A NEW TECHNIQUE FOR SYNTHESIS OF LOW NOISE AMPLIFIERS BASED ON GENETIC ALGORITHM AND MORPHOLOGICAL APPROACH

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Abstract — A new technique for automatic synthesis of linear and low noise amplifiers (LNAs) based on genetic algorithm and morphological approach is presented. The technique is implemented in the software tool GENEAMP. Efficiency of automatic synthesis is demonstrated in example design of 0.01—7 GHz single-stage feedback LNA.

I. Introduction

Microwave low noise amplifiers (LNA) are widely used in civil and military electronic systems for wireless communications, space applications, RADAR, radionavigation, etc. In general, modern CAD tools cannot generate circuit schematic and solve only the simulation task. The synthesis problem for active microwave circuits is much more complicated problem. Due to this, now the microwave amplifier design is mostly based on a heuristic approach with using engineer experience or a trial-and-error method.

For CAD of LNA's, several companies have developed specialized software such as MultiMatch Amplifier Design Wizard (Ampsa PTY Ltd., USA) [1], Linc2 (Applied Computational Science, USA) [2], and Genesys in ADS (Agilent Technologies, USA) [3]. These programs have the following disadvantages: high cost; a high skill level user is required; design process is laborious and lengthy (1-2 days on average); used techniques cannot precisely control all the amplifier characteristics. Thus, the development of fast software tool for automatic amplifier synthesis is a topical problem.

II. Morphological Approach

For amplifier synthesis, we use an advanced technique based on genetic algorithm (GA) and morphological approach. The theoretical basis of morphological approach is described in [4]. The idea is to represent amplifier structure and possible element types in the form of pattern (Fig.1) and morphological tree (Fig.2).

An amplifier may include several transistor stages (active elements) jointly with input, output, and interstage matching networks (MNs). In turn, an active element contains a transistor with connected correction one-ports (CO's) such as compensation and feedback networks.

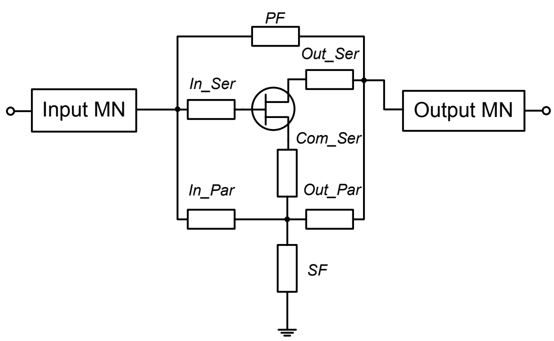

Fig. 1. The single-stage amplifier pattern

In our stage template we can use up to 7 CO's as illustrated in Fig. 1: input series CO (*In_Ser*), output serial CO (*Out_Ser*), common serial CO (*Com_Ser*), input parallel CO (*In_Par*), output parallel CO (*Out_Par*), series feedback (*SF*), and parallel feedback (*PF*).

All variants of an amplifier structure can be represented as a morphological tree. An example of a morphological tree for a two-stage amplifier is shown in Fig. 2.

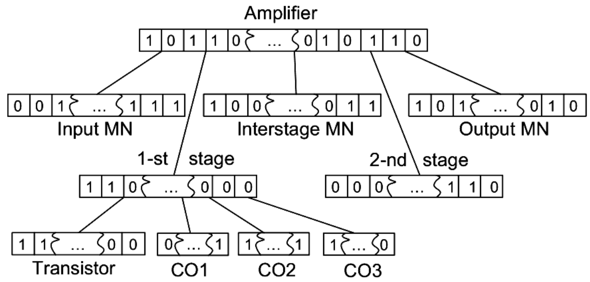

Fig. 2. A morphological tree for an amplifier

Every CO can contain from 1 to 4 both series and parallel "elementary networks" (ENs). In turn, each EN consists of one or two passive lumped elements (Fig. 3). Thus, CO may include from 1 to 8 elements.

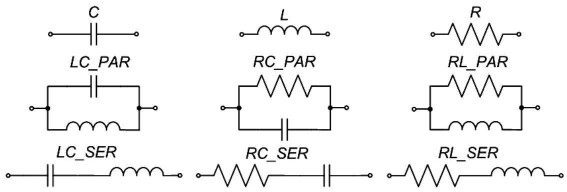

Fig. 3. Elementary networks

MN's can contain any number of series or/and parallel branches. The structure of branches in MN is identical to the CO structure.

Thus, with using morphological approach we can easily describe and control an amplifier structure during the synthesis.

III. Genetic Algorithm

For implementing GA-based synthesis, we must code all the information about amplifier structure and elements in "chromosome" [5] (Fig. 2). The feature of GA presented here is the use of binary coding with multiple populations. Example of coding-decoding of chromosome genes (parts) is shown in Fig.2 and Table 1.

Table 1. Example of decoding

	CO type	Gene	Interpretation
Amplifier	Parallel Feedback (*PF*)	0	Branch type: parallel
		1010	One-port circuit configuration: two elements
		011	First element type: capacitor
		1000101101	Value: 5.45 pF
		1	The next element in the chromosome isn't included in current CO
	…	…	…

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Thus, using a binary coding we code the morphological tree of an amplifier (Fig. 2).

To start the synthesis process, a user must specify primary parameters of GA [5]: number of populations, number of individuals (chromosomes) for each population, percentage of mutations, crossover and selection operator. Also, the user must specify limitations for the circuit structure and elements as well as the amplifier performance requirements.

GA in each population performs the following actions:

1) Random generation of initial set of individuals.

2) Decoding of chromosomes and computation of goal function (GF) for the newly created individuals (GF accounts for all the interested amplifier performances).

3) Sampling of the individuals according to the chosen selection operator.

4) Breeding of the produced individuals (population size is doubled).

5) The offspring of individuals are mutated according to the selected mutation operator.

6) The computation of the GF for children individuals.

7) Selection of individuals for the next generation by separating population into two parts.

8) Checking of GF improving.

9) Algorithm is terminated, when the user clicks on the "Stop" button or improvement of GF is very slow.

The approach presented is implemented in GENEAMP, a tool for automated synthesis of microwave amplifiers directly from a simultaneous set of performances (including gain, gain flatness, noise figure, input and output reflection coefficients, and stability factor). GENEAMP is able to synthesize linear and low noise, narrow- and wideband, one- and two-stage microwave amplifiers containing matching and correction networks on lumped elements.

IV. Example

We demonstrate efficiency of the proposed approach in example of designing a single-stage wideband 0.01–7 GHz LNA based on a AP344A2 mean power GaAs MESFET.

Amplifier specifications are as follows: noise figure $NF \le 3.5$ dB; power gain $G_T \ge 6$ dB; input and output reflection coefficients: $|S_{11}| \le 0.55$ (-5.2 dB); $|S_{22}| \le 0.33$ (-9.6 dB); amplifier must be absolutely stable in working frequency band. An amplifier stage structure includes all possible COs; input and output MNs are not used; element values are limited as follows: 0.01 nH ≤ L ≤ 10 nH; 0.01 pF ≤ C ≤ 10 pF; 0.1 Ohm ≤ R ≤ 1e+5 Ohm.

Several synthesized amplifier circuits with different topologies (solutions *A, B, C,* and *D*) are shown in Fig.4 with performances in Table 2. We see that GENEAMP tool can generate a number of different schematics satisfying requirements. In comparison with usual feedback amplifies, more interesting complicated parallel feedback networks are synthesized.

Table 2. Performances of synthesized circuits

Solution	$G \pm \Delta G$, dB	NF, dB	$\lvert S_{11} \rvert$	$\lvert S_{22} \rvert$	K	Synthesis time (mm:ss)
A	6.22±0.24	3.21	0.57	0.26	0.98	1:13
B	6.24±0.25	3.3	0.58	0.27	0.99	1:11
C	6.25±0.26	3.32	0.56	0.25	0.98	1:49
D	6.15±0.13	3.25	0.56	0.27	1.05	5:29
Mean:	6,215± 0.22	3,27	0,57	0,26	1	2:25

It should be noted that solution *D* could be conveniently realized, i.e., parallel resistors could be used for transistor biasing while the capacitors will be used for bias filtering; the parallel feedback has a series capacitor which is needed for DC decoupling. Also, in the obtained solutions there are no input and output DC block capacitors, thereby in practical amplifier implementation they must be added.

V. Conclusion

A new genetic-algorithm-based approach to LNA synthesis is proposed. There are two advantages of this approach: 1) design process is very simple and does not require a highly-skilled designer (the user defines only requirements for amplifier schematics and performances); 2) many variants of circuits can be generated and the user can select the most suitable ones.

A wideband 0.01–7 GHz LNA is designed demonstrating that the GENEAMP software can be a useful tool for a microwave engineer.

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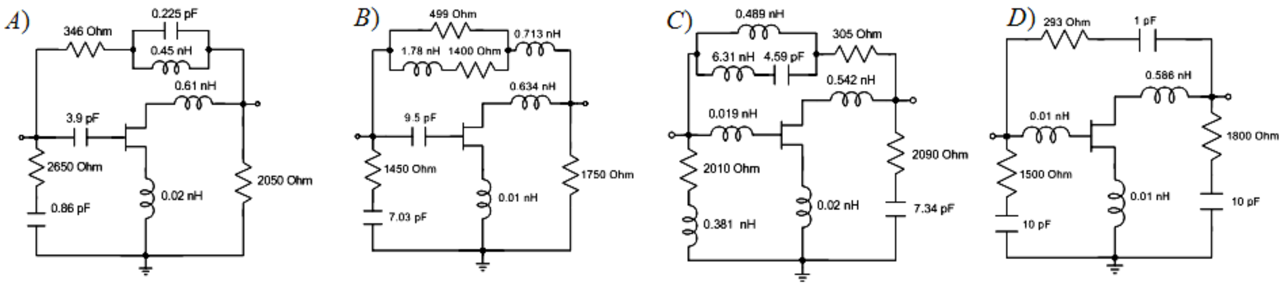

Fig. 4. Different amplifier schematics synthesized by GENEAMP

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