C_1/(2^{\alpha-1}|K|^\alpha)$, $K \to -\infty$; $r_0 \sim 1/2 - C_2K$, $P(A_0) \sim 1/2 - 2^{1-1/\alpha}C_2K$, $K \to 0$. We get, therefore, that $d_0 = |r_0 - 1/2| \sim 1/2 - C_1/|K|^\alpha$, $K \to \pm\infty$, and $d_0 \sim C_2|K|$, $K \to 0$. Similarly, since, by (30), $d_1 = |r_1 - 1/2| = |P(A_0) - r_0|/(2r_0(1 - r_0))$, one has that $d_1 \sim |1/2 - 1/2^\alpha| - |1/2 - 1/2^\alpha|C_1/|K|^\alpha$, $K \to \pm\infty$, and $d_1 \sim C_2|(2 - 2^{2-1/\alpha})K|$, $K \to 0$. Using the above relations and the fact that d_0 is increasing in $|K|$, it is not difficult to check that relations (15)-(17) indeed hold. Relation (18) follows from (15) and (17) and continuity of $d_1 - d_0$ in $K \in \mathbf{R}$.

<u>Proof of Lemmas 3 and 4.</u> Let $\alpha_1 \in (1, 2]$, $\alpha_2 \in (0, 1)$, and let $f_1 \in \overline{M}$, $f_2 \in \underline{M}$. For $j = 1, 2$, let $Y_1^{(j)}$ and $Y_2^{(j)}$ be i.i.d. r.v.'s such that $Y_i^{(j)} \sim S_{\alpha_j}(\sigma, \beta, 0)$, $\sigma > 0$, $\beta \in [-1, 1]$, $i = 1, 2$, and let $X_i^{(j)} = f_j(Y_i^{(j)})$, $i = 1, 2$, $j = 1, 2$. As in the proof of Lemmas 2.7 and 2.8 in Proschan (1965), we have $|f_1((y_1 + y_2)/2)| \geq |(f_1(y_1) + f_1(y_2))/2|$, $|f_2((y_1 + y_2)/2)| \leq |(f_2(y_1) + f_2(y_2))/2|$ for all $y_1, y_2 \in \mathbf{R}$. Since the functions $|f_j(x)|$ are increasing in $|x|$, we get that $|f_1((y_1 + y_2)/2^{1/\alpha_1})| \geq |(f_1(y_1) + f_1(y_2))/2|$, $|f_2((y_1 + y_2)/2^{1/\alpha_2})| \leq |(f_2(y_1) + f_2(y_2))/2|$, with strict inequalities for $y_1 + y_2 \neq 0$. Since $2^{-1/\alpha_1}(Y_1^{(1)} + Y_2^{(1)}) \sim S_{\alpha_1}(\sigma, \beta, 0)$ and the function f_1 is odd, this implies that, for all $x > 0$, $P((X_1^{(1)} + X_2^{(1)})/2 > x) = P((f_1(Y_1^{(1)}) + f_1(Y_2^{(1)}))/2 > x) < P(f_1((Y_1^{(1)} + Y_2^{(1)})/2^{1/\alpha_1}) > x) = P(f_1(Y_1^{(1)}) > x) = P(X_1^{(1)} > x)$ and, for all $x < 0$, $P((X_1^{(1)} + X_2^{(1)})/2 > x) = 1 - P((f_1(Y_1^{(1)}) + f_1(Y_2^{(1)}))/2 < x) > 1 - P(f_1((Y_1^{(1)} + Y_2^{(1)})/2^{1/\alpha_1}) < x) = 1 - P(f_1(Y_1^{(1)}) < x) = P(X_1^{(1)} > x)$. Similarly, we get that $P((X_1^{(2)} + X_2^{(2)})/2 > x) < P(X_1^{(2)} > x)$ for all $x > 0$ and $P((X_1^{(2)} + X_2^{(2)})/2 > x) > P(X_1^{(2)} > x)$ for all $x < 0$. This proves Lemma 4 and the first part of Lemma 3.

Let now $n = 2^k$, $k \geq 2$, and let $X_1, ..., X_n$ be i.i.d. r.v.'s such that $X_1 \sim \overline{\mathcal{CTSLC}}$. By definition of the class $\overline{\mathcal{CTSLC}}$, there exist i.i.d. r.v.'s Y_{ij}, $j = 0, 1, ..., k$, $i = 1, ..., n$, and functions $f_j \in \overline{M}$, $j = 1, ..., k$, such that $Y_{i0} \sim \mathcal{LC}$ and $Y_{ij} \sim S_{\alpha_j}(\sigma_j, 0, 0)$, $\alpha_j \in (1, 2]$, $\sigma_j > 0$, $j = 1, ..., k$, and $X_i = \gamma Y_{i0} + f_1(Y_{i1}) + ... + f_k(Y_{ik})$, $\gamma \in \{0, 1\}$, $i = 1, ..., n$. From the above we have that for all $i = 1, ..., n/2$ and $j = 1, ..., k$, the r.v. $(f_j(Y_{ij}) + f_j(Y_{n/2+i,j}))/2$ is strictly more peaked than $f_j(Y_{ij})$. In addition, by Proposition 2, $(Y_{i0} + Y_{n/2+i,0})/2$ is strictly more peaked than Y_{i0}.

According to Theorem 2.7.6 in Zolotarev (1986, p. 134) and Theorem 1.10 in Dharmadhikari and Joag-Dev (1988, p. 20), the densities of the r.v.'s Y_{ij}, $j = 0, 1, ..., k$, $i = 1, ..., n$, are symmetric and unimodal. This implies, as it is not difficult to see, symmetry and unimodality of the densities of the r.v.'s $f_j(Y_{ij})$, $f_j \in \overline{M}$, $j = 1, ..., k$, $i = 1, ..., n$. By Theorem 1.6 in Dharmadhikari and Joag-Dev (1988, p. 13), we get, in turn, that the densities of the r.v.'s $(Y_{i0} + Y_{n/2+i,0})/2$ and $(f_j(Y_{ij}) + f_j(Y_{n/2+i,j}))/2$, $j = 1, ..., k$, $i = 1, ..., n$, are symmetric and unimodal.

From Lemma in Birnbaum (1948) and its proof it follows that if V_1, V_2 and W_1, W_2 are independent absolutely continuous symmetric unimodal r.v.'s such that, for $i = 1, 2$, V_i is more peaked than W_i, then $V_1 + V_2$ is more

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[11]Note that the second term in relation (2.4.4) in Zolotarev (1989, p. 89) that implies asymptotic expansion (2.4.6) on the same page in the book should read $-1/2\alpha'(1 + \beta')$ instead of $1/2\alpha'(1 + \beta')$.

peaked than $W_1 + W_2$; furthermore, this peakedness comparison is strict if V_1 is strictly more peaked than W_1 or V_2 is strictly more peaked than W_2. This implies by induction (see also Theorem 1 in Birnbaum, 1948, and Theorem 2.C.3 in Dharmadhikari and Joag-Dev, 1988) that $\overline{X}_n = (1/n) \sum_{i=1}^{n/2} [\gamma(Y_{i0} + Y_{n/2+i,0}) + (f_1(Y_{i1}) + f_1(Y_{n/2+i,1}))... + (f_k(Y_{ik}) + f_k(Y_{n/2+i,k}))]$ is strictly more peaked than $\overline{X}_{n/2} = (2/n) \sum_{i=1}^{n/2} [\gamma Y_{i0} + f_1(Y_{i1}) + ... + f_k(Y_{ik})]$. This completes the proof of Lemma 3.

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